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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such
5 polynucleotides, along with uses for these polynucleotides and proteins, for example in
therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as
10 lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past
decade. The now routine hybridization cloning and expression cloning techniques clone novel
polynucleotides "directly" in the sense that they rely on information directly related to the
discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of
hybridization cloning; activity of the protein in the case of expression cloning). More recent
15 "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences
based on the presence of a now well-recognized secretory leader sequence motif, as well as
various PCR-based or low stringency hybridization-based cloning techniques, have advanced the
state of the art by making available large numbers of DNA/amino acid sequences for proteins
that are known to have biological activity, for example, by virtue of their secreted nature in the
20 case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based
techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for
example, diagnostics, forensics, gene mapping; identification of mutations responsible for
genetic disorders or other traits, to assess biodiversity, and to produce many other types of data
25 and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel
isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules,
30 cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic
variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more
epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression
vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such
35 polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1- 1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

5 The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the
10 protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA
15 or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as
20 expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide
25 of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition
30 which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein
35 expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides

5 a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the

10 invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal

15 antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate

20 (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a

25 compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a

30 polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that

35 modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited
5 for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological
10 macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

15 The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or
20 polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial"
25 defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

30 The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3)
35 appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

- 5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about
- 10 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a
- 15 listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*,
- 20 mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into
- 25 account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least
- 30 about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

5 The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

10 As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated
15 with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

20

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350 ; a polynucleotide encoding any one of the peptide
25 sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350 ; (b) nucleotide sequences encoding any one of the
30 amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in
35 receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

5 The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

10 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that
15 corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

20 The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

25 The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at
30 least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

 Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most
35 preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species.

Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

- 5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of
10 an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified
15 such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the
20 control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an *an*-omeric nucleic acid molecule. An *an*-omeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual *an*-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The
25 antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

30 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit
35 translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1350 or (b)

polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1351-2700.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either
10 cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

15 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or
20 deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the
25 molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved
30 systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to
35 retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active
5 portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to
10 the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which
15 the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.
20 The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays
25 to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for
30 appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can
35 subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked
5 in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or
5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or
10 indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation
15 or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant
20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic
25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as
30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of
35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its
5 receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch
15 and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional
20 sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the
25 polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

30 A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one
35 or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

- 5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in
 10 Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *I. Immunol.* 149:3778-3783, 1992; Bowman et al., *I. Immunol.* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,
 15 Kruisbeek, A. M. and Shevach, E. M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
 20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse
 25 and human interleukin 6--Nordan, R. In *Current Protocols in Immunology*. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In *Current Protocols in Immunology*. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin
 30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In *Current Protocols in Immunology*. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in*
 35 *Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce
5 autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and
10 identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be
15 used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition,
20 the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated
25 cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al.,
30 Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention
35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the
10 growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A
25 protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More
30 specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily
5 determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell
10 population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146,
15 1995; Muller et al. Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or
20 thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res.
30 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or
35 metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, 5 Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, 10 Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. 15 exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of 20 cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction 25 of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

30 4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and 35 their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant
5 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

10 Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988;
15 Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel
20 overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein
25 Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

30

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a
35 solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of
5 complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and
10 organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

15 The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a
20 review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein,
25 peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

30 Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested
35 for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be
5 complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying
10 previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number
15 of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the
20 invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and
25 inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a
30 protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not
5 limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- 10 (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human
15 immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral
20 sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus
25 callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular
30 neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, *J. Neurosci.* 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, *Exp. Neurol.* 70:65-82) or Brown et al. (1981, *Ann. Rev. Neurosci.* 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without
5 limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of
10 hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

15 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune
20 response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to
30 allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction
35 enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

10 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129.

15 Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

20 The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound
25 would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or
30 other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity.

5 Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the

10 biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and

15 polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine,

20 monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T

25 lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified

30 MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in

35 which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,
5 California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

10 The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the
15 art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting
20 dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such
25 as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using
30 oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of
35 monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

5 antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques,
10 including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans
15 in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and
20 Lonberg and Huszar (Intern. Rev. Immunol., 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host
25 have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The
30 preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as
35 hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

5 Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a
10 potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

 Antibody variable domains with the desired binding specificities (antibody-antigen
15 combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin
20 light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are
25 recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino
30 acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

 Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be
35 prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

20 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include
5 diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, *sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phcnomycin, enomycin, and the tricothecenes. A variety of
10 radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL),
15 active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987).
20 Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is
25 administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

30 In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM
35 and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of
5 a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

10 Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- 15 (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of
20 the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the
25 invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time
30 sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the
35 activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

5 Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.19 USE OF NUCLEIC ACIDS AS PROBES

 Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited
15 number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

 Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides
20 additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

 Other means for producing specific hybridization probes for nucleic acids include the
25 cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The
30 nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

10 4.20 **PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES**

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. Covalink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. Covalink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to Covalink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the
5 light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile
10 combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA,
15 including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples
20 may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

25 Low pressure shearing is also appropriate, as described by Schrieffer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA
30 fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviII, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid
5 being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations
10 may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and
15 variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

20 5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome
25 using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for
30 sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cyclic sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

5 Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

5 Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-1350. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927 976 1233 1319
adult brain	GIBCO	ABD003	41 49 74 101 111 120 132 141-142 151 217 225 238 271 317 404 446 469 503 513-514 535 550 564 573 666-669 798 898 910 927 976 1067 1083 1085 1178 1254
adult brain	Clontech	ABR001	39 216 238 327 356 535 927 1056 1121 1178-1180 1199 1251
adult brain	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145 147 188 197 208 225 227-239 250 300-303 312 316 328-331 340 357-362 374 380 384-391 408 414 446 448 464-467 483 488 495-496 505 512 521 535 550 566 571 577 585 590 594 598 634 641 658 666 683 725 742 764 767 786 801 805 810 823 826 829 831 836 841 887-923 927 934 943 950-951 963 976 995 1000-1001 1006 1026 1034 1048 1057-1067 1086 1088 1090 1118 1120 1122-1128 1142 1162 1181-1192 1199 1204 1218-1219 1225 1232 1253 1267 1271-1306 1342 1347 1349-1350
adult brain	Clontech	ABR011	49 238 1219
adult brain	BioChain	ABR012	74 238
adult brain	Invitrogen	ABR013	868 1268
adult brain	Invitrogen	ABT004	49 117 138 191 217 252 291 305 535 566 596 663 670 746 798 816-819 876 892 898 922 943 963 1034-1036 1121
cultured preadipocytes	Stratagene	ADP001	41 74 101 138 211 238 304 537 582 740 798 883 943 976 1067
adrenal gland	Clontech	ADR002	49 74 101 111 120 127 151 215 238 240-247 316 330 363-364 404 414 534-535 833 924-940 950 963 976 1001 1003 1067-1070 1118 1156 1193-1200 1325
adult heart	GIBCO	AHR001	38 49 71-72 74-77 79 92 99 101 111 118 129 132 138 151 158-163 182 195-203 215 217 238 264 269 353 384 398 408 434-439 446 504 512-513 519 537 562-573 577 611-614 616-619 658 661 671-672 722 734 757-773 815 828-835 874 891 898 919 926-927 976 988 1021 1037 1041 1062 1067 1071 1080 1083 1093 1122 1131 1185 1201 1254 1308 1331 1335
adult kidney	GIBCO	AKD001	41 49 51 71-74 78-85 94 100-101 103-107 111 119-120 138 151 157 215 217-218 238 250 264 294 304 384 404 440 446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859 877 909 918 927 956 963 976 1067 1074 1083 1095 1178 1302 1331 1335
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316 446 487 564 575 844 868 910 927 976 1116
adult lung	GIBCO	ALG001	8 101 111 151 187 402 446 490 514

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			518 537 545 549 580 582 592 594 634 640 651-652 676-678 725 851 873 918 952 976 1042 1067 1076 1083 1152
lymph node	Clontech	ALN001	8 111 121 151 180-182 188 215 537 545 549 651 679-682 789 804-810 868 873 927 952 976 1042 1059 1335
young liver	GIBCO	ALV001	8 64 79 111 186 215-216 238 446 514 519 537 564 653 683-684 698 753 798 813 833 840 858 927 976 1038-1039 1051 1085 1224 1245 1256
adult liver	Invitrogen	ALV002	40 71 292-293 305 384 468-469 496 505 657 675 714 753 832 844 941-942 976 1040 1076 1256 1293
adult liver	Clontech	ALV003	976
adult ovary	Invitrogen	AOV001	8 32 36 38 41 49 51 71 74 79-80 101 104 111 120 122-125 138 140 143-149 151 188-190 207-212 215-217 238 264 316 384 409 440 445-446 496 504 512 514 518-519 535 537 549-550 564 566 571 580 582 600 618 638 657 667 681 685-697 699 705 722 735-744 761 771 815 833 842-865 868 875-876 918 926- 927 950 952 963 976 1023 1042 1048 1051 1059 1072 1076 1083 1117 1120 1124 1131 1144 1174 1224 1268 1331 1335
adult placenta	Clontech	APL001	102 217 238 537 641 700
placenta	Invitrogen	APL002	663 851 1048
adult spleen	GIBCO	ASP001	8 45 74 111 132 140 151 185 217 238 294 414 446 477 504 514 534 545 549 592 722 873 883 952 976 1041-1042 1083 1093-1094 1152 1224
testis	GIBCO	ATS001	72 107 111 113 126 140 151 183 215 238 446 497 537 642 701-706 811 877 927 962 976 1083 1117 1131
adult bladder	Invitrogen	BLD001	41 151 191 402-405 409 414 496 545 592 607 706 873 952 1178 1329-1335
bone marrow	Clontech	BMD001	8 58-62 65-68 74 79 108 111 116 137 147 151 164-174 213-215 238 305-307 374 404 446 460 466 516 519 534 538- 541 544-546 549-554 566 584 586 592 596 607 610 628-629 643-645 652 707- 708 774-789 844 866-871 873 919 927 952 963 976 998 1034 1042 1064 1083 1085 1120 1132 1152 1225 1229 1268 1307 1310
bone marrow	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132 210 317 510-511 545 549 581 598 628 638 724 766 789 844 860 868 873 919 927 952 963 968 976 1042 1111 1141 1160-1161 1229 1266 1346
bone marrow	Clontech	BMD004	111 238 282 549 1083
adult colon	Invitrogen	CLN001	52 260 264 299 494 536 545 564 592 844 873 877 952 976 1042 1152 1268 1336-1337
adult cervix	BioChain	CVX001	49 51 129 132 151 205 207 238 332- 335 365-367 392-401 440 466 470-471 518 537 597 629 832 877 927 976 1006 1085 1117 1129-1134 1192 1202-1205 1219 1309-1328
diaphragm	BioChain	DIA002	74 976 1083

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
endothelial cells	Stratagene	EDT001	32 40-41 49 74 79 101 111 120 132 138 151 204-206 215-217 238 269 316 414 433 505 510 513 550 555 580 582 596 675 722 745 798 814 836-841 851 918 976 1041 1043 1073 1083 1131 1331
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	525-532 927
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	47 525
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	525 927
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM005	531
esophagus	BioChain	ESO002	74 138 238
fetal brain	Clontech	FBR001	441-442 927
fetal brain	Clontech	FBR004	215 893 927 1001
fetal brain	Clontech	FBR006	48 61 101 120 132 138 140 147 208 225 271 317 319 336 359 368 405-414 519 550 571 594 686 715 722 764 824 829 836 859 909 927 943 947 963 1057 1067-1068 1104 1135-1140 1162 1206- 1207 1235 1268 1288 1307-1308 1319 1338-1350
fetal brain	Clontech	FBRs03	111 446
fetal brain	Invitrogen	FBT002	41 51 120 151 192-194 264 504 512 535 683 761 798 820-827 844 876 909 963 976 1026 1048 1083 1144 1302
fetal heart	Invitrogen	FHR001	446 566 761
fetal kidney	Clontech	FKD001	51 74 111 127 140 151 184 294 537 550 630-631 1319
fetal kidney	Clontech	FKD002	111 976 1083
fetal kidney	Invitrogen	FKD007	238 974
fetal lung	Clontech	FLG001	463 566 976 1074 1083 1093
fetal lung	Invitrogen	FLG003	41 238 330 407 415-416 537 573 844 859 1048 1083 1116 1192
fetal liver-spleen	Columbia University	FLS001	8 14 34-35 37 41 43 49 51 54-56 63-64 69-71 74 77 79 87-90 101 107 110-111 114 120 128-131 138 140 147 150-155 197 210 215 217 225 238 312 367 384 414 440 446 460 468 483 496 504-507 511-515 518-519 523 533-535 537 541 544-545 547-550 555-560 564 566 571 577 582 585-586 598 636 646-647 649 652 664 698 709-710 714 722-723 731 735-736 746-753 761 784 798 823 829 832 844 851 858-859 868 873 876 898 927 943 949 952 963 976 984 1002 1021 1023 1040 1042 1044 1050 1083 1093 1116 1120 1129 1131 1144 1174 1217 1251 1254 1256 1302 1308 1311 1319
fetal liver-spleen	Columbia University	FLS002	8 36-37 41-46 49 54 64 71 74 79 101 111 120 129 147 207 210 215-216 238 250 330 353 359 366 383-384 414 478 505 508-509 511 515-524 534-535 537 544-545 564 566 571 577 591 598 638

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			663 671 698 714 722 725 727 751 798 851 859 873 876 909 927 949 952 983- 984 1002 1023 1042-1044 1085 1095 1131 1144 1178 1199 1233 1240-1270 1331 1340
fetal liver-spleen	Columbia University	FLS003	64 535 976 1256
fetal liver	Invitrogen	FLV001	8 101 120 138 217 446 468 535 566 580 722 730 749 844 918 943 976 1051 1256 1331
fetal liver	Clontech	FLV004	537 926 1256
fetal muscle	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421 425 535 537 577 598 614 836 857 1141 1208 1268
fetal muscle	Invitrogen	FMS002	537
fetal skin	Invitrogen	FSK001	13-26 32 41 51 89 107 111 147 151 225 264 316 405 422-429 488-494 496 519 534-535 537 566 675 732 859 876- 877 898 947 949-950 963 976 1001 1062 1076 1083 1117 1144 1165 1268 1281
fetal skin	Invitrogen	FSK002	537 812
fetal spleen	BioChain	FSP001	87 549
umbilical cord	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301 316 446 495-503 519 521 534-535 537 582 634 691 877 883 927 944-950 963 976 1001 1075 1142-1143 1171 1218 1243 1308
fetal brain	GIBCO	HFB001	41 49 57 79 87 103 111 120 132-135 138 145 151 188 197 207 215 238 264 271 294 316 367 414 440 446 466 504 513-514 535 542-543 550 564 571 596 635 648-654 675 711-715 722-723 798 832 872 876 883 927 976 1095 1144 1168 1171 1178 1211 1335
macrophage	Invitrogen	HMP001	238
infant brain	Columbia University	IB2002	49-50 77 81 89 105 111 136-138 140 151 161 175-179 185 216-217 264 295 299 308-310 371-373 462 476 504 511- 513 533 537 564 566 571 655-657 662 683 716-720 723 752 790-803 829 832 858-859 876 898 909 949 976 1045- 1047 1076-1087 1090 1093 1116 1122 1144 1209-1213 1225 1233 1256 1319 1341
infant brain	Columbia University	IB2003	41 50 77 104 132 215 238 508 512-513 519 566 655 714 794 918 943 976 1067 1092-1093 1233
infant brain	Columbia University	IBM002	311 472-473 753 1214
infant brain	Columbia University	IBS001	51 111 376 474 790 876 949 1144 1204 1221
lung , fibroblast	Stratagene	LFB001	151 316 462 514 534 582 675 939 1131
lung tumor	Invitrogen	LGT002	1-7 41 74 79 94 115 120 138-139 156 215 217 269 280 296 337 374-375 384 404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705 721-724 754-756 779 859 868 872-874 876-877 919 927 949 951-952 959 976 1002 1042 1048-1053 1076 1083 1088- 1089 1131 1144-1147 1216-1218 1229

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1293 1311
lymphocytes	ATCC	LPC001	41 74 111 132 151 253 316 446 550 634 844 927 976 1085 1268
leukocyte	GIBCO	LUC001	8 11 41 74 86 91-98 101 109 111 120 147 151 212 215 218 238 252 288 312- 314 316 338 359 408 427 443-447 505 510 512 514 518 534 545 549-550 561 564 566 571 577 580 582 587-609 615 632-638 658-659 698 714 725-728 832 836 841 859 866 873-874 882-883 918- 919 927 943 952 963 976 1042 1076 1083 1090 1148 1152 1168 1195 1219- 1220 1224
leukocyte	Clontech	LUC003	74 100 215 232 238 339-341 446 545 657 660 729 873 883 927 952 963 1008 1042 1116 1120 1149-1150 1215 1222
Melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	210 215 238 342 534 545 592 722 873 919 929 939 952 976 1071 1118 1218 1235 1245
mammary gland	Invitrogen	MMG001	8-10 40-41 49 73 80 114 138-140 147 217 250-256 264 297-299 305 377-378 398 446 481-486 505 512 537 545 549 571 592 725 730-733 816 829 836 844 868 873 876-877 898 926 943 951-960 963 976 995 1034 1042 1048 1054- 1055 1076 1083 1091 1093 1116-1117 1124 1152 1302
induced neuron cells	Stratagene	NTD001	39 101 111 138 238 361 1225 1251 1319
retinoid acid induced neuronal cells	Stratagene	NTR001	74 225 976
neuronal cells	Stratagene	NTU001	129 225 238 304 313 361 657 976
pituitary gland	Clontech	PIT004	976
placenta	Clontech	PLA003	38 976
prostate	Clontech	PRT001	111 188 238 257-258 564 724 961-966 1067 1095
rectum	Invitrogen	REC001	238 430-431 841 859 868 963 1001 1116
salivary gland	Clontech	SAL001	8 151 402 432-433 446 496 868 952 976 1083 1120 1151 1184
small intestine	Clontech	SIN001	8 101 147 215 259-266 446 462 505 545 592 660 789 836 866 873 927 952 963 967-978 1042 1120 1152 1223- 1224
skeletal muscle	Clontech	SKM001	238 302 927 943 992 1031
spinal cord	Clontech	SPC001	74 111 132 151 215-216 238 264 267- 270 343-344 353 379 516 537 566 740 828 927 976 979-994 1092 1153-1159 1225 1250
adult spleen	Clontech	SPLc01	698 859 1042
stomach	Clontech	STO001	210 238 271-272 537 580 705 918 952 995 1171
thalamus	Clontech	THA002	61 219-220 273-276 312 315 330 596 963 996-1007 1059 1093 1160-1162
thymus	Clontech	THM001	8 120 151 208 221 316-317 353 639 750 867 874 878-881 927 963 1023 1083 1094-1096 1124
thymus	Clontech	THMc02	8 61 114 129 132 210 225 231 306 317-319 336 340 359 380 398 446 448- 463 512 519 545 554 587 598 698 724- 725 789 812 836 868 873 927 947 952

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			976 1007 1042 1083 1085 1097-1116 1122 1147 1177 1226-1229 1234 1311 1313
thyroid gland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188 210 217 222 253 264 271 277-286 294 320-326 345-352 361 381-382 446 467 483 514 534 549-550 564 578 602 649 844 882-883 927 950 956 976 1008- 1028 1076 1083 1117-1120 1142 1163- 1175 1230-1238 1308
trachea	Clontech	TRC001	223-225 238 287 353-354 514 545 592 611 873 883-884 927 952 1029-1031 1042 1151-1152 1170 1176-1177 1239
uterus	Clontech	UTR001	151 226 288-290 355 537 877 885-886 976 1001 1032-1033 1232

TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.	460	100
2	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	111	51
3	R26173	Homo sapiens	Part of Major Yo paraneoplastic antigen (CDR62) encoded by clone pY2.	293	76
4	L29536	Homo sapiens	calcium channel L-type alpha 1 subunit	191	65
5	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	251	50
6	M11507	Homo sapiens	transferrin receptor	120	95
7	AF099100	Homo sapiens	WD-repeat protein 6	1941	93
8	Y92338	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-45.	245	82
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	91
10	AJ133798	Homo sapiens	copine VII protein	1127	68
11	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	99
12	X98330	Homo sapiens	ryanodine receptor 2	282	78
13	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase)))	293	100
14	AF045577	Pan troglodytes	olfactory receptor OR93Ch	191	36
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	93	39
16	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor	569	89
17	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	99	44
18	Y36203	Homo sapiens	Human secreted protein #75.	165	75
19	U15647	Mus musculus	reverse transcriptase	106	40
20	G02701	Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	544	100
21	Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 172.	1691	100
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 8111.	380	96
23	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	123	50
24	AF036329	Homo sapiens	gonadotropin-releasing hormone precursor, second form	284	90
25	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	96	32
26	S80119	Rattus sp.	reverse transcriptase homolog	100	34
27	U83303	Homo sapiens	line-1 reverse transcriptase	101	35
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	135	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
29	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	83	42
30	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	116	72
31	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	96	67
32	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	58	32
33	Y66688	Homo sapiens	Membrane-bound protein PRO1152.	2457	98
34	Y87071	Homo sapiens	Human secreted protein sequence SEQ ID NO:110.	348	95
35	U15131	Homo sapiens	p126	182	48
36	Y73464	Homo sapiens	Human secreted protein clone yl4_1 protein sequence SEQ ID NO:150.	982	90
37	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	687	99
38	AC067969	amino acids 3338-4088	Homo sapiens ryanodine receptor 1 (skeletal)	386	66
39	AL031588	Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN, FGENES and GENEWISE)	493	76
40	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	110	51
41	AF132969	Homo sapiens	CGI-35 protein	228	68
42	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	220	88
43	X61048	Hydra sp.	mini-collagen	105	35
44	M76546	Helianthus annuus	hydroxyproline-rich protein	110	31
45	U82288	Caenorhabditis elegans	Rac-like GTPase	139	70
46	G03477	Homo sapiens	Human secreted protein, SEQ ID NO: 7558.	118	58
47	AF090942	Homo sapiens	PRO0657	113	63
48	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	90	59
49	AJ005560	Mus musculus	SPR2B protein	72	56
50	G02450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	98
51	Y91649	Homo sapiens	Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.	973	94
52	U93563	Homo sapiens	putative p150	105	38
53	Y55927	Homo sapiens	Human STK2 protein.	699	85
54	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	145	56
55	AB008175	Mus musculus	hepatic nuclear factor 1-beta short form	356	74
56	M68941	Homo sapiens	protein-tyrosine phosphatase	165	41
57	AL031600	Homo sapiens	c390E6.1 (chloride channel 7)	338	76
58	AF011417	Mus musculus	putative pheromone receptor	143	55
59	AF167320	Mus musculus	zinc finger protein ZFP113	558	68
60	U73036	Homo sapiens	interferon regulatory factor 7	263	96
61	X07984	Mus musculus	protein-tyrosine kinase	297	69
62	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	791	98
63	U35376	Homo sapiens	repressor transcriptional factor	485	65
64	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	785	74
65	G03883	Homo sapiens	Human secreted protein, SEQ ID NO: 7964.	88	95
66	AF177390	Manduca sexta	antennal specific membrane protein AMP	274	54
67	AB040800	Homo sapiens	SREB2	614	100
68	AF030027	Equine herpesvirus 4	24	213	26
69	G02965	Homo sapiens	Human secreted protein, SEQ ID NO: 7046.	261	95
70	W75770	Homo sapiens	Human oxidoreductase YTF03.	1144	98
71	AB011135	Homo sapiens	KIAA0563 protein	239	76
72	AB014885	Halocynthia roretzi	HrPOPK-1	813	78
73	AF045454	Cavia porcellus	phospholipase B	955	73
74	J02870	Mus	laminin receptor	308	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		musculus			
75	Y00826	Rattus norvegicus	gp210 (AA 1-1886)	413	84
76	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	351	54
77	Y38422	Homo sapiens	Human secreted protein.	468	76
78	Y14596	Homo sapiens	Human T-type voltage-gated Ca channel alpha-1-I (hCavT3).	1357	99
79	Y14591	Human papillomavirus type 68	APM-1 protein	767	100
80	AL137802	Homo sapiens	dJ798A10.2 (KIAA0445 protein)	71	34
81	AP000383	Arabidopsis thaliana	protein arginine N-methyltransferase-like protein	359	65
82	L46815	Mus musculus	DNA binding protein Rc	895	75
83	G01600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681.	315	96
84	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	538	71
85	AB029002	Homo sapiens	KIAA1079 protein	134	42
86	Y28678	Homo sapiens	Human cw272_7 secreted protein.	325	62
87	Y99368	Homo sapiens	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.	156	48
88	AJ225124	Mus musculus	hyperpolarization-activated cation channel, HAC3	487	95
89	AF177203	Homo sapiens	cerebral cell adhesion molecule	290	56
90	Y28280	Homo sapiens	Human G-protein coupled receptor GRIR-2.	326	79
91	L39891	Homo sapiens	polycystic kidney disease-associated protein	1751	95
92	AF064876	Homo sapiens	ion channel BCNG-1	953	99
93	AF170723	Homo sapiens	protein kinase STK10	401	53
94	X13292	Trypanosoma brucei	GPI-phospholipase C (AA 1 - 358)	151	37
95	Y34127	Homo sapiens	Human potassium channel K+Hnov11.	661	99
96	X03638	Rattus norvegicus	sodium channel protein I (aa 1-2009)	1775	92
97	AF134213	Homo sapiens	ubiquitin-specific protease	1995	99
98	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	213	38
99	AF021935	Rattus norvegicus	myotonic dystrophy kinase-related Cdc42-binding kinase	675	48
100	AF279265	Homo sapiens	putative anion transporter 1	867	98
101	AC007878	Homo sapiens	match to nuclear protein, NP220; note: sequence difference at residue 58	160	60
102	U22829	Mus musculus	P2Y purinoceptor	264	42
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	516	99
104	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	787	98
105	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	343	57
106	AF169312	Homo sapiens	hepatic angiopoietin-related protein	212	67
107	AF116657	Homo sapiens	PRO1310	74	52
108	AE000401	Escherichia coli	sialic acid transporter	587	96
109	Y38395	Homo sapiens	Human secreted protein encoded by gene No. 10.	693	100
110	Y78801	Homo sapiens	Hydrophobic domain containing protein clone HP00631 amino acid sequence.	182	94
111	Z25535	Homo sapiens	nuclear pore complex protein hnup153	464	85
112	Y94939	Homo sapiens	Human secreted protein clone ye90_1 protein sequence SEQ ID NO:84.	274	51
113	AF016365	Homo sapiens	hexokinase 1 isoform td	301	71
114	AC007956	Homo sapiens	unknown	520	75
115	M83738	Homo sapiens	protein-tyrosine phosphatase	251	92
116	AL157952	Homo sapiens	dJ875K15.1.1 (ets homologous factor (ets-domain transcription factor ESE-3A, isoform 1))	484	91
117	W18084	Homo sapiens	Human Aurora-2.	546	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
118	L41816	Homo sapiens	cam kinase I	407	62
119	AJ006710	Rattus norvegicus	phosphatidylinositol 3-kinase	627	93
120	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP α	1646	94
121	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase (EC 3.1.3.48)	373	68
122	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit	262	88
123	Y44403	Homo sapiens	Human truncated tankyrase-1.	111	35
124	U88167	Caenorhabditis elegans	contains similarity to C2 domains	219	29
125	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	693	90
126	AB021861	Mus musculus	apoptosis signal-regulating kinase 2	153	65
127	AF305210	Homo sapiens	concentrative Na ⁺ -nucleoside cotransporter hCNT3	807	97
128	M90360	Homo sapiens	protein kinase	220	73
129	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	574	86
130	AF208043	Homo sapiens	IFI16b	496	67
131	AF201734	Mus musculus	testis specific serine kinase-3	800	87
132	AF112886	Bos taurus	differentiation enhancing factor 1	159	74
133	AJ278314	Homo sapiens	phospholipase C-beta-1b	554	85
134	W74802	Homo sapiens	Human secreted protein encoded by gene 73 clone HSQEL25.	1157	87
135	AB020335	Homo sapiens	Pancreas-specific gene	668	96
136	W80408	Homo sapiens	A secreted protein encoded by clone dt674_2.	866	98
137	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)	5041	99
138	Y96736	Homo sapiens	PRO3434, a novel secreted protein.	891	100
139	AB024034	Arabidopsis thaliana	DNA-damage inducible protein DDII-like	147	55
140	W97809	Homo sapiens	Human GTPase regulator GRAP.	248	56
141	Y51557	Homo sapiens	Human PLA2 protein.	125	46
142	AF090113	Rattus norvegicus	AMPA receptor binding protein	623	93
143	W26642	Homo sapiens	Human RECK cancer-inhibiting protein.	641	82
144	U87306	Rattus norvegicus	transmembrane receptor UNC5H2	578	84
145	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	727	92
146	W63683	Homo sapiens	Human secreted protein 3.	140	40
147	M96264	Homo sapiens	galactose-1-phosphate uridyl transferase	513	81
148	D64014	Escherichia coli	HrsA	818	90
149	M83316	Escherichia coli	pppGpp phosphohydrolase	915	95
150	AL163279	Homo sapiens	homolog to cAMP response element binding and beta transducin family proteins	1261	99
151	AF179867	Homo sapiens	STE20-like kinase	940	99
152	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	392	61
153	AF151859	Homo sapiens	CGI-101 protein	370	92
154	X66957	Homo sapiens	hexokinase type 1	489	81
155	Y16355	Homo sapiens	alternatively spliced form	432	92
156	G00857	Homo sapiens	Human secreted protein, SEQ ID NO: 4938.	349	78
157	AF159455	Mus musculus	zinc finger protein	352	74
158	L76191	Homo sapiens	interleukin-1 receptor-associated kinase	537	76
159	AP001743	Homo sapiens	putative gene, ankirin like, possible dual specificity Ser/Thr/Tyr kinase domain	670	98
160	AJ250425	Rattus norvegicus	Collybistin I	556	74
161	G02885	Homo sapiens	Human secreted protein, SEQ ID NO: 6966.	370	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
162	Z22968	Homo sapiens	M130 antigen	610	100
163	AF181121	Homo sapiens	ATP-dependent Ca ²⁺ pump PMR1	336	92
164	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	455	94
165	AF160798	Rattus norvegicus	calcium transporter CaT1	700	96
166	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	327	45
167	Y48607	Homo sapiens	Human breast tumour-associated protein 68.	1072	99
168	AB020741	Mus musculus	NIK-related kinase	197	43
169	AF252293	Homo sapiens	PAR3	596	44
170	U59429	Cricetinae gen. sp.	diacylglycerol kinase eta	481	82
171	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	386	42
172	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	507	82
173	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	653	99
174	G02979	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97
175	U36488	Mus musculus	embryonic stem cell phosphatase	168	55
176	W95629	Homo sapiens	Homo sapiens secreted protein gene clone gm196_4.	1022	100
177	AF289023	Homo sapiens	formiminotransferase cyclodeaminase form D	255	93
178	X04936	Homo sapiens	T-cell receptor alpha-chain (413 is 2nd base in codon)	710	99
179	AF127481	Homo sapiens	non-oncogenic Rho GTPase-specific GTP exchange factor	175	80
180	G00978	Homo sapiens	Human secreted protein, SEQ ID NO: 5059.	517	94
181	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	671	96
182	AF110640	Homo sapiens	orphan seven-transmembrane receptor	862	100
183	AB020854	Bos taurus	orphan transporter short splicing variant	766	84
184	AF169691	Homo sapiens	cadherin-like protein VR8	375	38
185	AF126372	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme	985	99
186	L20966	Homo sapiens	phosphodiesterase	541	76
187	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	254	93
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	301	98
189	Y66713	Homo sapiens	Membrane-bound protein PRO1309.	694	100
190	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	331	73
191	U36771	Rattus norvegicus	sn-glycerol 3-phosphate acyltransferase	707	92
192	R05935	Homo sapiens	Secreted GPIIb subunit of multiple subunit polypeptide (MSP)GPIIb-IIIa.	157	72
193	M92084	Theileria parva	casein kinase II alpha subunit	364	50
194	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	448	90
195	W95631	Homo sapiens	Homo sapiens secreted protein gene clone hj968_2.	382	49
196	AF255614	Rattus norvegicus	scaffolding protein SLIPR	680	99
197	AC021640	Arabidopsis thaliana	putative phosphatidate phosphohydrolase	300	41
198	AF073967	Mus musculus domesticus	olfactory receptor	316	43
199	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	617	98
200	AF117948	Homo sapiens	pancreas-enriched phospholipase C	625	89
201	AF128625	Homo sapiens	CDC42-binding protein kinase beta	636	94
202	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	1303	100
203	Y53021	Homo sapiens	Human secreted protein clone qc646_1 protein sequence SEQ ID NO:48.	701	99
204	AF227968	Homo sapiens	SH2-B beta signaling protein	182	79
205	S81752	Homo sapiens	DPH2L=candidate tumor suppressor gene	375	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			(ovarian cancer critical region of deletion)		
206	U18315	Sus scrofa	parathyroid receptor	122	60
207	AF255342	Homo sapiens	putative pheromone receptor V1RL1 long form	170	96
208	S52051	Rattus sp.	neurotransmitter transporter	715	94
209	W63683	Homo sapiens	Human secreted protein 3.	840	99
210	D79992	Homo sapiens	similar to Drosophila photoreceptor cell-specific protein, calphotin.	541	82
211	AF117948	Homo sapiens	pancreas-enriched phospholipase C	1348	99
212	U81035	Rattus norvegicus	ankyrin binding cell adhesion molecule neurofascin	471	69
213	AF154846	Homo sapiens	zinc finger protein	798	56
214	AF102777	Mus musculus	FYVE finger-containing phosphoinositide kinase	933	93
215	AL163303	Homo sapiens	putative gene containing transmembrane domain	523	89
216	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor	563	78
217	G04095	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	98
218	X75756	Homo sapiens	protein kinase C mu	314	81
219	Y66723	Homo sapiens	Membrane-bound protein PRO1100.	770	98
220	D88577	Mus musculus	Kupffer cell receptor	567	40
221	AF258465	Homo sapiens	OTRPC4	853	100
222	AF021935	Rattus norvegicus	myotonic dystrophy kinase-related Cdc42-binding kinase	636	96
223	AL136527	Homo sapiens	bA215B13.1 (A kinase (PRKA) anchor protein 11)	693	100
224	AB032417	Homo sapiens	WNT receptor Frizzled-4	690	99
225	AF030430	Mus musculus	semaphorin 11a	703	68
226	AF000218	Escherichia coli	putative dihydroxyacetone kinase (EC 2.7.1.2)	297	39
227	AF302150	Homo sapiens	phosphoinositide 3-phosphate-binding protein-2	2080	100
228	AB024573	Mus musculus	GTP-binding like protein 2	265	88
229	AF122924	Xenopus laevis	Wnt inhibitory factor-1	316	40
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.	229	100
231	X98260	Homo sapiens	M-phase phosphoprotein 11	265	92
232	R92754	Homo sapiens	Human growth differentiation factor-12.	682	95
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific phospholipase-D.	290	100
234	W69431	Homo sapiens	Human secreted protein cw1233_3.	235	97
235	Y08686	Homo sapiens	serine palmitoyltransferase, subunit II	859	81
236	AF118275	Homo sapiens	atrophin-related protein ARP	117	37
237	X81466	Mus musculus	Embryo Brain Kinase	460	62
238	U64857	Caenorhabditis elegans	similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor (TFPI)	284	33
239	AJ250840	Mus musculus	serine/threonine protein kinase	739	63
240	AJ223472	Mus musculus	transcription elongation factor TFIIS.h	222	38
241	Y94906	Homo sapiens	Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	353	52
242	AF169301	Homo sapiens	Na+/sulfate cotransporter SUT-1	591	99
243	L22022	Rattus norvegicus	orphan transporter v7-3	667	93
244	AF016191	Rattus norvegicus	potassium channel	1043	98
245	AF097366	Homo sapiens	cone sodium-calcium potassium exchanger	645	98
246	Y29868	Homo sapiens	Human secreted protein clone pp325_9.	497	98
247	AF180475	Homo sapiens	Not4-Np	188	83
248	Y17227	Homo sapiens	Human secreted protein (clone ya1-1).	690	99
249	AF250910	Manduca	death-associated small cytoplasmic leucine-rich	182	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		sexta	protein SCLP		
250	AF192756	Kaposi's sarcoma-associated herpesvirus	Orf73	134	34
251	AB022694	Homo sapiens	MOK protein kinase	209	83
252	W55045	Homo sapiens	Neural adhesion molecule (c8hb0018f2 product).	469	100
253	L46815	Mus musculus	DNA binding protein Rc	251	67
254	W68505	Homo sapiens	Human acid sensing ionic channel.	173	82
255	AF070066	Mus musculus	Citron-K kinase	1201	98
256	G02491	Homo sapiens	Human secreted protein, SEQ ID NO: 6572.	460	100
257	Z12841	Oryctolagus cuniculus	Phospholipase	368	80
258	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1857	99
259	AJ222968	Mus musculus	L-periaxin	430	72
260	AJ250839	Homo sapiens	serine/threonine protein kinase	861	100
261	AJ249977	Homo sapiens	AMP-activated protein kinase gamma 3 subunit	758	98
262	AF141386	Rattus norvegicus	SLIT-2	198	40
263	AF022859	Homo sapiens	neuropilin-2(a0)	335	62
264	AF160477	Homo sapiens	Ig superfamily receptor LNIR precursor	387	91
265	Y44662	Homo sapiens	Human 14273 G-protein coupled receptor (GPCR).	636	99
266	U27269	Mus musculus	sodium glucose cotransporter	204	56
267	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	159	75
268	AF127389	Rattus norvegicus	putative taste receptor TR1	209	39
269	X98296	Homo sapiens	ubiquitin hydrolase	215	95
270	X78482	Streptococcus pyogenes	Fc-gamma receptor	129	26
271	AB009883	Nicotiana tabacum	KED	109	26
272	AF137367	Mus musculus	VPS10 domain receptor protein SORCS	899	97
273	L34938	Rattus norvegicus	ionotropic glutamate receptor	460	86
274	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	188	74
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	173	94
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	56
277	L40380	Homo sapiens	thyroid receptor interactor	430	61
278	AB046851	Homo sapiens	KIAA1631 protein	283	96
279	AC008075	Arabidopsis thaliana	Contains PF00069 Eukaryotic protein kinase domain.	157	43
280	M83738	Homo sapiens	protein-tyrosine phosphatase	181	73
281	AK024397	Homo sapiens	unnamed protein product	439	91
282	AF141326	Homo sapiens	RNA helicase HDB/DICE1	497	84
283	AF156530	Mus musculus	ETS-domain transcriptional repressor PE1	605	76
284	Y29336	Homo sapiens	Human secreted protein clone cs756_2 alternate reading frame protein.	647	100
285	Y73402	Homo sapiens	Human secreted protein clone yc25_1 protein sequence SEQ ID NO:26.	300	90
286	AF016411	Homo sapiens	KCNA3.1B	137	100
287	W89253	Homo sapiens	Human ALP.	688	97
288	AF112886	Bos taurus	differentiation enhancing factor 1	750	96
289	AF113131	Homo sapiens	host cell factor homolog LCP	367	44
290	U52111	Homo sapiens	plexin-related protein	698	100
291	AF026504	Rattus	SPA-1 like protein p1294	603	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		norvegicus			
292	AF102854	Rattus norvegicus	membrane-associated guanylate kinase-interacting protein 2 Maguin-2	124	53
293	X99211	Drosophila melanogaster	ubiquitin-specific protease	143	38
294	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	185	94
295	Y94890	Homo sapiens	Human protein clone HP02798.	108	59
296	AF019767	Homo sapiens	zinc finger protein	154	96
297	Y28568	Homo sapiens	Secreted peptide clone bd577_1.	568	84
298	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	182	97
299	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	605	69
300	R58890	Homo sapiens	Human-32 cadherin-related molecule.	212	97
301	AF022859	Homo sapiens	neuropilin-2(a0)	277	100
302	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
303	Y44297	Homo sapiens	Human receptor tyrosine kinase.	228	97
304	D32050	Homo sapiens	alanyl-tRNA synthetase	192	80
305	U43586	Homo sapiens	protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author	428	72
306	R54872	Homo sapiens	Human H13 viral receptor mutant 4.	280	95
307	D78572	Mus musculus	membrane glycoprotein	199	41
308	AF255614	Rattus norvegicus	scaffolding protein SLIPR	639	88
309	S79463	Mus sp.	semaphorin homolog-M-Sema F	162	89
310	AF178941	Homo sapiens	ATP-binding cassette sub-family A member 2	736	100
311	U03413	Dictyostelium discoideum	calcium binding protein	151	36
312	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-124 SEQ ID NO:124.	744	100
313	Z97055	Homo sapiens	dJ388M5.4 (putative GS2 like protein)	789	99
314	AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	197	38
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and GENEWISE)	278	38
316	U70209	Mus musculus	polycystic kidney disease 1 protein	165	38
317	AF109643	Rattus norvegicus	coxsackie-adenovirus-receptor homolog	223	38
318	AF104923	Homo sapiens	putative transcription factor	138	84
319	AF100287	Trypanosoma vivax	activated protein kinase C receptor homolog	141	38
320	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	125	51
321	Y21591	Homo sapiens	Human secreted protein (clone CC332-33).	459	97
322	D26070	Homo sapiens	human type 1 inositol 1,4,5-trisphosphate receptor	232	97
323	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	306	88
324	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	70
325	M19650	Homo sapiens	2',3'-cyclic-nucleotide 3'-phosphodiesterase (EC 3.1.4.37)	214	97
326	W80396	Homo sapiens	A secreted protein encoded by clone bp646_10.	140	70
327	X75756	Homo sapiens	protein kinase C mu	540	78
328	G02292	Homo sapiens	Human secreted protein, SEQ ID NO: 6373.	721	99
329	AF168990	Homo sapiens	putative GTP-binding protein	877	99
330	S67984	Homo sapiens	anti-HIV gp120 antibody heavy chain variable region	581	80
331	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	2823	98
332	Y87330	Homo sapiens	Human signal peptide containing protein HSPP-107 SEQ ID NO:107.	1127	100
333	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	320	98
334	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95%	327	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similarity to P49205 (PID:g1345860)		
335	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-124 SEQ ID NO:124.	1111	67
336	AF006466	Mus musculus	lymphocyte specific formin related protein	193	75
337	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	632	97
338	Y13443	Homo sapiens	Amino acid sequence of hSlo3-2.	516	100
339	Y07637	Homo sapiens	putative GABA-gated chloride channel	189	100
340	Y05734	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
341	AE000497	Escherichia coli	L-idonate transcriptional regulator	928	98
342	D90855	Escherichia coli	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	769	99
343	D85613	Escherichia coli	membrane component	399	100
344	M93239	Escherichia coli	transmembrane protein	232	100
345	M60177	Escherichia coli	enterobactin	759	99
346	D90699	Escherichia coli	Sensor protein copS (EC 2.7.3.-).	638	97
347	D90843	Escherichia coli	CapB protein.	552	100
348	M13422	Escherichia coli	49 kd protein	1193	96
349	L10328	Escherichia coli	similar to drug resistance translocases	340	90
350	X69942	Mus musculus	enhancer-trap-locus-1	560	82
351	AF239613	Homo sapiens	apamin-sensitive small-conductance Ca2+-activated potassium channel	463	80
352	D90777	Escherichia coli	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (b-hydroxybutyryl-CoA dehydrogenase) (BhbD).	577	100
353	D90863	Escherichia coli	similar to	311	98
354	Y52386	Homo sapiens	Human transmembrane protein HP02000.	133	58
355	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-7).	482	55
356	Y58637	Homo sapiens	Protein regulating gene expression PRGE-30.	119	51
357	AF119226	Homo sapiens	dual-specificity tyrosine phosphatase YVH1	1788	100
358	Y87219	Homo sapiens	Human secreted protein sequence SEQ ID NO:258.	165	100
359	J00132	Homo sapiens	beta-fibrinogen	233	93
360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	70
361	R28916	Homo sapiens	Type III procollagen (prior art).	108	40
362	U16655	Rattus norvegicus	phospholipase C delta-4	649	65
363	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	95	42
364	U47276	Gallus gallus	chicken brain factor-2	104	34
365	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	65
366	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	118	46
367	X98258	Homo sapiens	M-phase phosphoprotein 9	564	75
368	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3387	99
369	U70932	Peromyscus leucopus	reverse transcriptase	92	59
370	X86400	Homo sapiens	gamma subunit of sodium potassium ATPase like	242	73
371	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	56
372	U49974	Homo sapiens	mariner transposase	257	55
373	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	21193	99
374	AF234765	Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	1182	78
375	U49974	Homo sapiens	mariner transposase	172	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
376	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	221	67
377	G00669	Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	600	100
378	X52574	Mus musculus	GTP binding protein	1456	91
379	R69095	Homo sapiens	Anti-HIV Fab tat31 light chain.	68	37
380	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
381	AB002405	Homo sapiens	LAK-4p	530	43
382	U64830	Dictyostelium discoideum	protein tyrosine kinase	115	44
383	G02916	Homo sapiens	Human secreted protein, SEQ ID NO: 6997.	618	98
384	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	617	93
385	AJ245822	Homo sapiens	type I transmembrane receptor	4560	100
386	D86974	Homo sapiens	KIAA0220	2148	98
387	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	142	50
388	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	99	59
389	M12140	Homo sapiens	envelope protein	197	51
390	AJ293309	Homo sapiens	NHP2 protein	461	77
391	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	181	94
392	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	241	66
393	Y14442	Homo sapiens	olfactory receptor protein	339	54
394	W85607	Homo sapiens	Secreted protein clone da228_6.	957	100
395	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	171	34
396	G03930	Homo sapiens	Human secreted protein, SEQ ID NO: 8011.	250	100
397	AB032904	Hylobates syndactylus	dopamine receptor D4	105	35
398	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	861	85
399	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	1047	92
400	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	162	37
401	D87002	Homo sapiens	similar to rat integral membrane glycoprotein; accession number Z21513.	527	78
402	AF100754	Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
403	X74904	Gallus gallus	alpha-2-macroglobulin receptor	258	60
404	AF075462	Mus musculus	ADP-ribosylation factor-directed GTPase activating protein isoform b	545	89
405	X92887	Human endogenous retrovirus K	pol/env	162	30
406	Y30162	Homo sapiens	Human dorsal root receptor 4 hDRR4.	325	72
407	AK022626	Homo sapiens	unnamed protein product	2833	99
408	L13802	Homo sapiens	ribosomal protein small subunit	264	92
409	Y91600	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:273.	1788	89
410	W88745	Homo sapiens	Secreted protein encoded by gene 30 clone HTSEV09.	2004	99
411	AB043953	Mus musculus	Chat-H	2628	82
412	Y86233	Homo sapiens	Human secreted protein HNTMX29, SEQ ID NO:148.	1014	92
413	U10542	Pan troglodytes	MHC class I A	265	71
414	AF155097	Homo sapiens	NY-REN-7 antigen	850	95
415	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	88	48
416	Y57911	Homo sapiens	Human transmembrane protein HTMPN-35.	266	89
417	W27651	Homo sapiens	Secreted protein AT205.	481	60
418	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	3077	87
419	AF255559	Notothenia coriiceps	alpha tubulin	289	68
420	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	209	74
421	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm antigen 4 (SPAG4)))	1446	96
422	AC008075	Arabidopsis thaliana	F24J5.4	112	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
423	AF231705	Homo sapiens	Alu co-repressor 1	1090	100
424	AF234887	Homo sapiens	FLAMINGO 1	6268	97
425	Y35942	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 191.	1961	99
426	AB009288	Homo sapiens	N-copine	635	98
427	L12392	Homo sapiens	Huntington's Disease protein	16080	99
428	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
429	AJ293573	Homo sapiens	zinc finger protein Cezanne	542	87
430	Y84441	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2074	100
431	G02850	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
432	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	73	42
433	AF159296	Lycopersicon esculentum	extensin-like protein	613	48
434	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	44
435	X73874	Homo sapiens	phosphorylase kinase	3442	97
436	AF161426	Homo sapiens	HSPC308	268	74
437	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
438	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	168	56
439	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
440	X02344	Homo sapiens	beta-tubulin	311	95
441	AF168418	Homo sapiens	activating signal cointegrator 1	1882	100
442	L11672	Homo sapiens	zinc finger protein	795	54
443	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
444	A52140	unidentified	HUMAN NDR	2451	100
445	X98330	Homo sapiens	ryanodine receptor 2	9356	99
446	AF116712	Homo sapiens	PRO2738	227	49
447	AF245447	Homo sapiens	sphingosine kinase type 2 isoform	576	99
448	AF133086	Homo sapiens	membrane-type serine protease 1	2630	94
449	U87305	Rattus norvegicus	transmembrane receptor UNC5H1	817	93
450	AF081249	Homo sapiens	JAW1-related protein MRV1A long isoform	4568	99
451	AC005498	Homo sapiens	R31665_1	316	62
452	M60235	Homo sapiens	granule membrane protein-140	464	73
453	AB036706	Homo sapiens	intelectin	730	88
454	G00918	Homo sapiens	Human secreted protein, SEQ ID NO: 4999.	263	81
455	Y22634	Homo sapiens	Human cytokine inducible regulatory protein-1 (CIRP-1).	192	67
456	Y36705	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	106	40
457	N91325	Homo sapiens	DNA encoding human growth hormone receptor.	3282	96
458	M19155	Plasmodium falciparum	S-antigen precursor	110	36
459	Y13377	Homo sapiens	Amino acid sequence of protein PRO257.	509	98
460	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	149	43
461	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	184	54
462	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	135	47
463	X84960	Triticum aestivum	low molecular weight glutenin	109	33
464	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	1781	85
465	AF189764	Mus musculus	alpha/beta hydrolase-1	502	59
466	U93569	Homo sapiens	p40	101	30
467	Y41528	Homo sapiens	Fragment of human secreted protein encoded by gene 77.	1172	99
468	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	149	52
469	AJ000008	Homo sapiens	PI3-kinase	5832	97
470	X70922	Mus musculus	neurotoxin homologue	118	47
471	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	75
472	Y36705	Homo sapiens	Fragment of human secreted protein encoded by	72	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 62.		
473	G02313	Homo sapiens	Human secreted protein, SEQ ID NO: 6394.	328	100
474	Y07007	Homo sapiens	Breast cancer associated antigen precursor sequence.	1013	97
475	W93254	Homo sapiens	Human ESRP1 protein.	943	80
476	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	236	65
477	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	202	60
478	G01870	Homo sapiens	Human secreted protein, SEQ ID NO: 5951.	267	100
479	AF102777	Mus musculus	FYVE finger-containing phosphoinositide kinase	3427	92
480	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	123	53
481	W87701	Homo sapiens	A human membrane fusion protein designated SYNTAX1.	221	77
482	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
483	AF210651	Homo sapiens	NAG18	124	59
484	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
485	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
486	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	149	73
487	Y76167	Homo sapiens	Human secreted protein encoded by gene 44.	627	100
488	AJ275213	Homo sapiens	stabilin-1	1244	91
489	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
490	L12392	Homo sapiens	Huntington's Disease protein	16081	100
491	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	197	66
492	J03799	Homo sapiens	laminin-binding protein	228	70
493	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	128	41
494	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	197	67
495	AC005175	Homo sapiens	R31449_3	889	94
496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	229	61
497	AB030237	Canis familiaris	D4 dopamine receptor	90	48
498	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
499	U70935	Peromyscus maniculatus	reverse transcriptase	213	52
500	U48508	Homo sapiens	skeletal muscle ryanodine receptor	26406	99
501	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
502	AF119851	Homo sapiens	PRO1722	156	62
503	AF113685	Homo sapiens	PRO0974	116	50
504	U79458	Homo sapiens	WW domain binding protein-2	322	59
505	W29651	Homo sapiens	Human secreted protein CD124_3.	608	55
506	W85459	Homo sapiens	Secreted protein encoded by clone dh1135_9.	986	70
507	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.	115	33
508	AL160175	Homo sapiens	bA243J16.3 (similar to MYLK (myosin, light polypeptide kinase))	184	92
509	U43360	Peromyscus maniculatus	reverse transcriptase	97	62
510	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	117	63
511	W79092	Homo sapiens	Human secreted protein dn740_3.	1058	100
512	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	205	64
513	AJ133439	Homo sapiens	GRIP1 protein	2151	100
514	AE003456	Drosophila melanogaster	CG6393 gene product	259	42
515	Z17206	Xenopus laevis	p46XIEg22	128	40
516	AF104413	Homo sapiens	large tumor suppressor 1	1766	94
517	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	40
518	AF151083	Homo sapiens	HSPC249	444	98
519	S80864	Homo sapiens	cytochrome c-like polypeptide	318	50
520	X92485	Plasmodium vivax	pval	170	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
521	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	59
522	AF121857	Homo sapiens	sorting nexin 7	259	40
523	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	82	37
524	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	253	73
525	AF119851	Homo sapiens	PRO1722	162	57
526	Y27761	Homo sapiens	Human secreted protein encoded by gene No. 47.	154	57
527	G02707	Homo sapiens	Human secreted protein, SEQ ID NO: 6788.	70	45
528	U47924	Homo sapiens	C8	1112	86
529	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	45
530	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	60
531	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	92	65
532	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	75	29
533	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	182	48
534	AF068286	Homo sapiens	HDCMD38P	861	100
535	U07707	Homo sapiens	epidermal growth factor receptor substrate	228	60
536	G01955	Homo sapiens	Human secreted protein, SEQ ID NO: 6036.	484	75
537	AF219232	Gallus gallus	qin-induced kinase	206	53
538	AF135022	Homo sapiens	mediator	128	100
539	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	141	59
540	AF016430	Caenorhabditis elegans	contains similarity to a BR-C/TTK domain	853	39
541	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059.(PID:g129308)	408	66
542	M29487	Homo sapiens	integrin alpha subunit precursor	517	81
543	AF102530	Mus musculus	olfactory receptor F3	327	73
544	Y73431	Homo sapiens	Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.	386	100
545	AE004833	Pseudomonas aeruginosa	probable TonB-dependent receptor	279	42
546	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	264	53
547	Y69192	Homo sapiens	A human monocyte-macrophage apolipoprotein B receptor protein.	1772	67
548	Y91493	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:166.	176	100
549	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
550	AF044588	Homo sapiens	protein regulating cytokinesis 1; PRC1	1953	88
551	Y29332	Homo sapiens	Human secreted protein clone pe584_2 protein sequence.	1224	94
552	X98330	Homo sapiens	ryanodine receptor 2	24621	99
553	Y42782	Homo sapiens	Human UC Band #331 protein.	684	95
554	AB025258	Mus musculus	granuphilin-a	501	41
555	AJ010346	Homo sapiens	RING-H2	1468	100
556	W92388	Homo sapiens	Human TR-interacting protein S239a.	538	92
557	AF119851	Homo sapiens	PRO1722	175	59
558	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	183	32
559	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	319	68
560	D86214	Mus musculus	Ca ²⁺ dependent activator protein for secretion	1010	93
561	AF187325	Canis familiaris	melanoma antigen	287	55
562	AJ001981	Homo sapiens	OXA1L	2512	99
563	Z17238	Rattus norvegicus	glutamate receptor subtype delta-1	338	66
564	W30638	Homo sapiens	Partial human 7-transmembrane receptor HAPO167 protein.	371	100
565	AC005620	Homo sapiens	R33590_1	467	97
566	Y99358	Homo sapiens	Human PRO1722 (UNQ834) amino acid sequence SEQ ID NO:63.	1138	78
567	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1002	58
568	AF151043	Homo sapiens	HSPC209	798	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
569	AF097518	Homo sapiens	liver-specific transporter	231	100
570	AB035698	Homo sapiens	Missshapen/NIK-related kinase MINK-1	1532	100
571	Y07096	Homo sapiens	Colon cancer associated antigen precursor sequence.	1064	100
572	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	735	55
573	Y66639	Homo sapiens	Membrane-bound protein PRO290.	254	45
574	AB037108	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
575	D43949	Homo sapiens	This gene is novel.	836	100
576	Y48596	Homo sapiens	Human breast tumour-associated protein 57.	108	50
577	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	141	75
578	R95913	Homo sapiens	Neural thread protein.	140	65
579	AK025116	Homo sapiens	unnamed protein product	201	70
580	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.	77	70
581	AF196779	Homo sapiens	JM10 protein	450	100
582	AF188706	Homo sapiens	g20 protein	330	98
583	AB030234	Canis familiaris	D4 dopamine receptor	64	56
584	G02621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
585	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	268	85
586	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	235	35
587	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	132	56
588	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	182	79
589	AF235017	Mus musculus	2P1 protein	764	80
590	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	329	81
591	Y30709	Homo sapiens	Amino acid sequence of a human secreted protein.	110	43
592	Y53875	Homo sapiens	A human seven transmembrane signal transducer polypeptide.	1369	92
593	Y53051	Homo sapiens	Human secreted protein clone dd119_4 protein sequence SEQ ID NO:108.	1112	97
594	Y27658	Homo sapiens	Human secreted protein encoded by gene No. 92.	763	79
595	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	156	58
596	AF151110	Mus musculus	COP1 protein	2215	95
597	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	157	65
598	AF192499	Mus musculus	putative secreted protein ZSIG37	143	40
599	AF119855	Homo sapiens	PRO1847	236	76
600	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	73
601	Y00295	Homo sapiens	Human secreted protein encoded by gene 38.	567	88
602	AF184971	Homo sapiens	class II cytokine receptor ZCYTOR7	2015	74
603	AF061936	Homo sapiens	diacylglycerol kinase iota	773	96
604	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	1333	93
605	AB033106	Homo sapiens	KIAA1280 protein	3915	100
606	X75756	Homo sapiens	protein kinase C mu	3916	99
607	D86983	Homo sapiens	similar to D.melanogaster peroxidase(U11052)	5758	99
608	W69341	Homo sapiens	Secreted protein of clone CG279_1.	1377	99
609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	339	82
610	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	116	62
611	AF202636	Homo sapiens	anglopoietin-like protein PP1158	2164	100
612	AF090944	Homo sapiens	PRO0663	218	82
613	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	195	59
614	M87053	Rattus norvegicus	lens membrane protein	450	84
615	AC004232	Homo sapiens	FPM315	163	37
616	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	205	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
617	Y91524	Homo sapiens	Human secreted protein sequence encoded by gene 74 SEQ ID NO:197.	821	99
618	AJ245621	Homo sapiens	CTL2 protein	2258	99
619	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	108	64
620	AF067864	Homo sapiens	transferrin receptor 2 alpha	3922	94
621	D90721	Escherichia coli	Transmembrane protein dppC	573	90
622	W75858	Homo sapiens	Human secretory protein of clone CS752-3.	730	100
623	Y94982	Homo sapiens	Human secreted protein vb12_1, SEQ ID NO:4.	733	100
624	AF034745	Mus musculus	LNXP80	637	83
625	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, IPPPNMSLPLS (3x)	94	46
626	U79260	Homo sapiens	unknown	194	70
627	R95913	Homo sapiens	Neural thread protein.	99	50
628	G03450	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.	427	100
629	Y36281	Homo sapiens	Human secreted protein encoded by gene 58.	590	100
630	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	165	76
631	G02139	Homo sapiens	Human secreted protein, SEQ ID NO: 6220.	268	96
632	U16996	Homo sapiens	protein tyrosine phosphatase	351	80
633	AF121857	Homo sapiens	sorting nexin 7	2019	100
634	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	340	77
635	Y07090	Homo sapiens	Renal cancer associated antigen precursor sequence.	277	64
636	AB013382	Homo sapiens	DUSP6	414	76
637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
638	M95762	Rattus norvegicus	GABA transporter	924	89
639	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
640	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	137	79
641	AC008075	Arabidopsis thaliana	F24J5.4	121	33
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96 clone HAQBK61.	615	62
643	AB015982	Homo sapiens	serine/threonine kinase	485	98
644	Y25806	Homo sapiens	Human secreted protein fragment encoded from gene 23.	162	46
645	AF122904	Homo sapiens	membrane protein DAP10	474	100
646	AF233323	Homo sapiens	Fas-associated phosphatase-1	200	38
647	W48804	Homo sapiens	Homo sapiens clone BK158_1 protein.	1203	99
648	AF257330	Homo sapiens	COBW-like protein	1440	98
649	Y36203	Homo sapiens	Human secreted protein #75.	233	73
650	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	173	78
651	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
652	AB032909	Hylobates agilis	dopamine receptor D4	122	32
653	AK021848	Homo sapiens	unnamed protein product	186	69
654	W73411	Homo sapiens	Human secreted protein encoded by Gene No. 15.	57	37
655	L22455	Rattus norvegicus	mu opioid receptor	116	34
656	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	110	45
657	G02345	Homo sapiens	Human secreted protein, SEQ ID NO: 6426.	459	97
658	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	291	75
659	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	65
660	Y91423	Homo sapiens	Human secreted protein sequence encoded by gene 11 SEQ ID NO:144.	333	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
661	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	168	68
662	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	375	43
663	W75771	Homo sapiens	Human GTP binding protein APD08.	629	100
664	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	480	55
665	AB037734	Homo sapiens	KIAA1313 protein	978	96
666	W82841	Homo sapiens	Human cerebral protein-1.	192	84
667	W82841	Homo sapiens	Human cerebral protein-1.	182	87
668	AB030184	Mus musculus	contains transmembrane (TM) region and ATP binding region	757	68
669	AB032919	Hylabates muelleri	dopamine receptor D4	85	37
670	AF107295	Rattus norvegicus	outer membrane protein	746	81
671	Z33642	Homo sapiens	leukocyte surface protein	394	93
672	W85608	Homo sapiens	Secreted protein clone du410.5.	261	91
673	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
674	AL035587	Homo sapiens	dJ475N16.4 (KIAA0240)	2388	99
675	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	1134	53
676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	174	74
677	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPr	1013	95
678	L11625	Mus musculus	receptor protein-tyrosine kinase	545	96
679	AL031427	Homo sapiens	dJ167A19.3 (novel protein)	745	100
680	AJ133430	Mus musculus	olfactory receptor	528	77
681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	70
682	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	336	76
683	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	118	100
684	U43360	Peromyscus maniculatus	reverse transcriptase	100	37
685	G00885	Homo sapiens	Human secreted protein, SEQ ID NO: 4966.	162	60
686	AK001518	Homo sapiens	unnamed protein product	590	100
687	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
688	Y92241	Homo sapiens	Human cancer associated antigen precursor (MO-REN-46).	2405	99
689	AC024792	Caenorhabditis elegans	contains similarity to TR:P78316	423	36
690	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	183	81
691	Y56514	Homo sapiens	Human Jurkat cell clone P2-15 AIM10 longest ORF protein sequence.	180	88
692	Y27795	Homo sapiens	Human secreted protein encoded by gene No. 79.	1539	99
693	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	428	98
694	U12465	Homo sapiens	ribosomal protein L35	308	89
695	Y45272	Homo sapiens	Human secreted protein encoded from gene 16.	1517	99
696	AF191838	Homo sapiens	TANK binding kinase TBK1	1242	98
697	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	275	75
698	Y87280	Homo sapiens	Human signal peptide containing protein HSPP-.57 SEQ ID NO:57.	576	90
699	Y97999	Homo sapiens	Human SCAD family molecule HSFM-1, SEQ ID NO:1.	729	99
700	AJ006701	Homo sapiens	putative serine/threonine protein kinase	610	79
701	AF209198	Homo sapiens	zinc finger protein 277	2357	100
702	AJ298841	Mus musculus	torsinA protein	709	45
703	AK021729	Homo sapiens	unnamed protein product	622	98
704	Z46787	Caenorhabditis elegans	similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger)	920	51
705	G02882	Homo sapiens	Human secreted protein, SEQ ID NO: 6963.	589	98

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
706	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	125	58
707	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 2DD).	121	95
708	G03002	Homo sapiens	Human secreted protein, SEQ ID NO: 7083.	125	39
709	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	516	98
710	M63577	Saccharomyces cerevisiae	SFP1	131	59
711	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	467	85
712	D21211	Homo sapiens	protein tyrosine phosphatase (PTP-BAS, type 3)	368	44
713	AF044033	Marmota marmota	olfactory receptor	615	83
714	G03561	Homo sapiens	Human secreted protein, SEQ ID NO: 7642.	251	100
715	AB033062	Homo sapiens	KIAA1236 protein	1380	100
716	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	73
717	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	835	99
718	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	234	100
719	U47334	Homo sapiens	similar to chicken gamma aminobutyric acid receptor beta4 subunit	578	99
720	AB020598	Homo sapiens	peptide transporter 3	1096	100
721	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	570	74
722	J05046	Homo sapiens	insulin receptor-related receptor	6787	100
723	AF001958	Ambystoma tigrinum	electrogenic Na ⁺ bicarbonate cotransporter, NBC	111	41
724	AF127084	Mus musculus	semaphorin cytoplasmic domain-associated protein 3A	5253	94
725	X54673	Homo sapiens	GABA transporter	3114	99
726	AF016191	Rattus norvegicus	potassium channel	370	100
727	AB029559	Rattus norvegicus	BAT1	139	35
728	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	2186	97
729	AJ011415	Homo sapiens	plexin-B1/SEP receptor	729	56
730	Z93096	Homo sapiens	bK390B3.1 (manic fringe (Drosophila) homolog)	142	68
731	Z10062	Homo sapiens	cDNA encoding a human vanilloid receptor homologue Vanilrep1.	675	99
732	AF161382	Homo sapiens	HSPC264	492	94
733	AB029033	Homo sapiens	KJAA1110 protein	3826	99
734	AE000493	Escherichia coli	putative transport protein	592	97
735	AL033379	Homo sapiens	dJ417022.2 (novel 7 transmembrane receptor (rhodopsin family) protein similar to high-affinity lysophosphatidic acid receptor homolog)	2173	99
736	AF132599	Homo sapiens	RANTES factor of late activated T lymphocytes-1	245	56
737	X55019	Homo sapiens	acetylcholine receptor delta subunit	883	99
738	X91906	Homo sapiens	voltage-gated chloride ion channel	1978	100
739	AB026116	Homo sapiens	organic anion transporter 4	1444	98
740	D00570	Mus musculus	open reading frame (196 AA)	83	24
741	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	118	40
742	U66059	Homo sapiens	V ₂ segment translation product	614	100
743	AF119815	Homo sapiens	G-protein-coupled receptor	2751	99
744	X16663	Homo sapiens	haematopoietic lineage cell protein (AA 1-486)	148	93
745	W67838	Homo sapiens	Human secreted protein encoded by gene 32 clone HLTJC163.	448	95
746	W57260	Homo sapiens	Human semaphorin Y.	2414	100
747	W21578	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS2232.	968	65
748	Y94935	Homo sapiens	Human secreted protein clone yd218_1 protein sequence SEQ ID NO:76.	622	100
749	AL022238	Homo sapiens	dJ1042K10.5 (novel protein)	314	85
750	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	391	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
751	AB025258	Mus musculus	granuphilin-a	773	41
752	Y52386	Homo sapiens	Human transmembrane protein HP02000.	900	99
753	Y48586	Homo sapiens	Human breast tumour-associated protein 47.	2527	99
754	AJ272207	Homo sapiens	putative G protein-coupled receptor 92	694	100
755	M85183	Rattus norvegicus	vasopressin receptor	979	68
756	AF190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	71
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
758	Z22535	Homo sapiens	ALK-3	439	98
759	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	564	97
760	W74902	Homo sapiens	Human secreted protein encoded by gene 175 clone HE8BI92.	1217	99
761	G03706	Homo sapiens	Human secreted protein, SEQ ID NO: 7787.	223	88
762	AB020676	Homo sapiens	KIAA0869 protein	4433	99
763	AK026992	Homo sapiens	unnamed protein product	2283	99
764	AF173358	Homo sapiens	glucocorticoid receptor AF-1 coactivator-1	573	100
765	AF268066	Mus musculus	netrin 4	2019	89
766	Y48585	Homo sapiens	Human breast tumour-associated protein 46.	1169	89
767	AF230378	Mus musculus	interleukin-1 delta	309	45
768	AF121975	Mus musculus	odorant receptor S18	268	62
769	AB008515	Homo sapiens	RanBPM	611	57
770	Y09945	Rattus norvegicus	putative integral membrane transport protein	458	50
771	AF226731	Homo sapiens	AD026	688	99
772	Y27132	Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
773	X87832	Homo sapiens	NOV/plexin-A1 protein	1821	98
774	AB025258	Mus musculus	granuphilin-a	500	41
775	AF125101	Homo sapiens	HSPC040 protein	232	93
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6896.	314	95
777	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	191	68
778	R03301	Homo sapiens	Sequence of pre-human atrial natriuretic peptide.	213	45
779	AL357374	Homo sapiens	bA353C18.2 (novel protein)	232	100
780	AF100346	Homo sapiens	neuronal voltage gated calcium channel gamma-3 subunit	1434	89
781	Y19566	Homo sapiens	Amino acid sequence of a human secreted protein.	103	52
782	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	1098	93
783	AF084464	Rattus norvegicus	GTP-binding protein REM2	141	30
784	W49042	Homo sapiens	Human low density lipoprotein binding protein LBP-3.	2693	99
785	AF238381	Homo sapiens	PTOV1	1904	91
786	Y91870	Homo sapiens	Human apoptosis related protein.	547	100
787	Y71062	Homo sapiens	Human membrane transport protein, MTRP-7.	1062	94
788	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	8684	98
789	AL049569	Homo sapiens	dJ37C10.3 (novel ATPase)	2848	96
790	AF151848	Homo sapiens	CGI-90 protein	745	96
791	Y08639	Homo sapiens	nuclear orphan receptor ROR-beta	1421	95
792	Y41706	Homo sapiens	Human PRO381 protein sequence.	644	99
793	AF121228	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP95	1037	100
794	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124	62
795	Y69384	Homo sapiens	Amino acid sequence of a 14274 receptor protein.	119	100
796	W40215	Homo sapiens	Human macrophage antigen.	1358	99

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
797	AF258340	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
798	AF159615	Homo sapiens	FGF receptor activating protein 1	461	98
799	Y59863	Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
800	W70459	Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
801	L00073	Homo sapiens	renin	1913	93
802	P92219	Homo sapiens (human)	CR1 protein.	11963	97
803	X15357	Homo sapiens	ANP-A receptor preprotein (AA -32 to 1029)	5199	98
804	W64473	Homo sapiens	Human secreted protein from clone EC172_1.	4018	95
805	AJ243874	Homo sapiens	oligophrenin-4	2067	100
806	G01731	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
807	Z24680	Homo sapiens	garp	1562	83
808	AF171669	Homo sapiens	glycoprotein-associated amino acid transporter LAT2	1364	90
809	W70321	Homo sapiens	Secreted protein CC198_1.	1154	96
810	W74843	Homo sapiens	Human secreted protein encoded by gene 115 clone HOVBA03.	855	99
811	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
812	AF092135	Homo sapiens	PTD014	862	100
813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	784	100
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone gn114_1.	358	100
817	G01082	Homo sapiens	Human secreted protein, SEQ ID NO: 5163.	549	100
818	AF151800	Homo sapiens	CGI-41 protein	1106	95
819	L00352	Homo sapiens	low density lipoprotein receptor	3980	100
820	X04434	Homo sapiens	IGF-I receptor	5832	99
821	G03844	Homo sapiens	Human secreted protein, SEQ ID NO: 7925.	572	100
822	AF212220	Homo sapiens	TERA	396	48
823	Y50125	Homo sapiens	Human glycoposphatidylinositol-anchored protein GPI-122.	4897	99
824	AF156778	Homo sapiens	ASB-3 protein	2675	98
825	AF096322	Homo sapiens	neuronal voltage-gated calcium channel gamma-2 subunit	1105	100
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded from gene 28.	1540	100
827	AB032013	Homo sapiens	potassium channel Kv8.1	2435	95
828	Y13620	Homo sapiens	BCL9	5284	96
829	Y91474	Homo sapiens	Human secreted protein sequence encoded by gene 24 SEQ ID NO:147.	541	98
830	X54232	Homo sapiens	glypican	1625	87
831	X14830	Homo sapiens	acetylcholine receptor beta-subunit preprotein	2540	100
832	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1002	100
833	G03873	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	638	96
834	AC003030	Homo sapiens	R29828_1	1389	93
835	Y38422	Homo sapiens	Human secreted protein.	964	87
836	U41557	Caenorhabditis elegans	glycine-rich	85	36
837	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	998	75
838	AJ011415	Homo sapiens	plexin-B1/SEP receptor	1580	60
839	W80398	Homo sapiens	A secreted protein encoded by clone cw1543_3.	1105	67
840	G00862	Homo sapiens	Human secreted protein, SEQ ID NO: 4943.	255	92
841	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
842	AF036717	Homo sapiens	FGFR signalling adaptor SNT-1	2629	99
843	Y73446	Homo sapiens	Human secreted protein clone yc27_1 protein sequence SEQ ID NO:114.	1089	100
844	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	357	69
845	AF151810	Homo sapiens	CGI-52 protein	1443	88
846	X83378	Homo sapiens	putative chloride channel	1620	99
847	AC004883	Homo sapiens	similar to general transcription factor 21; similar	655	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			to AF038969 (PID:g2827207)		
848	X99886	Homo sapiens	monocyte chemotactic protein-2	160	76
849	AC005587	Homo sapiens	similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)	963	98
850	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
851	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
852	Y86217	Homo sapiens	Human secreted protein HWIIGU54, SEQ ID NO:132.	1189	99
853	AF224741	Homo sapiens	chloride channel protein 7	3748	99
854	X17094	Homo sapiens	furin (AA 1-794)	3550	99
855	W78245	Homo sapiens	Fragment of human secreted protein encoded by gene 19.	1245	99
856	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	1926	100
857	Y41765	Homo sapiens	Human PRO1083 protein sequence.	3211	99
858	AF057306	Homo sapiens	transmembrane proteolipid	481	84
859	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone HLDRM43.	824	100
862	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived protein #375.	96	30
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	211	67
866	X54870	Homo sapiens	Type II integral membrane protein	1201	100
867	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
868	Y07894	Homo sapiens	Human secreted protein fragment encoded from gene 43.	388	88
869	J00123	Homo sapiens	preproenkephalin (1349	95
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:305.	1048	98
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	237	93
872	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	960	94
873	AF161382	Homo sapiens	HSPC264	1124	99
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573	96
876	M15530	Homo sapiens	B-cell growth factor	171	56
877	W63681	Homo sapiens	Human secreted protein 1.	1652	99
878	L27867	Rattus norvegicus	neurexophilin	1448	98
879	Y10835	Homo sapiens	Amino acid sequence of a human secreted protein.	321	100
880	W88991	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
881	AF118670	Homo sapiens	orphan G protein-coupled receptor	1971	100
882	AF208865	Homo sapiens	EDRF	528	100
883	Y18462	Homo sapiens	cathepsin L	209	72
884	Y94950	Homo sapiens	Human secreted protein clone dh1073_12 protein sequence SEQ ID NO:106.	348	100
885	AF070661	Homo sapiens	HSPC005	404	100
886	Y04315	Homo sapiens	Human secreted protein encoded by gene 23.	385	100
887	X92744	Homo sapiens	hBD-1	375	100
888	Y22496	Homo sapiens	Human secreted protein sequence clone cn621_8.	994	94
889	Y41293	Homo sapiens	Human soluble protein ZTMPO-1.	4595	99
890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	63
891	AF208856	Homo sapiens	BM-014	1012	99
892	U29195	Homo sapiens	neuronal pentraxin II	2002	98
893	X68149	Homo sapiens	Burkitt lymphoma receptor 1	1953	100
894	Y94914	Homo sapiens	Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	537	100
895	W61630	Homo sapiens	Clone HNFGW06 of EGFR receptor family.	326	63
896	M24110	Homo sapiens	G0S19-2 peptide precursor	481	100
897	Z68747	Homo sapiens	imogen 38	2018	99
898	AF186112	Homo sapiens	neurokinin B-like protein ZNEUROK1	619	100
899	AF225420	Homo sapiens	AD025	734	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
900	P60657	Homo sapiens	Sequence of human lipocortin.	1835	100
901	M27288	Homo sapiens	oncostatin M	1297	99
902	W85737	Homo sapiens	Polypeptide with transmembrane domain.	749	100
903	G01349	Homo sapiens	Human secreted protein, SEQ ID NO: 5430.	650	99
904	Y00261	Homo sapiens	Human secreted protein encoded by gene 4.	1133	99
905	AF039688	Homo sapiens	antigen NY-CO-3	771	99
906	AB007836	Homo sapiens	Hic-5	2544	100
907	AB017507	Homo sapiens	Apg12	224	100
908	AK000056	Homo sapiens	unnamed protein product	1537	98
909	Y86299	Homo sapiens	Human secreted protein HFOX55, SEQ ID NO:214.	427	100
910	AF231023	Homo sapiens	protocadherin Flamingo 1	7393	99
911	Y14134	Homo sapiens	Vascular endothelial cell growth inhibitor beta protein sequence.	1319	100
912	Z90420	Homo sapiens	Human GDF-3 (hGDF-3) polypeptide encoding cDNA.	1950	100
913	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	1361	100
914	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	48
915	U14971	Homo sapiens	ribosomal protein S9	886	90
916	AF172854	Homo sapiens	cardiotrophin-like cytokine CLC	1204	99
917	AC005525	Homo sapiens	F22162_1	1963	100
918	AF166350	Homo sapiens	ST7 protein	4711	99
919	Y87285	Homo sapiens	Human signal peptide containing protein HSPP-62 SEQ ID NO:62.	430	100
920	Y36131	Homo sapiens	Human secreted protein #3.	465	88
921	AF193766	Homo sapiens	cytokine-like protein C17	724	100
922	Y95013	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.	357	100
923	X75208	Homo sapiens	protein tyrosine kinase-receptor	5256	100
924	Y96202	Homo sapiens	IkkappaB kinase (IKK) binding protein, Y2H56.	813	98
925	AB039886	Homo sapiens	down-regulated in gastric cancer	785	78
926	G03368	Homo sapiens	Human secreted protein, SEQ ID NO: 7449.	55	50
927	Y48606	Homo sapiens	Human breast tumour-associated protein 67.	539	100
928	Y36151	Homo sapiens	Human secreted protein #23.	668	100
929	AF110399	Homo sapiens	elongation factor Ts	1666	100
930	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2763	99
931	Y73328	Homo sapiens	HTRM clone 082843 protein sequence.	931	100
932	G01959	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
933	U47924	Homo sapiens	B-cell receptor associated protein	1469	100
934	G03827	Homo sapiens	Human secreted protein, SEQ ID NO: 7908.	529	93
935	AB039371	Homo sapiens	mitochondrial ABC transporter 3	196	63
936	X56385	Canis familiaris	rab8	1064	100
937	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	117	44
938	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	1064	99
939	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	515	42
940	Y16630	Homo sapiens	Human Putative Adrenomedullin Receptor (PAR).	1904	99
941	AC005102	Homo sapiens	small inducible cytokine subfamily A member 24	627	99
942	M12886	Homo sapiens	T-cell receptor beta chain	1289	81
943	AF226046	Homo sapiens	GK003	1049	98
944	Y36078	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 463.	667	100
945	M22877	Homo sapiens	cytochrome c	565	100
946	W67869	Homo sapiens	Human secreted protein encoded by gene 63 clone HHGDB72.	551	93
947	W67859	Homo sapiens	Human secreted protein encoded by gene 53 clone HBMCL41.	283	100
948	W85726	Homo sapiens	Novel protein (Clone BG33_7).	789	100
949	AJ242015	Homo sapiens	eMDC II protein	4236	100
950	G04075	Homo sapiens	Human secreted protein, SEQ ID NO: 8156.	567	99

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
951	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog	1314	100
952	Y36111	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 496.	402	70
953	AB012109	Homo sapiens	APC10	990	100
954	AF246221	Homo sapiens	transmembrane protein BRI	1405	100
955	AF054986	Homo sapiens	putative transmembrane GTPase	1883	100
956	W74726	Homo sapiens	Human secreted protein fg949_3.	1879	100
957	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	1581	100
958	AJ222967	Homo sapiens	cystinosis	1920	100
959	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	587	100
960	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	283	100
961	AF151855	Homo sapiens	CGI-97 protein	1214	96
962	U26592	Homo sapiens	diabetes mellitus type I autoantigen	250	65
963	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	3796	100
964	AF078859	Homo sapiens	PTD004	2089	100
965	AB020315	Homo sapiens	homologue of mouse dkk-1 gene:Acc# AF030433	1466	100
966	X04571	Homo sapiens	precursor polypeptide (AA -22 to 1185)	6580	99
967	AF146019	Homo sapiens	hepatocellular carcinoma antigen gene 520	993	99
968	AF071002	Homo sapiens	minK-related peptide 1; MiRP1	632	100
969	AB021227	Homo sapiens	membrane-type-5 matrix metalloproteinase	3545	100
970	AF180920	Homo sapiens	cyclin L ania-6a	1579	100
971	AF105365	Homo sapiens	K-CI cotransporter KCC4	5621	99
972	AF083248	Homo sapiens	ribosomal protein L26 homolog	739	100
973	AJ132429	Homo sapiens	hyperpolarization-activated cyclic nucleotide gated cation channel hHCN4	6295	100
974	W61619	Homo sapiens	Clone HTPEF86 of TM4SF superfamily.	454	100
975	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
976	AF275948	Homo sapiens	ABCA1	11763	99
977	AB026891	Homo sapiens	cystine/glutamate transporter	2552	100
978	AF117657	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP80	3348	99
979	AF044201	Rattus norvegicus	neural membrane protein 35; NMP35	1570	92
980	AF119297	Homo sapiens	neuroendocrine-specific protein-like protein 1	1170	99
981	AF155652	Homo sapiens	potassium channel modulatory factor	1983	99
982	W88499	Homo sapiens	Human stomach carcinoma clone HP10412-encoded protein.	1553	99
983	Z56281	Homo sapiens	interferon regulatory factor 3	2012	98
984	AB026125	Homo sapiens	ART-4	2160	100
985	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	172	70
986	AB023888	Homo sapiens	b-chemokine receptor CCR4	1895	100
987	W27291	Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
988	AF153450	Manduca sexta	juvenile hormone esterase binding protein	226	32
989	G03697	Homo sapiens	Human secreted protein, SEQ ID NO: 7778.	194	88
990	AF204159	Homo sapiens	potassium large conductance calcium-activated channel beta 3a subunit	1486	100
991	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
992	AL031266	Caenorhabditis elegans	VM106R.1	327	40
993	Y66749	Homo sapiens	Membrane-bound protein PRO1124.	4730	99
994	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	141	77
995	AF133845	Homo sapiens	corin	5811	99
996	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	4999	100
997	W62066	Homo sapiens	Human stem cell antigen 2.	284	93
998	Y87173	Homo sapiens	Human secreted protein sequence SEQ ID NO:212.	725	100
999	Y13379	Homo sapiens	Amino acid sequence of protein PRO263.	1654	99
1000	Y95008	Homo sapiens	Human secreted protein v3_1, SEQ ID NO:56.	676	47
1001	AF190167	Homo sapiens	membrane associated protein SLP-2	1747	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1002	G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	398	96
1003	W73420	Homo sapiens	Human secreted protein encoded by Gene No. 24.	2150	100
1004	X12791	Homo sapiens	19kD SRP-protein (AA 1 - 144)	742	100
1005	M23323	Homo sapiens	membrane protein	642	100
1006	X63745	Homo sapiens	KDEL receptor	326	98
1007	Y35997	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO: 382.	824	99
1008	AB032918	Hylobates moloch	dopamine receptor D4	92	35
1009	Y91680	Homo sapiens	Human secreted protein sequence encoded by gene 81 SEQ ID NO:353.	1372	99
1010	AL136125	Homo sapiens	dJ304B14.1 (novel protein)	825	98
1011	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	379	98
1012	Y17531	Homo sapiens	Human secreted protein clone BL205 14 protein.	818	97
1013	G00724	Homo sapiens	Human secreted protein, SEQ ID NO: 4805.	462	100
1014	AF288092	Naegleria gruberi	haem lyase	114	37
1015	AB045292	Homo sapiens	M83 protein	3867	99
1016	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	644	100
1017	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
1018	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	589	100
1019	X83425	Homo sapiens	Lutheran blood group glycoprotein	3054	99
1020	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	100
1021	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.	768	100
1023	AE000660	Homo sapiens	hADV36S1	573	100
1024	AF132965	Homo sapiens	CGI-31 protein	1550	100
1025	W92380	Homo sapiens	Human TR-interacting protein S103a.	1466	97
1026	R66278	Homo sapiens	Therapeutic polypeptide from glioblastoma cell line.	830	100
1027	X65614	Homo sapiens	S100P calcium-binding protein	476	100
1028	Y41741	Homo sapiens	Human PRO704 protein sequence.	1323	100
1029	AJ001014	Homo sapiens	RAMP1	806	100
1030	W63682	Homo sapiens	Human secreted protein 2.	1354	99
1031	AK023007	Homo sapiens	unnamed protein product	766	100
1032	W97900	Homo sapiens	Human SR-BI class B scavenger.	2672	99
1033	Y82453	Homo sapiens	Human TGC-440 secretory protein SEQ ID NO:1.	639	99
1034	Y73473	Homo sapiens	Human secreted protein clone yd178_1 protein sequence SEQ ID NO:168.	752	93
1035	Y86468	Homo sapiens	Human gene 48-encoded protein fragment, SEQ ID NO:383.	96	90
1036	U09813	Homo sapiens	mitochondrial ATP synthase subunit 9 precursor	698	100
1037	AJ242832	Homo sapiens	calpain	3699	99
1038	X66403	Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
1039	AJ242730	Homo sapiens	polyhomeotic 2	1310	100
1040	AF169968	Mus musculus	DNA binding protein DESRT	1453	80
1041	X52563	Bos taurus	permeability increasing protein	383	29
1042	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	75	50
1043	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	60	53
1044	M94582	Homo sapiens	interleukin 8 receptor B	1850	100
1045	AL080239	Homo sapiens	bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))	1704	50
1046	AF125101	Homo sapiens	HSPC040 protein	580	100
1047	W74809	Homo sapiens	Human secreted protein encoded by gene 81 clone HMWDN32.	176	100
1048	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	2201	100
1049	W88667	Homo sapiens	Secreted protein encoded by gene 134 clone HAIBP89.	1559	99
1050	AF097518	Homo sapiens	liver-specific transporter	2820	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1051	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1052	Y21851	Homo sapiens	Human signal peptide-containing protein (SIGP) (clone ID 2328134).	1643	95
1053	AL163815	Arabidopsis thaliana	putative protein	661	62
1054	Y76200	Homo sapiens	Human secreted protein encoded by gene 77.	262	100
1055	AJ276567	Homo sapiens	TC10-like Rho GTPase	1160	100
1056	Y27620	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
1057	D14530	Homo sapiens	ribosomal protein	745	100
1058	AF132000	Homo sapiens	TADA1 protein	1132	100
1059	AL031778	Homo sapiens	dJ34B21.1 (novel BZRP (benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)	920	100
1060	AF227135	Homo sapiens	candidate taste receptor T2R9	134	33
1061	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
1062	Z11697	Homo sapiens	HB15	1088	100
1063	AF123757	Homo sapiens	putative transmembrane protein	819	100
1064	AF155135	Homo sapiens	novel retinal pigment epithelial cell protein	2932	99
1065	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
1066	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	2575	100
1067	Y36087	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 472.	770	85
1068	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	301	100
1069	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	301	100
1070	W64535	Homo sapiens	Human leukocyte cell clone HP00804 protein.	2014	99
1071	X03145	Homo sapiens	pot. ORF III	148	50
1072	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	821	91
1073	X82200	Homo sapiens	gpStat50	249	62
1074	G03213	Homo sapiens	Human secreted protein, SEQ ID NO: 7294.	99	47
1075	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	506	55
1076	G03187	Homo sapiens	Human secreted protein, SEQ ID NO: 7268.	424	98
1077	L25899	Homo sapiens	ribosomal protein L10	332	76
1078	Y91447	Homo sapiens	Human secreted protein sequence encoded by gene 48 SEQ ID NO:168.	898	97
1079	G01862	Homo sapiens	Human secreted protein, SEQ ID NO: 5943.	290	89
1080	AB039723	Homo sapiens	WNT receptor frizzled-3	1376	92
1081	AB020527	Homo sapiens	Na/PO4 cotransporter homolog	269	100
1082	L13802	Homo sapiens	ribosomal protein small subunit	499	80
1083	W75098	Homo sapiens	Human secreted protein encoded by gene 42 clone HSXB125.	143	81
1084	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	83	51
1085	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88	43
1086	AF090942	Homo sapiens	PRO0657	124	64
1087	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	129	41
1088	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	126	36
1089	AF140631	Homo sapiens	G-protein coupled receptor 14	364	82
1090	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	114	32
1091	S72304	Mus sp.	LMW G-protein	146	83
1092	W88708	Homo sapiens	Secreted protein encoded by gene 175 clone HEMAM41.	405	100
1093	W85612	Homo sapiens	Secreted protein clone fh123_5.	4358	97
1094	Y53012	Homo sapiens	Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30.	1013	99
1095	Y92345	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-62.	409	100
1096	AF090942	Homo sapiens	PRO0657	147	60
1097	L24521	Homo sapiens	transformation-related protein	166	58
1098	X56932	Homo sapiens	23 kD highly basic protein	490	70
1099	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	35
1100	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	149	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1101	AF119851	Homo sapiens	PRO1722	183	72
1102	G04086	Homo sapiens	Human secreted protein, SEQ ID NO: 8167.	207	62
1103	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	91	52
1104	X74856	Mus musculus	ribosomal protein L28	128	69
1105	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	130	62
1106	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	48
1107	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	69	43
1108	AF039942	Homo sapiens	HCF-binding transcription factor Zhangfei	744	99
1109	AF201951	Homo sapiens	high affinity immunoglobulin epsilon receptor beta subunit	738	94
1110	AF111108	Mus musculus	transient receptor potential 2	223	79
1111	AF119900	Homo sapiens	PRO2822	144	59
1112	Y16589	Homo sapiens	A protein that interacts with presenilins.	265	39
1113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	178	67
1114	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	164	63
1115	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	1217	99
1116	X51394	Xenopus laevis	APEG precursor protein	130	40
1117	M27826	Homo sapiens	neutral protease large subunit	442	65
1118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	72	60
1119	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	491	97
1120	Y35906	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 155.	244	97
1121	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	65
1122	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	110	90
1123	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1124	AF212862	Homo sapiens	membrane interacting protein of RGS16	442	88
1125	W64469	Homo sapiens	Human secreted protein from clone CW795_2.	191	53
1126	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	154	100
1127	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
1128	Y84320	Homo sapiens	Human cardiovascular system associated protein kinase-1.	815	99
1129	G02105	Homo sapiens	Human secreted protein, SEQ ID NO: 6186.	88	73
1130	Y32923	Homo sapiens	Transmembrane domain containing protein clone HP01512.	700	100
1131	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	260	91
1132	Y91644	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:317.	525	96
1133	Y91449	Homo sapiens	Human secreted protein sequence encoded by gene 49 SEQ ID NO:170.	542	100
1134	AB017908	Homo sapiens	4F2 light chain	2399	93
1135	X51760	Homo sapiens	zinc finger protein (583 AA)	312	55
1136	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	917	72
1137	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
1138	AF155106	Homo sapiens	NY-REN-36 antigen	768	91
1139	AL031055	Homo sapiens	dJ28H20.1 (novel protein similar to membrane transport proteins)	117	50
1140	AF011359	Bos taurus	regulator of G-protein signaling 7	138	96
1141	Y70018	Homo sapiens	Human Protase and associated protein-12 (PPRG-12).	623	100
1142	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	38
1143	AB030235	Canis familiaris	D4 dopamine receptor	89	48
1144	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	539	88
1145	X99962	Homo sapiens	rab-related GTP-binding protein	398	96
1146	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	168	79
1147	G03712	Homo sapiens	Human secreted protein, SEQ ID NO: 7793.	512	85
1148	Y28279	Homo sapiens	Human G-protein coupled receptor GRIR-1.	705	76
1149	U13642	Caenorhabditis	exon 5 similar to transmembrane domain of S.	247	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>s. elegans</i>	cerevisiae zinc resistance protein		
1150	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	117	62
1151	G01003	Homo sapiens	Human secreted protein, SEQ ID NO: 5084.	181	80
1152	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	198	63
1153	X88799	Oryza sativa	DNA binding protein	95	41
1154	D85245	Homo sapiens	TR3beta	155	96
1155	R74272	Homo sapiens	Tumour suppressor protein, p53.	341	87
1156	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.	99	41
1157	G02577	Homo sapiens	Human secreted protein, SEQ ID NO: 6658.	263	98
1158	AF104334	Homo sapiens	putative organic anion transporter	185	42
1159	G01393	Homo sapiens	Human secreted protein, SEQ ID NO: 5474.	173	57
1160	W75771	Homo sapiens	Human GTP binding protein APD08.	224	81
1161	AF216833	Homo sapiens	M-ABC2 protein	410	83
1162	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1163	AF119851	Homo sapiens	PRO1722	230	70
1164	Y87252	Homo sapiens	Human signal peptide containing protein HSPP-29 SEQ ID NO:29.	113	31
1165	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	82
1166	AF269286	Homo sapiens	HC6	134	64
1167	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	149	51
1168	D90789	Escherichia coli	Dipeptide transport system permease protein DppC.	411	90
1169	R63783	Homo sapiens	TG0847 protein.	344	90
1170	Y45274	Homo sapiens	Human secreted protein encoded from gene 18.	478	98
1171	D64154	Homo sapiens	Mr 110,000 antigen	347	96
1172	AB026256	Homo sapiens	organic anion transporter OATP-B	311	67
1173	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	60	52
1174	D87717	Homo sapiens	similar to human GTPase-activating protein(A49869)	178	59
1175	M64716	Homo sapiens	ribosomal protein	391	78
1176	R08330	Homo sapiens	Human IL-7 receptor clone H6.	285	67
1177	L06505	Homo sapiens	ribosomal protein L12	242	72
1178	AJ251885	Homo sapiens	organic cation transporter (OCT2)	276	88
1179	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	155	71
1180	G01207	Homo sapiens	Human secreted protein, SEQ ID NO: 5288.	282	90
1181	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	249	62
1182	AF161524	Homo sapiens	HSPC176	138	90
1183	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	282	66
1184	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	71
1185	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	88	69
1186	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	118	46
1187	AB032905	Hylobates concolor	dopamine receptor D4	96	37
1188	G00956	Homo sapiens	Human secreted protein, SEQ ID NO: 5037.	292	78
1189	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	178	79
1190	G03361	Homo sapiens	Human secreted protein, SEQ ID NO: 7442.	324	76
1191	AF117755	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP230	187	70
1192	Y70455	Homo sapiens	Human membrane channel protein-5 (MECHP-5).	202	67
1193	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	99	42
1194	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	192	76
1195	W29661	Homo sapiens	Homo sapiens C1542_2 clone secreted protein.	2001	98
1196	Y14104	Homo sapiens	Human GABAB receptor 1d protein sequence.	239	69
1197	X61972	Homo sapiens	macropain subunit iota	149	90
1198	G00534	Homo sapiens	Human secreted protein, SEQ ID NO: 4615.	145	51
1199	Y86260	Homo sapiens	Human secreted protein HELHN47, SEQ ID NO:175.	1089	89
1200	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	154	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1201	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	404	50
1202	M27826	Homo sapiens	neutral protease large subunit	202	49
1203	Y73424	Homo sapiens	Human secreted protein clone yi4_1 protein sequence SEQ ID NO:70.	265	61
1204	AF264014	Homo sapiens	scavenger receptor cysteine-rich type I protein M160 precursor	625	98
1205	Y36203	Homo sapiens	Human secreted protein #75.	219	59
1206	U78111	Gallus gallus	AQ	205	57
1207	AF095448	Homo sapiens	putative G protein-coupled receptor	416	76
1208	AF116715	Homo sapiens	PRO2829	127	75
1209	AF099137	Homo sapiens	MaxiK channel beta 2 subunit	475	95
1210	AF205718	Homo sapiens	hepatocellular carcinoma-related putative tumor suppressor	423	79
1211	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	224	70
1212	G00719	Homo sapiens	Human secreted protein, SEQ ID NO: 4800.	117	44
1213	G01009	Homo sapiens	Human secreted protein, SEQ ID NO: 5090.	351	73
1214	AF090942	Homo sapiens	PRO0657	124	70
1215	Y14427	Homo sapiens	Human secreted protein encoded by gene 17 clone HSIEA14.	99	77
1216	G03905	Homo sapiens	Human secreted protein, SEQ ID NO: 7986.	173	57
1217	Y57897	Homo sapiens	Human transmembrane protein HTMPN-21.	1173	100
1218	J00194	Homo sapiens	hla-dr antigen alpha chain	454	78
1219	Y59709	Homo sapiens	Secreted protein 76-28-3-A12-FL1.	470	92
1220	W81576	Homo sapiens	EBV-induced G-protein coupled receptor (EBI-2) polypeptide.	725	100
1221	W96745	Homo sapiens	High affinity immunoglobulin E receptor-like protein (IGERB).	650	98
1222	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 160.	135	31
1223	Y00278	Homo sapiens	Human secreted protein encoded by gene 21.	260	95
1224	AF161422	Homo sapiens	HSPC304	568	90
1225	U14970	Homo sapiens	ribosomal protein S5	202	95
1226	G01733	Homo sapiens	Human secreted protein, SEQ ID NO: 5814.	610	100
1227	AF099973	Mus musculus	schlafen2	333	56
1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	155	81
1229	AF217188	Mus musculus	YIP1B	801	63
1230	AF176813	Homo sapiens	soluble adenylyl cyclase	275	100
1231	X98333	Homo sapiens	organic cation transporter	1704	100
1232	W74955	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	212	53
1233	Y94940	Homo sapiens	Human secreted protein clone yi62_1 protein sequence SEQ ID NO:86.	526	100
1234	U76618	Mus musculus	N-RAP	482	82
1235	AF044924	Homo sapiens	hook2 protein	380	97
1236	G01459	Homo sapiens	Human secreted protein, SEQ ID NO: 5540.	417	100
1237	AF000018	Homo sapiens	adapter protein	164	84
1238	W88633	Homo sapiens	Secreted protein encoded by gene 100 clone HE8EU04.	250	90
1239	W29660	Homo sapiens	Homo sapiens CH27_1 clone secreted protein.	697	98
1240	AF004161	Oryctolagus cuniculus	peroxisomal Ca-dependent solute carrier	154	52
1241	Y92710	Homo sapiens	Human membrane-associated protein Zsig24.	709	97
1242	Y95002	Homo sapiens	Human secreted protein vc34_1, SEQ ID NO:44.	908	88
1243	Y44905	Homo sapiens	Human potassium channel molecule ERG-LP2 partial protein.	325	100
1244	AF284422	Homo sapiens	cation-chloride cotransporter-interacting protein	511	97
1245	Y53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	1888	93
1246	AB039371	Homo sapiens	mitochondrial ABC transporter 3	389	97
1247	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	168	39

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			ID NO. 160.		
1248	AF072509	Rattus norvegicus	glutamate receptor interacting protein 2	559	90
1249	AF247042	Homo sapiens	latter pore domain potassium channel TRAAK	661	98
1250	B08974	Homo sapiens	Human secreted protein sequence encoded by gene 27 SEQ ID NO:131.	1087	97
1251	L15313	Caenorhabditis elegans	putative	858	59
1252	Y29338	Homo sapiens	Human secreted protein clone it217_2 alternate reading frame protein.	278	75
1253	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	211	92
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 7155.	294	83
1255	G01818	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	253	91
1256	AF286368	Homo sapiens	eppin-1	222	54
1257	AF220264	Homo sapiens	MOST-1	87	93
1258	G02227	Homo sapiens	Human secreted protein, SEQ ID NO: 6308.	281	78
1259	Y07970	Homo sapiens	Human secreted protein fragment #2 encoded from gene 26.	81	94
1260	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	986	100
1261	AF140674	Homo sapiens	zinc metalloprotease ADAMTS6	172	36
1262	U28369	Homo sapiens	semaphorin V	237	67
1263	Y07049	Homo sapiens	Renal cancer associated antigen precursor sequence.	288	71
1264	Y36153	Homo sapiens	Human secreted protein #25.	187	80
1265	Y78114	Homo sapiens	Human cytokine signal regulator CKSR-2 SEQ ID NO:2.	723	93
1266	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	191	100
1267	AF030558	Rattus norvegicus	phosphatidylinositol 5-phosphate 4-kinase gamma	859	95
1268	U73167	Homo sapiens	candidate tumor suppressor gene LUCA-1	159	96
1269	AF190664	Mus musculus	LMBR2	552	76
1270	AL050332	Homo sapiens	dJ570F3.1 (homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP)	820	98
1271	G02126	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	131	95
1272	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	253	92
1273	AL035661	Homo sapiens	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	1280	100
1274	AF064748	Mus musculus	S3-12	3523	61
1275	D17554	Homo sapiens	TAXREB107	377	78
1276	Y30715	Homo sapiens	Amino acid sequence of a human secreted protein.	643	90
1277	AF146760	Homo sapiens	septin 2-like cell division control protein	707	100
1278	Y05069	Homo sapiens	Human PIGR-2 protein sequence.	281	46
1279	X59668	Oryctolagus cuniculus	aorta CNG channel (rACNG)	267	85
1280	G01051	Homo sapiens	Human secreted protein, SEQ ID NO: 5132.	489	98
1281	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	120	43
1282	AF055084	Homo sapiens	very large G-protein coupled receptor-1	1635	100
1283	AF117814	Mus musculus	odd-skipped related 1 protein	357	98
1284	U87318	Xenopus laevis	NaDC-2	535	60
1285	AF061346	Mus musculus	Edp1 protein	452	68
1286	AB030182	Mus musculus	contains transmembrane (TM) region	582	68
1287	A13595	synthetic construct	immunosuppressive protein PP15	185	97
1288	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1	837	100
1289	AF084205	Rattus norvegicus	serine/threonine protein kinase TAO1	319	98

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1290	AF038563	Homo sapiens	membrane associated guanylate kinase 2	523	100
1291	AF034837	Homo sapiens	double-stranded RNA specific adenosine deaminase	468	100
1292	M15888	Bos taurus	endozepine-related protein precursor	937	87
1293	AB010692	Arabidopsis thaliana	ATP-dependent RNA helicase-like protein	636	45
1294	AF209923	Homo sapiens	orphan G-protein coupled receptor	1570	100
1295	W67828	Homo sapiens	Human secreted protein encoded by gene 22 clone HFEAF41.	504	98
1296	AC004832	Homo sapiens	similar to 45 kDa secretory protein ; similar to CAA10644.1 (PID:g4164418)	648	65
1297	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	575	70
1298	G02645	Homo sapiens	Human secreted protein, SEQ ID NO: 6726.	223	97
1299	Y59440	Homo sapiens	Human delta3 fragment #4.	122	32
1300	W70504	Homo sapiens	Leukocyte seven times membrane-penetrating type receptor protein JEG18.	459	81
1301	Y67315	Homo sapiens	Human secreted protein BL89_13 amino acid sequence.	3916	99
1302	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	174	96
1303	G01331	Homo sapiens	Human secreted protein, SEQ ID NO: 5412.	254	69
1304	G01491	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	747	99
1305	AF148509	Homo sapiens	alpha 1,2-mannosidase	602	98
1306	G01658	Homo sapiens	Human secreted protein, SEQ ID NO: 5739.	333	98
1307	Y90899	Homo sapiens	D1-like dopamine receptor activity modifying protein SEQ ID NO:1.	332	98
1308	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	348	52
1309	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	147	66
1310	AF063243	Bos taurus	ribosomal protein L30	296	90
1311	AF224494	Mus musculus	arsenite inducible RNA associated protein	688	70
1312	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	1154	100
1313	Y99419	Homo sapiens	Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.	1145	78
1314	AF116667	Homo sapiens	PRO1777	433	97
1315	W75100	Homo sapiens	Human secreted protein encoded by gene 44 clone HE8CJ26.	807	97
1316	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	789	100
1317	AB041533	Homo sapiens	sperm antigen	2607	98
1318	U19617	Mus musculus	Elf-1	806	92
1319	U82598	Escherichia coli	ferric enterobactin transport protein	768	100
1320	D90892	Escherichia coli	SORBITOL-6-PHOSPHATE 2-DEHYDROGENASE (EC 1.1.1.140) (GLUCITOL-6-PHOSPHATE DEHYDROGENASE) (KETOSEPHOSPHATE REDUCTASE).	709	100
1321	W67847	Homo sapiens	Human secreted protein encoded by gene 41 clone HPBCJ74.	601	92
1322	AJ276101	Homo sapiens	GPRC5B protein	466	93
1323	AJ276101	Homo sapiens	GPRC5B protein	504	97
1324	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1584	100
1325	U91561	Rattus norvegicus	pyridoxine 5'-phosphate oxidase	1277	89
1326	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1606	100
1327	Y32206	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2825826.	1531	90
1328	AF151048	Homo sapiens	HSPC214	657	85
1329	Y10530	Homo sapiens	olfactory receptor	1645	100
1330	AF180681	Homo sapiens	guanine nucleotide exchange factor	4314	99
1331	AF111856	Homo sapiens	sodium dependent phosphate transporter isoform NaPi-3b	3591	99
1332	Y13583	Homo sapiens	G-protein coupled receptor	2171	100
1333	AF078866	Homo sapiens	SURF-4	1395	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1334	Y25755	Homo sapiens	Human secreted protein encoded from gene 45.	1380	96
1335	AF152325	Homo sapiens	protocadherin gamma A5	4742	99
1336	X74070	Homo sapiens	transcription factor BTF3	639	81
1337	AF095927	Rattus norvegicus	protein phosphatase 2C	1931	95
1338	G03877	Homo sapiens	Human secreted protein, SEQ ID NO: 7958.	621	100
1339	AL008582	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	626	100
1340	X61615	Homo sapiens	leukemia inhibitory factor receptor	5820	99
1341	Y01519	Homo sapiens	A carcinogenesis-inhibiting protein.	7528	97
1342	AF207600	Homo sapiens	ethanolamine kinase	2372	100
1343	U54807	Rattus norvegicus	GTP-binding protein	1167	97
1344	AC020579	Arabidopsis thaliana	putative phosphoribosylformylglycinamide synthase; 25509-29950	3283	51
1345	Y28576	Homo sapiens	Secreted peptide clone pc503_1.	944	100
1346	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFH61.	1171	100
1347	M55542	Homo sapiens	guanylate binding protein isoform I	2636	87
1348	AF183428	Homo sapiens	28.4 kDa protein	1329	100
1349	U70669	Homo sapiens	Fas-ligand associated factor 3	167	24
1350	AF295530	Homo sapiens	cardiac voltage gated potassium channel modulatory subunit	562	99

TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
1	1351	A	2	337	1	TPSLIHQAPTPCPAGLWG/PPNGHYHGS*PGC HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAAGRLPGPAWSWHASGAAPA QPGL*LLVPGSSGLPDRDP
2	1352	A	27	100	366	IRNSSIRPMKERETKLSAKHMITCSASYDIRGL QIETTYHHTPIRMAKIQT/GHHQC**ECGAT GTLIHGWGWCKVVEPLGKTVWQIPK
3	1353	A	40	3	314	HASAHASVVLKDNSELEQQLGATGAYRARA LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVDTHRTPI*R SCNYTLALILFL
4	1354	A	74	2	292	TASALFSCPDGGSAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQARQSPG*RTNPE/ALQWVLPVSDGWH VLPLP
5	1355	A	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRIASHP NAGGEVSNGPKRKLTLMLNFSPLSSGLNAGA FYALSTLLNRMVIVHYPGEEVNAGRIGLTVI AGMLGAVISGIWLDRSKTYKETILVVYIMDT GGAWWCYTFYLTGDTG*CFITAGTMGFF MTGYLPLGFFAVELASYPESEGISSGLLNISA QVFGIIFTISQGOIDNYGTPGNIFLCVFTLG AALTAFIKADLRROKANKETLEN
6	1356	A	81	97	376	EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A YLRVPFIRILLNAR*IRKAYKRMSLEIKLLI/RE *CLFQEMGLSLQWLYSARGDFFRATSL
7	1357	A	93	2	872	TLSSACLIQDAWKELTVAGAVSNQLLVWYP ATALADNKPVPADRRISGHVGIFSMYSLESK GLLATASEDSRVRIWKGGLRVPGGRVQNG HCFGHSARVWQVKLLNYLISAGEDCVCLV

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						WSHEGEILQAFRGHQGRGIRAAHERQAWV ITGGDDSGIRLWHLVGRGYRGLG/DLGSLLQ VP*ARYTQGCDSGWLLATAGSD*YRGPVSL *RRGQVLGAAARG*TFPVLLPAGGSSWSRGL RIVCYGQWGRSQCGCPHQHSNCCCQDPVVS WEGAQLELGPWL
8	1358	A	106	3	350	FSSLLSGRISTLRDETGAILEDGPAACAPIIKF LLTEELHLRGVSIYVLRHEAQIYGITPLVICAL LI/CRRL*SDSCMRAALNDRGLYQVLLDGLV QCLGFVDSDSRKMVSTLT
9	1359	A	115	49	186	QAWAIFKKGKYKEGDTGGPAVWKTRLRCALN KSSEFNEGFERERMDV
10	1360	A	123	2	1249	KGCRTOEKVDRTEVIRTICINPVYSKLFTVDFY FEEVQRLRFEVHDISSNNHGLKEADFLGME CTLGQIVSQRLSKSLLKHGNTAOKSSITVIA EELSGNDDYVELAFNARKLDDKDFFSKSDPF LEIFRMNDATQQLVHRTEVVMNLSPAWK SFKVSVNSLCSGDPDRRLKCIWWDWDSNGK HDFIGEFTSTFKEMRGAMEGKQVQWECINPK YKAKKKNYKNSGTIVLNLCKIHKMHSFLDYI MGGCQIQFTVAIDFTASNGDPRNSCSLHYIHP YQPNEYLKALVAVGEICQDYDSDKMFAFGF GARIPPEYTDSDFAINFNEDNPECAGIQGVV EAYQSCFPKAPTFTGPTNICPHSSRKVAKFRR SEGN*HQGRAFAIFILVDPGQVGVYSQDMGP DNPGGHFV
11	1361	A	147	614	9	ACARKQLLGRVFIWVFGQLLGGELKGYSKT NTTSSRPASSRGVTLSSSSSSSLTKDALPSSL KSDSTTITSGLVFPRSLCVNPAKSSVSESVSSI KILLSVVKYLE*KRTSCCFDSSSEKLSQLSS DERVSMGTSSRKPTNSSSLGALKMSATS*G SGSESPTPFFLTGLQSPSTRPREPLTTARN TTLTRDC
12	1362	A	177	12	416	LIPSEPALDSLVDPRVRSRKQPFVIYVYDTAI DTKIHFSLLDGNVGEFDMASAGFCFNHKAAM VLFLDRVYGEVQDFLLHLEGGFLPLDRAA ASLDT/AEIGAMDFLS*LFTLCLMMFFFIYPI NLLTMNVY
13	1363	A	249	535	105	WTFHRHLSAPLIVCDQGTCCVVSYPQNIQV MPDQTMEQGLN/HLFLDGA*PHSVECYCPS TFEIAIKITSFVLYFHRYRAPEVLLRSSVSSPI DVWAVGSIMAEYMLRPLFPGTSEVDEIFKIC QVLGTPKKVSTLVPKLL
14	1364	A	254	572	201	YLLTXIGNLMMLLVINADSLRTXM*FFLGH FFFLDICYSSVTAQDAAEFPVS*KPILVWGYYT *SFFFIFSWGTCCLLSAITYACYAAICPLLS TMVMNRPLCTATVNATNKMGLNSQVN
15	1365	A	257	425	68	THAKFLNKKFNIPKLVLFPKLVYIVKAIPTKM AIEFLLECDQNTKLCICENT*KNIKNI*KRRV TFTPIET*HPVQMIK WQ*LTAWLRNRGYKKI KQTPNSETAPSVCRNLVFDKCG
16	1366	A	263	104	481	FCIFRTTEEDRGDDCVSVVWTKQRNNSCVK SKDVFSKPVNIFWALEESVLGVKARQPKPFA AGNTFEMTCVSSKNKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV
17	1367	A	298	68	208	RKRTNPNIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM
18	1368	A	300	904	1	LVVGITGRHHARVIFLIVETGFPHVGQAGL ELLTSGDPPALASQSAGITGMSCARPKGHFG

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						IHLK*MFYTMSQKMP*PTNLILLIIPGNLNI KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR WK*DY*C/LQEVTDPIMEKCKKKKRTASFFK GQPHQSTNALLRRCVR*RYHLS/TVETAGLP* KNTGHIHPGQPFLLFKLVFKC*NVICI**QYKW*Q NIGVKNKSF CPH*SSSPSL*FIGHHSRNF/CSFK TEPHSVVQAGGQWRNLSLQAPPPGLMPLSR ISLMSSWDYRRPPO
19	1369	A	302	3	445	NSPSRWAKIQMFEHTFCG*GCG/ER/NVHIHCS WICRLRPLL WRAVREYLSKLKNAELSFDPGV SLLRIYAIMPTS*DEKEALLFAFLAFHE*HC KSRIWAVIQ/CIHLWDWLRKL*CFHRMKFYA AV*NKPRHLLSHIWKDVQNILLK
20	1370	A	304	1	1339	FFFCQKEVPLFEQNKHPGRATTSPGA/HARA LLSAGEFTAGVGLSP*AIHSFVWLCTFIQHGA GGPCHQPGGSPGPMHTTQAGHL WEGAYPG GSSTWHQVPGQLGGSWGPRERSLLGSFIKCS CPHPPGFRLLWMSNPQKPTENPGVMGRVWR LMPGESPLIWEAEGKEDHLSPEGQGHSE/PVA PLHSSLGNTVKP*PKNQKPKQNRSRHGGV MAGQQQSRPAAR*PPCPALTPASHSAGTWPP RICRTVPGGPCPSPSGFRSCR*GFS*TRSWP DAEPPSTPDTAPRCCTQSDTSSQGPQ*S*WRR CRALPGRLCSAPAAGLRARPRLESRRGNP PASPAASARCPSPWGPSCPARPPSRPAAGTEP AAPSRCATWLRGEREPGRPPGRRPRSGRGP VSFAPEVLSLPAVRQTKSWRWRNEEITRPW ALVRSRGG
21	1371	A	326	799	1587	GSQVLPPPSQDSATLPQDA*GPRAAFGQFVC E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCLP HLSFSPRQGAAPDTEPSAWGPAFTGATGPGLP LRHVRLFSAGAPRGAATPCPALLHGPWPP ARPMFRGHPPVRPLGPWGKVAAGPRALCLA GVPAVQGECAKPSG*GL*PAHLRGPPGPEVL QWHWQLSAGRDPVPAEDPPL*EGPLGPGGPA AAQAEFGADPEPEDKDQAESRPAGAMSLSA QSGSPVGGQGLR
22	1372	A	327	146	652	PHLENPHFHSFPGAPLT*STLSWSILSPREPSP GAPCYPGHPHLENPHLEHLLTWRTVTWSTLL PGAPCYPEHPHLEHPLTWSTPHLEHPSGPEPL SCRTPTRSILHRDHPLP*CLSTEEPI*GWGSLP APPSTPLVLDVAPPGPQPASSCPGRDSCYSVP GTVVSP
23	1373	A	348	397	2	CIVSSCQGTRKPCHELEDANKINKQSPTEKIES LQESL*VKQ*LIVAEKYVQILHPRKKYFORPL NNEKRKMKKRKEKKKCRERMQRRSKWRR EEKKE*REEEERKKEKEDRKERRKETSPRG SRLLRD
24	1374	A	362	170	352	GRALDTAAGSPVQTAHGLPSDALAPLDDSM WEGRTTAQWSLHRKRHLARTLLVSRVRGPQ
25	1375	A	384	373	128	YLITITLETGYLWKNRHSQ*KRTENPERDQH KYPKVDCKSNSMKNLCKNKHWTNWIFTD KKINLNLKPHTKLTPNIKK
26	1376	A	397	383	165	EVKNTNPFIFSGTNLTWIRSI*RKSDENQRTK *MEKYSISLDRRLNTVKMSFLPNLYKFNITSI KIPANF
27	1377	A	406	103	380	KSKATGYMVNI*KLIVFLYANDEQLEIEMNK IVPFGSKNKLAFTNLTKYQNIQNRHAENYKI LVNKIEDLNKWRNVLLSWIGRRNIINTMT

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28	1378	A	408	14	427	TICTNKFNNLDEIK/FLERHKL SKLTQEEVENL ITLKTSRETEL VINK*VIPHKEKPGPDSFTGEF YQTFKEEL/ILHLKLFQITKYGRILPNSVYETSI TLKPKPEKDLAKENYRPLPLSNIDAKVLNKTALA NRI**HIR
29	1379	A	434	395	128	IYSKMCMERQRLNN*ILKKNKVRGLAVPDVK VYYKPTVIK/TSWL*KDSHIVEWNRLENLEID PN/IKRLILDKGAEATEWRKDSFFRQWQ
30	1380	A	455	2	228	FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS SWDYRYAPPRP/ANF*FLVETGFFYYVAQAGL KLLSPGDLPALAS
31	1381	A	462	393	2	QLMFDKGVKNIH/WGWTPTPTK*YWKNIWISI CRRMNLNPYLSRYIKINSR/KDLTVRPEIKLV EENTGKTIQDTGLGK*FIKTSKAQSTKTKN* KRQTRYIKLKVKKSTASKENNRVKRQPLE*EK IFAN
32	1382	A	474	125	471	VKPYELA VFLVKPIEYK*HLLSDPAIPLSGI*LK EIKAYT/RRICTPMFAAPVSVIA/RN*KQSK/CQ KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT ILRETDRIHKTTYDVISLI
33	1383	A	488	1825	2	KSACSFICSEEQPASPSFLKPGTYASETRPRDP HAAGPRRDSSEAE TRRPRGA/DGSGTVVKGT PGSPAPPCSWGHGGVETEGAG*CPAAPGTDLR APGGSAGS*GLPSAGGSRGRKGWRAAGRQP STR*GRPGRHGGROE*AGHPEPRQSALQSAG L/ASSPEPMGAALAE DSGDSRGAGPRPQE*P PSVLSRS/SGS*G*G*AASGTASSPRSHSRLGPP SAGFHGLRCGQPPFAAAPPGPWGTGRPAGG AGSPAAAGTAPPATRG AQSRQRNRTAGRNA SPQTAAGAGSPVQWALS RATG*TGETGSWC AGGTHQATHLTAAWVCPTTWSVRPGSGPA AGLGR*GRHPAQSPPLVFRG*PAWPQEAPSP SPASSEVALSSGSCWPDQAPGARGSPAPLA PAWPAAGRGRQR*GRQSAHPPRR*STAVSL SGTS*WRRSP*AGTRTQCC*SPWLVPACSSRP L*RGTRRPSTQSPQTGTGTPRSAGPHPRS* GGRSPAGTGHLGAQTVASPH*GHWPTALSCL WASASPPGPEAPPQTGACIGTNCRYRAASAR RSSVAPACA*GWQ*AGSPPAVLRGPP*RVRRER GALTHRPRAPDE
34	1384	A	497	422	2	APGASVGRAQAAEG*RGGPTGRPPSALGVSE AGRAGRAGEGRPVPPAYPLCKSAQTS GPPKA RLS/PLASCGGRGPPGGAACATCAPPAGPAR SSRCRRRSPPE*GPR*PSRPARPSGSAASRRQ KLTPCRCQFRGLCA
35	1385	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN LTELVAVTDENIVGLFAALLAERRVLLTAS KLSTLTSCDHAFCALLYPMRWEHVLITLPPH LLDYC*CPPLPRT
36	1386	A	512	3	1631	FFFSFVCHLYCVSPTPGPHGRLATWL/PGLLA FLGLAAGQTLCPAGELPGHARAQASGAPGS VLIAVPGRRRVHTCGPGPAAPSTRGECPPPAL GHTRPARPRPVFPAPAVPOEPGGQGHGAA/P PATGHSAPRGCPPARAAPTGSATPAPPPAACAA AFHSAWSVPPAGRQCG*RVPAFAFRRTTPTGT PGQHLLDRPGAPPAQSGGPAPAPPPRLAGPA GPAAPPPGPPAASWHSSLSKSSSL/GWSPPLP VGPGSLQ*TPPPQGPLSGSCGGTSSWRGQR AAVARRLRSWNACGLSRVAGRSSASYPGRE

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						GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD GPGHPASTWLRAGKTGPSPPACGCA*LPPPS VSAAPQSPRTRCPRGCAAAAGLCVLAAGAS HGA\GLPGVRVHTQRVHIIH*GAG/GCQTPRPR LRSLPVLGLPAPRCPVSAHPWHRRSGSSCHA ARLVPRHPAPGCP**TG*PLITGFPEP*A*GLP NHQAVGLEASGALQAGHRDELPTMVQLLDH SPDYPLKGRPHAP
37	1387	A	620	828	1	FRLLAAGA/RGAAEPRVAVSMAPDPSAKIH WEASPEMQSKCHQKGNQTECFNHVRFLQ RLNSTHLYACGTHAFQPLCAIDAFAFTLPTS FEEGKEKCPYDPARGFTGLIIDGGLYTATRYE FRSIPDIRRSRHPHSLRTEETPMHWLNG*EDE AQDDGG*GTISSFLPWPADHPTPKSPGEPVH SIPVCCQVRGQPSGGKESACLKSLSNCLTH DAEFVFSVLVRESKASAVGDDDKVYFFTE RATEKESGSFTQSRSSHRVARGIFPL
38	1388	A	739	1	427	FRAMVSSTLKLGISLNGGNAEVQ/QGNRGKG TSEEGKEG*EVPV*LPVSPPLPRPLQKMLDYL KDKKEVGFFQSIQALMQTC\GEKVMADDEFT QDLFRFLQLLCEGHNDFQNYLRTQTGNTTT INIICTVDYLLRLQESI
39	1389	A	767	1	1030	TLDTGPLLGGVPNVFKDFRGNRQFGGCM RNLSDVGKNVDMAGFIANNGTREGCAARRN FCDGRRRQNGGTCVNRWNMYLCECPLRFGG KNCEQGEWPASSIPPVTAWEALLLDVPGTT VRGLHIQVRQPLVVYAAFTVDSHRPLQETVL RRAPAPASGVSPSGVGWDR*AGPAEPSPTIP ATVHSVPWYLGMLFRTRKEDSVLMEATSGG PTSFRQLQVTGAPCHQGT*VGARGRDPMLSG LRVTDGEWHLLIELKNVKEDSEMHLVTM TLDYGMDOVSWHLHLLWG*TLFPAQKGTGA SEDKVSVRRGFRGCMQVRGCGGRGEACPS QAAPRL
40	1390	A	801	69	399	IHKIIHKEDLNKWKYILCSGMRSLSTMIPVV PQIYKFNA*QVILKFTW*E*GAKITLRKNKL RGLVLVPLSTC*VKYLLDKVLPHIKTYEAR VNKSVVLVQVTIM
41	1391	A	835	7	195	SMLKERVQFPSCLEFFQYITWLGPYPHVLF SSVINFSIGAK*DLQSVMNCLYAKRIPCVT
42	1392	A	841	1	415	GSTHASGYDKTPDFILQVPVAVEGHIHWIES KASFGDECSHHAYLHDQFWSYWSNLKHRTW QGIGTVASNLSQL*TLNAPFPELLFRSLARTG FVLT*TRFGPGLVIYWGFIQELDCNRERGILL KACFPTNIVTL
43	1393	A	845	358	92	PALSPAPVPQKKGSPPLDPCLGPSWLLSVG LGWPRP*PRRGPDGSLPATPPLTPPHILLP QRPMLPFSHAGLARPPPEPISVP
44	1394	A	853	452	1	LPQYCFPPRLSPKSKLVKHSAL**PSALKPPTK SPRCIPRTSLYFTICC/PPALQLSPIDPPAIYRS PPTHMLRSASQPLNQAPTLVKGHPPSRFLQG QVSCFPQPTLPREKPLPLHLRPPRPAQPPLPR PLTFSTRNVDPPIPERFR
45	1395	A	894	379	162	GVYPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTL*PQTSFVICFSIGNLEFIYGT WLSMSMGK
46	1396	A	900	1	366	TTKKTLSNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLPR VFLFHQLNIT**CLHFFITMTIFAIFFSFLGR

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						D/KSLAMLPRLVSNWPQVILPP
47	1397	A	944	162	2	QLQNLASRGCL*SQLLRRLRRENRLNPGGGG CSEIAF/CTPAWVTQRDFFRKKK
48	1398	A	963	216	308	HFTPDRIAIVKNTRDSDHCWRGC*EEGAPARC
49	1399	A	967	466	1	PRKRESW/GERLP/PRGFFPAEDAPAGWK GRKHASRTARAHVFHPIRQSIRSPVGRPGDP RAAHTRSAGTRLQCKASRGG*GKGPAATR*E GGPGSAPAPLPASSGCSLFPDSSPWTPPPAPG AAAAQP**TPRCPAALRAGAHIGRVGRPY
50	1400	A	973	45	421	EKCIQALDVFVFCYIDHSSHCLMSCD*E/DQA LNFMPLEMEPKMSKLAFCGQRSSTSDDDSGC ALEEYAWVPPGLRPEQIQLYFACLPEEKVVPY VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLSE E
51	1401	A	992	2095	194	IRIRHEAARSCLGCAAGHVPAAGLRLPLTVRG PPGRRGPAAPGCVCY*SGESTFVSHVFORMA WPGSAPPRGFHPLQSQTSPTDVTSSPQLSKEE DGPWEHPLSSSL*SLGQAGGNH*QPEELAG WEPRGPPSLAPSSPT/TMWTALVLIWIFSLSL ESHAASNDPRNFVFNKMWKGLVKRNASVET VDNKTSSEVTMAAASPVTLTKGTSAAHLNS MEVTTEDTSRTDVSEPATSGVAADGVTSIAPT AVASSTTAASITTAASSMTVASSAPTTAASST TVASIAPTTAASSMTAASSTPMTLALPAPTST STGRTPSTTATGHPSLSTALAQVPKSSALPRT ATLATLATRAQTVATTANTSSPMSTRPSPSKH MPSDTAASPVPMPRQAQGPISQVSDQPVV NTINKSTPMPSNTTPEPAPTPTVVTITKAQAR EPTASPVPVPHTSPIPEMEAMSPITQSPMPYT QRAAGPGTSQAPEQVETEATPGTDSTGTPRS SGGTMKPAATDSCQSTQGOYMV/DHH*APHP GRGRQNSPGGAVTRGDPFHSLGFVCPAGL *ELQEEGLHPGGLLNQRDVCGLRNVRGAGA WREAWPLPRPFLPLRPNQVLPNSFGAIEEIC QMLKHI
52	1402	A	994	1	462	ESGEFLVSFTLKKPTNVFHHINGMKFFNK/LIF *SHTDIAFYKIQHPFMLKALTQWA*EGT*PDR RYLH*SLRLNGEQLKTFPLRSGMR*G/CAILPL VLNAMLSIVPAVVPAGKTRHEKEITCPLIGQE EK*FS*FVGDMNTCVENKESKILLE
53	1403	A	1011	1	630	PEVIQQSAYDSKADIWSLGTIELAKGEPNS DMHPMRVLFIPKNNPPTHCWRRLESFKEV *LMLA*TKDPSNRPTAKELLKHKFTVKNKKT SYLTELIDRFKR WKAEGHSDDSDSEGSSES TSRENNTHPEWSFTTVRKKPKVQNGAEQ DLVQTLSCLSMIITPAFAELKQDENNASRNQ AIEELEKSIAVAEAAGPG
54	1404	A	1016	1	222	ISIDA*KAFDKIQH/CFMITTLKKLGIDGKYLN TIKAIDDRHTVSTILNVEKLKAF*RSQTRQRF PISGSGARI
55	1405	A	1033	3	366	HASVDGDEGSDDVYYYYPAILRELQALNTA EAAEHRPEEDRMLSEDPWPAHMIKGYMPL HNIPHTEVIDVTGLNQSHLYQHNLKGTMPKT QKRAALYTWVLEQLEILRQINQQSHGPG
56	1406	A	1044	5	429	SVTLTQTRSPSKPLSRKLMDEWVVSRSISE DRLETQSRASRSPVTPNQSQETPVDGKPLAL PPNQSQKNIRYHIHYLHLQYYLDRHISATLPI SSSGIPTPIAVITDALTDLVELLGQPCSEESGR APGTLFLLAL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
57	1407	A	1050	11	430	GAYAFETNGFPIMLVLTDDKIEGVDVGIAGLYD MHNSLPMAFLRLVRCSTSYIPVTHVLTSTPV TCLRRREKDGIVVDVLTASDASNHNGFPVEEH ADDTHPARLQGPILRSQPMGPLKHKAFFERA NLGLVQRRRLLED
58	1408	A	1058	258	419	LKHRDTPVVGANNRALSCTPLTSLTLCALCPL PCLGCPTXATCRLYQTTVAUVF
59	1409	A	1064	3	425	KAFSFTTSLIGHQRMHTGERPYKCKEKGKTF KGSSSLNNHQRIHTGEKPYKCNCGRAFSQC SSLIQHRIHTGEKPYECTQCGKAFTSISRLSR HRIHTGEKPFHCNECKVFSYHSALIIHQRIH TGEKPYACKDVGK
60	1410	A	1065	204	419	GGPPGPFLAHTHAGLQAPGPLLAPAGDEGDL LLAVQQSCLADHLLTASWGGK/DPIPTKALG EGQEGPLTV
61	1411	A	1079	3	383	RHSRAHLCQPFHLVMDLLQLGQDIPQGCYH LEENHLIHRDIAARNCLLSCAAPTRAATIGDF GMARYTYRTRYQGLDRAL/LPRKWMPPEAL LEGIFTYNTDSWTFGVLLWEIFSLGYMPYPGR TN
62	1412	A	1080	1	859	VVEFLWSRRPSGSSDPFRPRPASKCQMMEER ANLMHMMKLSIKVLLQSALSLSGRSLDADHA PLQOFFVVMCHLKHGLKVKKSFIGNKSF GPLELVEKLCPEASDIATSVRNLPKLTAVGR GRAWLYLALMQKKLADYLVLDNKHLLSE FYEPEALMEEEGMTVIGLLVGLNVLDANLA CLKGEDLDSQGVDFSLYLKDVQDLDDGKE HERITDVLQKNYVEELNRHLSCTVGDLDQTK IDGLEKTNKQLQERVSAATDRICSLQEEQQQL REQNELIR
63	1413	A	1083	2	615	SSFAKHKRIHTGEKPFICLCEGKAFTSSTTLTK HRIHTGEKPYTCECOKAFRQSAILYVHRI HTGEKPYTCGCGKTFRQSANLYAHKKIHTG EKPYTCGDCGKTFRQSANLYAHKKIHTGKPK YKCKEKGKAFKSYYSILKHKRTHTRGMSYEG DEC/QRSLN/RSSILSNHKKIHNEEK/PLKCKE KAFNHTSICCRHKKN
64	1414	A	1084	946	1	KKQDLSSSLTDDSKNAQAPLALTESHLATLA SSSQSPFAIKQLDLSGLPSLLVRLASFCSHIS SSESIAQSIDISQDKLRRHHVPOCNKMPITAD LVAPILRFLTEVGNSHIMKDWLGGSEVNPLW TALLFLLCHSGSTSGSHNLGAQQDQCKISFS FFSWLTGTLTQRTAENATVAFPLQCNCS HPNNQKLMAQVLCFLQTSFQRGNLPTSGNI SIGFIRLRLFLQMLEDEKVTMFLQSPCLYKG RINATSHVIQHPMYGAGHKFRTLHLPVSTTL SDVLDVSDTPSITAKLISKQKDDKKKK
65	1415	A	1087	103	324	PRAFEFVHTEMIVG/RVQNIHLFTLVLEDRAL LFTMSVGSSLWSTYLHVMALP/DRELLKPNA SVALHKLNALV
66	1416	A	1095	3	493	HETCSVTHIVSFLPFLNPSHPASTPGHTENEQ PSLVWFDGRGKFLTFEGSSRGPSPLTMGAQD TLPVAAAFETETVNAFYKGADPSKCIKVTGE MVLSEFAGITRHFANNPSAALTFRVINFSRLE HVLNPNQLCCDNTQNDANTKEFWVNMNPNL MTHLK
67	1417	A	1098	57	356	LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYVFLDLCCSDILRSAICFPFVFNVSVKNGST WTYGTLTCKVIAFLGVLSCFHTAFMLFCISVT

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						RYL
68	1418	A	1106	1	1326	MGKISATGINMGTKCSWALVWHLESYDPKH YEREGMQDWKTASGQSEEAQQSSQKQPH YTTYQSSSFLKYSSSESHLLAWRENSSEGSFQF PGRSRARPPRTROQRRGAAAGPGRGAVRLG HPQSAAPQLRAAARIPESPAAPQPRPGSA RNSDASGPAASLRTLGASSPFPQAPDVTAP SPAALAPRAAGGSRAAALAGAEAEELRTL APRPTRAAAFPPPPPPPLPPGAPPPVRCVSR RARAPPWR/PAATGPPPARPVAPSRKLGSARAP APALQIRKGTSSGLPGRGGSGPGNNLSSVA GNWRGSSFAVERPGMAKYQGEVQSLKLDLDD SVIEGVSDQVLVAVVVSFALIATLVYALFRNV HQNIHPENQELVRVLEQLQTEQDAPAAATRO QFYTDMYCPICLHQASFPVETNCGHLFCGSLT PNSIW
69	1419	A	1107	2	466	FDTARLHEFGTSITQIFAVDNREDLQKWMEA FWQHFFDLQWKHCCELMKIEIMSPRKPLF LTKEATSVYHDMSIDSPMKLESLTDIIQKKIEE TNGQFLIGQREESLP/SS/CGPHSLMVTIKWSS RKRY/SYPASEPLHDEKGGKROAPLPSPDK
70	1420	A	1111	698	23	ALRRLHYVRATKVFLSFRPFWREEHIEGGH SNTDRPSRMIFYPPREGALLASYTWSDA AFAGLSREEALRLALDDVAALHGPVVRQLW DGTGVVVKRWAEQHSQGGFVVQPPALWQT EKDDWTVPYGRIFYAGEHTAYPHGWVETAV KSALRAAIKINSRKGPASDTASPEGHASDMEG QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL QNTHTIRTS
71	1421	A	1119	2	385	QKQTLQNGYLDSSMDILYLGSLPPELQVSSDE PPGPPEQAGLSQFHLEPETQNPETTEEIQSSLQ QEAAAQLPQLPEVVELSSTKAIEAPALPSQSL EGVHSSTEQKAPAQQLPAFEELAPLIIHE
72	1422	A	1127	1	906	HAQVVGPPYRLEKTLGKGQTLVKLGVCIT GQKVAIKIVNREKLSVLMKVEREIALRLI EHPHVLKLGHYENKKYFPPDELTSGPSMLA QVSPHGKLSARRSWDLLSQFPYLVLEHVSQ GELFDYLKKGRLTPKEARKFFRQIVSALDFC HSYSICHRDLKPENLLDEKNRIADFGMAS LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLE KVKRGVFMHPHFIPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS
73	1423	A	1128	1	802	LRNALDVLHREVPRVLVNLVDLNFNTIMRQV FLGNPDKCPVQQA/MLEPLGSKTETLDRAE MPITCPTQNEPFLRTPRNSNYTIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSDLPTSWRGLSWSIG GDGNLEHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAEAGARARMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE
74	1424	A	1139	60	480	FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCVEVAIPCCKGAHSGVLKGLWLLAQG VLGMRDITPQEHPESTPDLCFCRDPEEIEVE EQPAADAAVAKGEF/QGEQIAPVPAIIAAHPE AADPAPVHTTAHPKGA
75	1425	A	1147	2	413	PFPHQHPQEPKGCWQPSALRGQCQPPVLGV TTTSDLCSLQVPVSSHRNPLDLAAYDQEGR

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						RFDNFSSLSIQWESTRPVLASIEPELPMQLVSQ DDESGQKKLHGLQAILVHEASGTTAITATAT GYQESHLSAR
76	1426	A	1155	38	410	PIISAPAQDDPILLSFIHCLHANLLCVWRRDVK PDCKEIWFWWGDEPNLVVQYIMNCMLWK KDSGKMAFFPMNVGRC/FFKEIHNLRLCLMD KNFVLIGKWFVRPYKDEKPVNKSEHLSCAF T
77	1427	A	1162	526	350	RFPQGLDVSITYPVILIEELSRGWSEELQGV LRGNLLRVFRQVEKVQEENKWSQPLED
78	1428	A	1171	1	1293	MAESASPPSSSSAAAPAAEPGVTEQPGPRSP SSPPGLEPLDGDAPHVPHDLAPIAFFCLRQT TSRPNWCIMVCNPNWFECVSMVLVLLNCVTL GMYQPCDDMDCLSDRCKILQVDFDFIFIFA MEMVLKMVALGIFGKKCYLGDTWNRDLFFI VMAGMVEYSLDLQNNLSAIRTVRVLRPLKA INRVPSMRILVNLLDITLPM LGNVLLLCFFVF FIFGIHVQLWAGLLRNRCFLEENFTIQGDVAL PPYYQPEEDDEMPFICSLSGDNGIMGCHEIPP LKEQGRECCSKDDVYDFGAERQDLNASGL CVNWNRYYNVCRTGSANPHKGAINFDNIGY AWIVIFQVITLEGWVEIMYYVMDAHSFYNFI YFILLIIVSVREPGLLGGSFSTAQSPKCQGDSPF GVAESLLLRGWVWLWLPGGG
79	1429	A	1175	1	405	PNDFFKDMFPDLPGGPLGPIKAENDYGAYLN FLSATHLGGFPWPVLEERKLKPKASQQCPI CHKVIMGAGKLPRHMRTHITGEKPYMCTICE VRFRQDKLKIHMRRKHTGERPYLCHICNAKF VHNYDLKNHMR
80	1430	A	1182	25	198	EMNELSQQLSQGGRGASQCPSPPAPTLPNPT PLCQLQLQRVNTGLTPPCHPGAGAA
81	1431	A	1186	254	583	KTVLVDVGAGTGILSIFCAQAGARRVYAVEAS AIWQQAREVVRFNGLDRVHVLPGPVEIVEL PEQVDAIVSEWMGYGLLHESMLSSVLHARTK VVKDGGFFLPXSSELFM
82	1432	A	1187	2	716	DFVDAARNLPLESTKSPAEPKSVSPSLEDPRA SSQGLPSQGPVQNGRRGEQRPKKF/TVIQT SSFESDSLEQPSGLEGEDKPLAQFSPPPAPH GRSAHSLQPKLVRQPNIQVPEILVTEEDRPD TEPEPPKPEKTEEFQWPQGSQTLAQFPVEK LPPKKRLGLAKMAQSSGESSFESSVPLFRSP SQESNVSLSGSSRSALFERDDHGKAEAPSPSF DMGPKPLGTHMLTV
83	1433	A	1188	517	804	ESPGLSKVLRTGAFAYPFLFDNLPLFYRLGLC WGRGHGCCQALSTSHGYHLFCALLTGFLFA SHLPERLAPGRFDYIGHSHQLFHICAVLGTHT Q
84	1434	A	1192	45	476	LGDVGFVVVERTPVHEAAQRGESLQLOQLIES GACVNVQTVDSITPLHAASLQGAQRCVQLLL AAGAQVDARNIDGSTPLCECLRLGQHRVCEA LAVLRGQGPSPVHSPVARGHLHREFRMC* GFLFDVGXNLEAHEFHGEP
85	1435	A	1194	69	410	KRSEEAAPPFPPLGGTGAAPTRASLPEQILLPR SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ HRLVSPVHPGRRGSSPGVAECKLTSAYFT GRSPCPSLPGTTRTNSLL
86	1436	A	1215	3	405	LPSHTCONPGRLPNIGIQGGSTFNLGDKVRYSC NLGFFLEGHAVLTCHAGSENSATWDFPLPSC RADDACGGTLRG/AEWHHLQPPLPLG/ATKN

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						NADCTWTLAELGDTIALVFIDFQLEDGYDFL EVTGTEGSSLW
87	1437	A	1216	226	964	GTARFGPMVGFGANRRAGRLPSLVGLVLLV VTVVLAFFNYWSISSRHVLLQEEVAELQGGVQ RTEVARGRLKRNSDLFAVVGHAQETDRPEG GRLPPQQAAGQGRPREEMEDDKVKLQNN ISYQMADIHHLKEQLAELRQEFRLQEDQLQD YRKNNTYLVKRLEYESFQCGQMKELRAQH EENIKKLADQFLEEQKQETQKIQSNDGKELDI NNQVVPKNIPKVAENVADKNEEPSSNHPHG
88	1438	A	1218	1	534	PEFGTTISCGYLMATDVSRSPSVHKAVEIEQE RVKSAGAWIHPYSDFRFYWDLIMLLLMVGN LIVLPVGITFFKEENSFPWIVFNVLSDTFFLLD LVNFRGTGVVEEGAEILLAPRAIRTRYLRTW FLVDLISSIPVDYIFLVLELEPRLDAEVYKTAR ALRIVRFTKILSLLRL
89	1439	A	1223	1	743	MGFDEVFMINLRRQDRRERMLRALQAQIE CRLVEAVDGKVGMLTRSNAAPGRHMLAMLET LVVVAAPRFVDADNLILNPDTLSELLAENKTVV APMLDSRAAYSNFWCGMTSQGYKRTPAYI PIRKDRRGCFVPMVHSTFLIDLKKAASRNL VAFYPPHPDYTWSDDIIVFAFCKQAEVQMY VCNKEEYGFPLPVPLRAHSTLQDEAESFMHVQ LEVMPVSSPSSAQSMVVSADHIGLVISYL
90	1440	A	1227	2	349	NKTSFIFYLKNIVVADLIMTLTFFPRIVHDAQF GPWDFKFLCRYTSVLFYANMDTSIVVLGLIT/ YDRY/WKVVRHL/WDSWMTGI/SFTRVYLLG LGARLVWFGKLLAKGGHGGISWL
91	1441	A	1245	3	1937	LGSSDVRAPOSELGAESPSRMVASQAYNLT SALTPILTRSRVLNNEEPLTAGFSRAPANLSD VVQLIFLVDNPNFFFGYISNYTVSTKVASMAF QTQAGAQPPIERLASERAITVKVPNNSDWAAR GHRSSANSVIVQPAQFVAVVTLDSNPAAV LHLQLNYTLDDGRYLSEEPYLAAYLHSEPR PNEHNCASRRIRPESLQADHRPYTFISPPT RDPVGSYRLNLSSHFRWSALEVSVGLYTSLC QYFSEEDVVWRTEGLLPLEETSPRQAVCLTR HLTAFGTSLVPPSHIRFVFPEPTADVNIYVML TCAVCLVTYVMMAAILHKLDQLDASRGRAIP FCGQRGRFKYEILVKTGWGRSGTTAHVGIM LYGVDSRSGHRHLDGDRAFHRNSLDIFQIATP HSLGSMWKIRVWHDNKGSLPAWFLQHIIVRD LQTARSTFFLVNDWLSVETEANGGLVEKEVL AASKASFRVPTPSAALLRFRRLVAELQRGF FDKHIWLSIWDPRPSRSCFTRIQRATCCVLLICL FLGANAVWYGAVGDSAYSTGRVSRLNPLSV DTVAVGLVSSVVVPVYLAILFLFRMSRSKV GWGWGPGSTGNGAWASAPCEPPLSSAAAR GKGVHQRLLGKQHT
92	1442	A	1246	5	562	VFDEENILNELNDPLREEIVNFNCRKLVAATMP LFANADPNFVTAMLSKLRFEVFPQGDYIREG AVGKKMYFIQHGVAAGVITKSSKEMKLDGGS YFGEICLLTKGRRASVRADTYCRLYSLSD NFNEVLEEYPMRRAFETVAIDRLDRIGKKN SILLQKFQKDLNTGVFNQENELKQIVKH
93	1443	A	1249	180	901	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPASSPMVSSAHNP KAEIPERRKDSTSTPNLPPSMMTRNTYVCT ERPGAERPSSLNPKENSSGTPRVPPASPSHS

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						LAPPSGERSRLARGSTIRSTFHGGQVRDRRAG GGGGGGVQNGPPASPTLAHEAAPLPAGRPRP TTNLFKLTSLKLTTRVADERIGGPEVTRRP RQEDHLSPPGGRGCSEL
94	1444	A	1261	3	385	KFSQWGLTKPKLSNAP/WISLVKKLMKKWS VTQNLTFREQLEAGIRYFDLRVSSKPGDADQ EIYFIHGLFGIKVWDGLMEIDSFLTQHPQEIIFL DFNHFYAMDETHHKCLVLRQEAFGNKLCPA CR
95	1445	A	1282	2	550	GPRDNPGEPRFEIVEHFHGIWFTFELVARFA VAPDFLKFFKNALNLDLMSIVPFYITLVVNL VVESTPTLANLGRVAQVLRMLMRIFRILKLARH STGLRSLGATLKYSYKEVGLLLL YLSVGISIFS VVAYTIEKEENEGLATIPACWWWATVSMIT VGYGDVVPGT TAGKL TASACILA
96	1446	A	1294	1	1456	QLLPPSNRENAGLLVGRCLCSAALRPVGDLLT SSGQVAVRNAPQAGSAKAGKGFQDNFEFIQ YFKKFFDANCNEKDYNPVAAGQGOETEVA SIVAPVLNKNPQCPEGYICVKAGRPNPNYGYT SFDTFSWAFLSLFRLMTQDYWENLYQLTLRA AETTYMIF/LV/LVILLGSLYLVTLLAV/VAMA YEEQNQATLEAEQKEAEFQQMLEQLKKQQ EAAQQAATATASEHSREPSAAGRLSDSSSEAS KLSSKSAKERRNRKRKQKEQSGGEEKDED EPQKSESEDSIRRKGFRRSIEGNRLTYEKRYSS PHQSLLSIRGSLFSPRRNSRTSLFSFRGRAKDV GSENFADDEHSTFEDNESRRDSLFPVRRHGE RRNSNLSQTSRSSRMLAVFPANGKMHSTVDC NGVVSLVGGPSVPTSPVGQLPEVIIDKPADT DNGTTTETEMRKRRSSSFHVSMDFLEDPSQR QRAMSLASILTNTVE
97	1447	A	1295	2	2057	IQTQLPTKSSQQLRKGONCVRCKMQMNFIAE EVLLKYRITFYNNKGNMPLYIEIKAFVHFMI NRYLSYSGGPKRFPLVDVLQYALEFASSKPV CTSPVDDIDASSFPGSIPSQTLPTTIEQQGALS SELPSTSPSSVA AISRSVIHKPFTQSRIPDL MHPAPRHITTEELSVLESCLHRWRTEIENDTR DLQESISRIHRTIELMYSDKSMIQVPYRLHAV LVHEGQANAGHYWAYIFDHRESRWKMYNDI AVTKSSWEELVRDSFGGYRNASAYCLMYIN DKAQFLIQEADLIKTGQPLVGIELPPDLRDFV EEDNQRFEEKELEWDAQLAQKALQEKLLAS QKLRESETSVTTAAAGDPKYLEQPSRSDFSK HLKEETIQTITKASHEHEDKSPETVLQSAIKLE YARLVKLAQEDTPPETDYRLHHVVYFIQNO APKKIEKTLLEQFGRNLSFDERCHNIMKVA QAKLEMIKPEEVNLEEEYEWHDYRKFRETT MYLIGLENFQRESYIDSLFLICAYQNNKELL SKGLYRGHDEELISHYRRECLLKLNEQAAELF ESGEDREVNNGLIIMNEFIVPFLPLLVDMEEE KDILAVEDMRNRWC SYLGQEMEPHLQEKLT DFLPKLLDCSMEIKSFHEPPKLP SYSTHEL CER FARIMLSLSRTPADGR
98	1448	A	1304	118	453	SGPSSRAIYLHRKEYSQNLTSPTLLQHRVEH LMTCKQGSQRVQGPEDALQKLFEMDAHGRV WSQDLILQVRDGLWLQLLDIETKEELDSYRLD SIQAMNVALNTCSYNSILS
99	1449	A	1306	3	1660	CGYFCHTTCAPQAPPCPVPPDLLRTALGVHPE TGTGTAYEGFLSVPRPSGVRRGWQRVFAALS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DSRLLLFDAPDLRLSPPSGALLQVLDLRDPQF SATPVLASDVIHAQSRDLPRIFRVTTSQLAVPP TTCTVLLAESEGERERWLQVLGELQRLLLD ARPRPRPVYTLKEAYDNGLPPLPHTLCAAILD QDRLALGTEGLFVHILRSNDIFQVGECCRRVQ QLTSPSAGLLVVLGCRGPSVRLFALAELENI EVEVPKIPESRGCQVLAAGSILQARTPVLCVA VKRQVLCYQLGPGPGPWQRRIELQAPATVQ SLGLLGDRLCVGAAGGFALYPLLNEAAPLAL GAGLVPEELPPSRGGLGEALGAVELSLSEFL LFTTAGIYVDGAGRKSREGHELLWPAAPMGW GYAAPYLTVFSSENSIDVFDVRAEWVQTVPL KKIVRPLNPEGSFLYGTKEVRLTYLRNQLAE KDEFDIPDLTDNSRRQLFRTKSKRRFFFRVSE EQQKQQRREMLKDPFVRSKLISPTNFNHLV HVGPAANGRPGARDKSP
100	1450	A	1318	918	190	SLCVPGPVDGTGFAVMSVMVGSVTESLAPQA LNDSMINETARDAARVQVASTLSVLVGLFQV GLGLIHFGFVVTYLSEPLVRGYTTAAAVQVF VSQKLYVFGHLSSHSGPLSLIYTVLEV CWKL PQSKVGTVVTAAGVAVVVLVVKLLNDKLLQ QLPMPPIGELLTLIGATGISYGMGLKHRFEAG PPVAPNTQLFSKL VGSAFTIAVVGFAIAISLGK IFALRHGYRVDSNQVWVMRDV
101	1451	A	1353	220	445	DWPDLFITYPLIGSPKCFQSARPEIRMYRRTVR SSHGNHALQEVLP RSGHGTEFTKQKHLEAAD HGHPPARMSIFSR
102	1452	A	1363	542	2	AHLLMLNLALVTDLLVLTSLPFLIHYASGEN WIFGDFMCKFIRFSHFNLVSSILFLTCFSIFRY CVIIHPMSCFSIHKTRCAVAVACAVVWISLVA VIPMTFLITSTNRTNRSACLDLTSSDELNTIKW YNLLTAALLCLPLVIVTLCYTTIHTLTHGHAN VDSCLKQKARRLTLLL
103	1453	A	1371	2	410	CHTSESSDFILPGDYLLGGLCPHSGCLQVC SFNEHGYHLFQAMRLAVEEINNSTALLPNITL GYQLYDVCSDSANVYATLRVLSLPGQHIEL QGDLLHYSPTVLA VIGPDSTNRAATTAALLSP FLVPMLEQ
104	1454	A	1376	3	432	NSRVEDRS/NMSLWTQNTVCPVRNVTRDGG FGPWPWPQCEHL DGDNSGSLCRARSCDSP RPRCGGLDCLGPAIHLANCSRNGAWTPWSSW ALCSTSCGIGFQVRQSCSNPAPRHGGRICVG KSREERFCNENTPCFVPIF
105	1455	A	1379	2	396	GLGLLYLIFAAVEGVMRVIGGSNHLAVVLLD IILAVIDSIFVWFIFISLAQTMKTLRLRKNVVF SLYRHFKNLIFAVLASIVFMGWTTKTFRIAK CQSDWMERWVDDAFWSFLFSLILVIMFLW RPSA
106	1456	A	1383	1	432	EDGHGGWSSRCLVDHAEEGHREPWKRLCTW QRGGEHIFAFYFPGHPLSPQICLAPETPPRG CPPVSSLHFISLQ/RLPRDCQELFQVGERQSG FEIQPGSPFLVNCKMTSGTFWTCRTDSRVF QANPNSNAHSEDQPTP
107	1457	A	1386	719	558	FFFVTRSHSVAQAECGVTFAHRSLLDVGSSN YPALSLQSSWDHRHTWLIFAF
108	1458	A	1397	631	2	RVAISLLCAAIFISFMVQSAGKRWPTGVMLM VVVLFALYSWPIQALLPTYLKTDLAYNPHT VANVLSFSGFGAAVGCVCV/GGFLGDWLGTRK AYVCSLLASQLLIIPVFAIGGANVWVLGLLLF

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						FQQMLGQGIAGILPKLIGGYFDTDQRAAGLG FTYNVGALGGALAPIIGALIAQRLDLGTALAS LSFSLTFVVILRNRRPGKSLVR
109	1459	A	1402	15	387	VLVALPDTVTSETVVTEVLGHRVTLPCLYSS WSHNSNSMCWGKDQCPYSGCKEALIRTDGM RVTSRKSAYRLQGTIPRGDVSILTNPSESDS GVYCCRIEVPGWFNVDKINVRNLQRASTT
110	1460	A	1421	3	350	HEDLSSLLTRGSGNQERERQLKKLISLRDWM LAELAFPGVLTCA*SLISC*YCVILFPCSCF FFHSPDALFSLLLSCYFPYCYFFYYLFFSSPL CLLLASSPFPLFILLASL
111	1461	A	1426	2	344	FTSTMTPFEKESEQA*ATLAFGAQTSTTAD QCALKPDLSYLNNSSSSSTPATSGGGIFGSS TSSSNPPVATFVPGQSSDPVSSYGFVNTAESST SDSLFSQDSKLATTS
112	1462	A	1434	46	372	TTSWTTSCTRSCT*SGASSGPGWTPRTTWWR SRRSSQRTCSRACSGAWSRTW*RSS*TSSSSC STSCSSSSSRSCGRPGGPLGARGVHITSCLNSC MSSSTTSSTSTF
113	1463	A	1439	3	292	HEDIMTHYDRLVDE*ALNAGKQRYEKMISG MYLGEIVRNILIDFTKKGFLLRQJSEMLKTR GIFLTFLLSNFLIVCVLLFYVSFYLFQSCINFL
114	1464	A	1463	1	396	KQQAVPEPHSSTTTPQEQQNWWYQDILLNLQ QRTKVHLPGHKTGPAVAKDTPEPVKKEFTVP ATSQGP*SPFSEEPPLPPSNEEVPTLP*EPQS EDP*KNA*LKQMHAATTHWQQHQHQVGC QYHGIMQ
115	1465	A	1464	291	2	AGSYPSMVWSCHWGVTOKRRAL*VVSFEEG GRRKCGQYWPLEKDSRIRFGFLTNSNLGVEN MNHYYKSTLEILNPEVNPFFFFLTLWKQGEN NYCN
116	1466	A	1465	667	337	LPPQORPA*TDSYSTCNVSSGFLAQSHNIHLQ YWTQYQVWVWLQHFLDTNQLDANCIPQEF DINGEHLCSMSLQEFTRAAGTAGQLLYSNLQ HLKWNGDSLFLCLSLPC
117	1467	A	1479	1	381	GTSGGPKRVLVTERFPWQNPVNRGQAQR VLGPNNSFQRPVLQAQKLVSCHKPQGNQKHK QLQATSVHPVCMPLNNTQSKQPLPSAPEN NPEELASDPNNEESL*RPWALEDFEIGRPLG KKG
118	1468	A	1485	3	385	TYLWL*GNPPFYEKNDGGLFELILRAKDEFNS PYWDDMSDSAKHFIRPLTGRDP*KFPDQPL QHPWIEGHTCLDNNHQAASEPNNNFAESKR NLAFLATGVVRHMRKLFMGANLEGPGPTVS H
119	1469	A	1486	1	398	GTTSKHH*LARSLIRGPFDDHDLKPAATRDQL NIIVSYPTKQLTYEEQDLGWKFRYYLTNQE KALTCKFLKVVNWDLQPEAKQALELLGKWK PMDVKDSLELLSSHYTNPTVRRYAVARLQA DDEDLLMYL
120	1470	A	1497	3	999	MGESPAV*GYFVLAGMNSAGLSFGGGAGKY LAEWMVHGYPSENVWELDKRFGALQSSRT FLRHRVMEVMPMLMYDLKVPHWDFQTGRQL RTSPLYDRDLAQGARWMEKHGFERPKYFVP PDKDLLALEQSKTFYKPDWFDIVESEVKCK EAVCVIDMSSFEFETSTGDQALEVLQYLF NDLDVPVGHIVHTGMLNEGGGYENDCSIALR NKRSSFMSPTDQQVHCWAWLKKHMPKDSN LLEDVTWKYTALNLIGPRAVDVLSLSYAP

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						MTPDHFPFLCKEMSVGVYANGIRVMSMTHI GEPGFMLYPIEYRWGFTMLSTLVNS
121	1471	A	1498	3	306	AQFLLVGWDHIL*LVIL*TNLTGRTTCDQN WPNSPDVLNHGCFYMQCLSKDCTIGYVSRE MLVAHTHTVEEHTGTHLQYVSWPDHVSPPD SSDFVEFEN
122	1472	A	1533	121	329	LGLFSFVWTEVLEPKDFSCETEDFKTLHCT WDPGTD TALGW SKQPSQSYTLFES*VGSGYII DNFFLA
123	1473	A	1547	111	408	DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE RGHVEMIEKLTFNLHTSEKDKGGNTALHLA AKHGHSPAVQVLLAQWQDINEMNEKQQTPL HVAADRG
124	1474	A	1555	1	745	MTFDDDDKNTYGV ALVWKKFQTQSLRLSDL HRKSHLWRGIVSITLIEGRDLKAMDSNGLSDP YVKFRLGHQKYKSKIMPKTLNPQWREQDF HLYEERGGVIDITAWDKDAGKRDDFIGRCQV DLSALSREQTHKLELQLEEGEGHLVLLVTLT ASATVSISDLSVNSLEDQKEREELKRYSPRLI FHNLDVGFLOVKVIRAEGLMAADVTKSD PFCVVELNNDRLLTHTVYKLNLPENKVFIL *VALVWKKFQTQSLRLSDLHRKSHLWRGIVS ITLIEGRDLKAMDSNGLSDPYVKFRLGHQKY KSKIMPKTLNPQWREQDFHLYEERGGVIDIT AWDKDAGKRDDFIGRCQVDLSALSREQTHK LELQLEEGEGHLVLLVTLASATVSISDLSVN SLEDQKEREELKRYSPRLIFHNLDVGFLOV KVIRAEGLMAADVTKSDPFCVVELNNDRLLT HTVYKLNLPENKVFIL
125	1475	A	1556	57	509	GGPAPNSRYAEP*KNSLAMT*AHADCENYVA CGGLDNICSIYNLKTREGNVRVSRELPGHTGY LSCCRPLDDSQIVTSSGDTTCALWDIETAQQT TFTGHSGDVMSSLSLSPDMRTFVSGACDASS KLWDIRDGMCRQSFTGHVSDINAVS
126	1476	A	1592	3	178	KSEKSCVSSLAHFGTSCQRDYDAMVKLVETL EMLPTCDLADQHNKIFHYAFALNR*ER
127	1477	A	1612	1	497	TESPLLVRPYLPYITKSELHAIMTAGFSTIAGS VLGAYISFGVPSSHLTASVMSAPASLAAAKL FWPETEKPKITLKNAMKMESGDSGNLL*AAAT QGASSISLVANIAVNLI AFLALLSFMNSALA WVGNMFDYPQLSFELICSYIFMPFSFMMGV WPDSFM
128	1478	A	1619	286	486	CCMNSKAQESVFNVLNPPALSEMPDVKA EDEVDFRASSISEEVAVGSIATLKMKGQPM TQAINR
129	1479	A	1627	1	395	PTRGALRYWIFGRFLCNIWAAVDVRCCTATI MGLCHSIDRYVGVSYPLRYPTIVTQRRGLMA LLCVWALSIVYIGPLLGWRHPAPEDETICQI NEEPGYVLFSTPGSFYPLAIMLVMN*RVYRV AKTE
130	1480	A	1638	2	466	DPRVRTKJVNKRTTIEIQDKTGSMVVGKG ECHNIPCEKGDKLRLFCFLRKRENMSKLMS EMHSFIQIKNTNQRSHDSRSMALPQEQSQHP KPSEASTTLPESHLKTPQMPTTIPSSSFTKVT KDKDIK*LLFNLYSSVEILPEVLHLKT
131	1481	A	1651	607	3	LAEGGDVDFDCVLNGGPLPESRAKALFROMVE AIRYCHGCGVAHRDLKCENALLQGFNLKLT FGFAKVLPKSHRELSQTFCGSTAYAAPEVLQ GIPHDSKKGDVWSMGVVLVYVMLCASLPFDD

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						TDIPKMLWQQQKGVSFPHTLSISADCDLLKRLLEPDMILRPSIEEVSWHPWLAST**KQWQVLSNKVGGESKPKKKK
132	1482	A	1656	150	48	LVAKSLLYCGCLFLLQLAKNVGNNSFNDIMEANLTSPSPKPTPSSDM*VFLIY*TYFGAWHV VDAQ
133	1483	A	1660	3	406	RKHHLIQLKLSQV*ECQNNQL*KLTEICEKEKKEFKKKMDDQREPKITEA*SKDKSPMEEEKTEMIRSYIQEVGRYIKRLEEAQSKRLEKLRKHKEIRQFILDKPKGEGSSSFLSETHEDTSWF PNFTP
134	1484	A	1666	1276	466	PGSTHASARITTY*L*ILSNATEVDNNSKPPFFPAGAPPASSSSSSSSPPTVSTAPPLIPPFGPPPPGAPPSLIPTIESGHSYDSRSARAFYGNVAFPHLPGSAPSWPSLVDTSKQWDYYARSSSSSSSSSSSSSPDRDRER*RTREERERDRHSPTPSVFNSEERYRYREYAERGYERHRASREKEERHRRRHREKEETRHKSSRSNSRRRHESEBGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE STEATPAE
135	1485	A	1673	1	417	PTRPVNSSQAFALVYYTLGALGGNLIAMGLGYRYWAGIGVLQSCSALTHYRLVANHVASDISLTGGSVVQRIRLPDEVENPGMNSGMLQEDLIQYYQFLAEKGDVQAQVGLGQLHLHGGRGV*QNHQRAFDYFNLA
136	1486	A	1678	525	9	ANTSLSSAAVSAVSPPPCRTSTATTLPMPSPFCVFPSPSPSPSEFLSCLASVSRVHLSSSSSSSSTASSLNFSAIMGSSSATASWVLSTASTPPCPSALPSSPAQES*SLAASSAWPVAGISPSGACTFPAGSASGAAPSPSWRCPSFRALFSLDSSSLSL
137	1487	A	1680	1	2999	AHRDEIQKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASGANDEIVQLRS EVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEKERQWEAWRSVLGDEKSQFEQVRELQRMLEDTEKQSRARADQRITESRQVVELAVKEHKAELALQALKEQKLKAEISDKLNDLEKKHAMLEMNARSLQQLLETERELKQRLLEEQAQLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERSLEYQLENIQVLYSHEKVKMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEKEKARCAELEALQKTRIELRSAREEAHRKATDHPHPSTPATARQ QIAMSIVRSPEHQPSAMSLAPPSSRRKESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFRQASKCLECQVMCHPKCSTCLPATCGLPAEYVTHFTEAFCDKMNPSGLQTKESPSSSLHLEGWMKVFRNNKRGQGWDRKYTVLEGSKVLIDNEAREAGQRPVEEFELCLPDGDVSIHGA VGASELANTAKADVPIYLMKESHPHTTCWPGRITLYLLAPSFDPKQRWVTALESVVAGGRVSREKAADAKLLGNSLLKLEGDDRLDMNCTLPFSDQVVLVGTEEGLYALNVLKNLTHVPGIGAVFYIYIKDLEKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQDPISNIFEAVKGCHLFAGAKIENGLCICAAMPSKVILRYNENLSKYCIRKEIETSEPCSHFTNYSILIGTNKFYEIDMKQYTL EEFLDKNDHSLAPAVFAASSNSFPVSIQVNSAGQREYLLCFHEFGVFVDS

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						YGRRSRTDDLKWSRLPLAFAYREPYLFVTHF NSLEVIEIQARSSAGTPARAYLDIPNPRYLGP ISSGAIYLASSYQDKLRVICCKGNLVKESGTE HHRGPSTSRP*PASPLPOYQOQRAFLQGRRK
138	1488	A	1686	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV PLCCLGGAAGRL*ARSGKSLRRRAHAGPP PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS CWTRGCQTTARTAAAAAAPGAGRPPGGA PQNGSCAASASQEAAPPMCPPGRRWAVAS PPETRCPAAPGTRCRRLEAA
139	1489	A	1693	3	376	LPSMSNCTSCFRLQSRTE*IRQAGHLLGRNE FIETKALGCAWFSLCYYLVLYFESSHKVDFVF IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR RWAGIAKGVGTQKIIGRVHLGEQKALCL
140	1490	A	1704	3	376	ERTNKFELIMDGKNLIAATKSLVAQRKFA HSLRDFKFEFIGDAVTDDERCIDASREFSNFL KNLEEQRDMVS*EGCKLISQLSRGKKIWTWK LVLVEVVKHLSLGTVVHCNGKMRFPPEP
141	1491	A	1743	1	362	LITNKVFVARELSCLDVHLDSTGSTAVVADQ DKLELELVKGSYEDTQTSFLGTASAFRFHY MAAL*TELSGRLRSSKSNWNGDNSTGYLTV PLRPLTIVKEVTMDVPAFNVRLGNWVG
142	1492	A	1769	1	406	NNPSTLPRGS*PMSPRTTMGRRRQRREHKSS LSLASSTVPGGQIVHTTETEVVLCGDFLSGF GLQLGGIFATETLSSPPLVCFIEPDSPAERCG LLQVGDRLVLSINGIATEDGTMEANQLLRDA ALAHKVV
143	1493	A	1789	1	447	QMLRNGGDQNTVPDYHFAADRIRELL*PTEDQ KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA NELCEVNRKGGCTSGDPCLPYFCVQGCCKLQQA SDFIARQGTLIQVPSSAGEVECYKICSCGQSG LENCMEMHCCMDLPTDTSALVR
144	1494	A	1814	1	404	PGRFRPRLSQAGTDSGS*VFPDSFSPAPAEPL PYFLQEPQDAYTVKNKPVELRCRAFPATQIYF KCNGEWVSQNDHVTQEGLEATGLRVREHV IEVSRQQVEELFGLLEDYWCQCVAWSSAGTTK SRRAYVRI
145	1495	A	1827	26	448	XVEEKHADTWRSXCLSDFFHAAKXLCXE*N CGDAISLSVGDHFGKGNGLTWAKEFQCEGSE THLALCPVQHPEDTCIHSREVGVCVSRVTDV RLVNGKSQCDGQVEINVLGHWGSLCDTHWD PEDARVLCRQLNCGTAL
146	1496	A	1828	574	333	QHEGGDLRRRLQGEIQLTVRYVCLRAASAC* SMAAET*HHVPASGADPYVRVYLLPERKWA CRKKTSVKRKTLEPLFDET
147	1497	A	1855	1	372	ERLVLTSHECLVLTWFPSWTYHTLLLSRQH VRLPKLTHAEHDHLASIMNKLLTNYDNLFE TSVTYSMG*HGAPTGEAGANWNH**LHAH YYPPLLRSDTVRKFMVGSQMLAQALQDLTPE Q
148	1498	A	1879	568	7	LLSALDDKGGTQPSASFSNAPTIVCVTACPAG IAHTYMAAEYLEKAGRKLGNNVYVEKQGAN GIEGRLTADQLNSATACIFAAEVAIKESERFN GIPALSVPAEPIRHAEALMQQALTLKRDEET RTVQQDTQPVKSVKTELKQALLSGISFAVPLI VAGGTQVA*AV*ROGISSLHDVQVRTWNS
149	1499	A	1880	611	24	GLNSENALSNEAMERGWQCLRLFAERLQDIP PSQIRVVATATLRLAVNAGDFIAKAQELGCP VQVISGEEEARLIYQGVAAHTTGGADQRLVVD

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						IGGASTELVTGTGAQTT*LFSLSMGCVTWLER YFADRNLGQENFDAAQKAAREVLRPVDEL RYHSWKEVRGASVTVQALQEIMMAQGMDE RITMEIWPVD
150	1500	A	1894	2	750	GRVDFHFDYRPLRDSNNYVLDEQTTQQA LMPPPFLVDVDGNPHPTKYQRLVPGRENSAD EHLIPQLGYVATSDGEVIEQIISLQTNNDERS PESSILDGMIQQLQQQDQRMGADQDTIPRG LSNGEETPRRGFRRLSLDIQSPNIGLRSSQV EGVRQMHQNAFRSQIATERDLQAWKRRVVV PEVPLGIFRKLEDFRLEKGEERNLYIGRKRK TLQLSHKSDSVGLVSQSFRPTCRKRYF
151	1501	A	1900	141	785	GKTIQIQTMMQNKYKTVQKQYKTIKPKKA MEMQIKKQFQDTCKVQTKQYKALKNHQLEV TPKNEHKTILKTLKDEQTRKLAIAEQYEQSI NEMMASQALRLDEAQEAECQALRLQLQOEM ELLNAYQSKIKMQTEAQHERELQKLEQVRSL RRAHLEQKIEELAALQKERSERIKNLLERQE REIETFDMESLRMGFGNLVTLDFPKEDYR
152	1502	A	1915	2	377	LVRLDLDQDGLQNYEALLGLTNLSGRSDKL RQKIFKERALPDINYMFEHNDQLRQAATEC MCNMVLHKEVQERFLADGNDRLKLVLLCG EDDDKVQNAAGALAMLTAAHKKLCLKMT QVTT
153	1503	A	1921	1	237	AYQSLRLEYLQIPPVSRAYTTACVLTSAAVQL ELITPFQLYFIPFLIFKHFQIWRLLTNLFFVPFG FNFLLYMIFLYT
154	1504	A	1928	2	354	EMVEGEGGKMCINTEWGGFGDNGCIDDITR YDTEVDEGSLNPGKQRYEKMTSOMYLGEIV RQLIDLTKQGLLFRGQISERLRTRGIFETKFLS QIESDRLALLQVRRILQQLGLD
155	1505	A	1929	2	369	TEIAKIKMEAKKKYEKELTMFQNDFEKACQA KSEALVLRKSTLERIHKHQEIEKIEYARQ LLKDMDLLRGREAELKQVEAFESYQLELK DDYIIRTYRLIEDDRINIQISGHWQESP
156	1506	A	1935	1	270	VTRKLPFIVDAFTARAFRGSPAADCLLENEL DEDMHQKIAREMNLSETAFIRKLHPTDNFAQ RSCFGLIWFITPTDLQILTSSILPSIL
157	1507	A	1936	584	305	ESKVNNEKFRKSPKPAESQSATKQLDQPTA AYEYDAGNHWCKDCNTICGTMDFDFTMHM NKKHTQGQFQKSSDFQKEELQOTFLPPERQG
158	1508	A	1939	1	423	TTHRLNVTAEPPCTSMPIYWMPDVPHRCTTA NTCPVDLTDYCAQNGFYCLVYGFLPYGSLED RLHCQTQACPLSWPQRLDILLGTARAIQFLH QDPSLHGDIKSSNVLLDERLTPKLGDFGLA RFSRFAGSSPIQSSM
159	1509	A	1974	3	401	HTSTARLLLHRGAGKEAVTSDGYTALHLAAR NGHLATVKLLVEEKADVLARGPLNQALHL AAAHGHSEVVEELVSADVIDLFEQGLSALH LAAQGRHAQTVETLLRHGAHNLQSLKFQGG HGPAATLLR
160	1510	A	1982	2	417	KFLKDLEKQYNKEEPLHSEIGSCLFQNGEFA IYSEYCNNHPGACLELANLMKQKQYRHFEEA CRLLQQMIDIAIDGFLTPVQKICKYPLQLAEL LKYTTOEHGDYSNIKAAYEAMKNVACLNER KRKLESIDKIA
161	1511	A	1984	4	770	RETGSVSLSPSGLEGAESYAVSPILYSSPDVKE LWLETQGGQRHSHTGVKSTPGQSAAILMKLR SSHNAKTLNANNMETLIECQSEGDIEHPLL

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						ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS PASDFSGALETDLKASLFDQPLSHCGSDTLP RPIQDILTILCLKGPSTEGIFRRAANEKARKEL KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP RKLLSSDLFEEWMGALEMQDEEDRJEALK
162	1512	A	1986	864	501	LLNSGLFSAPDGSNLEMLRTRGGMCSGRIE KFQGRWGTVCDDNFNIDHASVICRQLECGSA VSFSGSSNFGECSGPIWFDLINCNGESALWN CKHQGWGKHNCDAEDAGVICSSKD
163	1513	A	2001	419	187	AVDLSIDESSLTGETTPCSKVTAQPAATNGD LASRSNIAFMGTLVRCGAKGVVIGTGENSE FGDIINLSTFVVHS
164	1514	A	2012	284	597	SLCLFPGTSTVVCKPIVIETQLYVIVAQLFGG SHIYKRDSFANKFIKQAEILKIRKPNDIETFKI ENNWFYFVADSSKAGFTTITKWERETGFYSH QSFR
165	1515	A	2013	2	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY NVDLPFMYSTYAAFAIATLLMLNLLIAMMG DTHWRVAHERDELWRAQIVATTVMLEKRLP RCLWPRSGICGREYGLGDRWILRVEDRQDLN RQRIQRYA
166	1516	A	2019	2	927	CCQREGGLGKAVVQILLSHGRNGLPGEFAS QGLSAASSTPVFHLALQIDSDNDWVEMLF NKNMVTERRLQNMVLEQCFSDSSSLYRFLTY SYLLAFNVWLLAPVTLCDYDQVGSIPLVETI WDMRNLATIFLAVVMALLSLHCLAAFKRLE HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER VLYMPMGYCILFVHGLSKLCTWLNRCGATT LIVSTVLLLLFSWKTQVQNEIWSRESLFRS GVQTLPHNAKVHYNANFLKDQGRNKEAIY HYRTALNNNAWDYLCWRFRKTLTDLP
167	1517	A	2025	696	71	AAASAASSLTVTGLRLASACSHSLRPSGGA ASLWSASRRFNSQSTSYLPGYVPKTSLSPPW PEVVLDPVEETRHAEVVKVNMIVTGQY GRLFAVVFASRQWKVTSEDLILIGNELDLA CGERIRLEKVLVGADNFTLLGKPLLKDLV RVEATVIEKTESWPRIMRFRKRKNFKKKRIV TTPQTVLINSIEIAPCLL
168	1518	A	2046	2	366	HLQVAARVFMPLQAVDSAPKPLKGQAQAPQ RLQGAARVFMPLQAQVKAASKPLQMQIKA PPRLRRAARVLMPLQAQVRAFRLQVQSQVS KKQQAQTQTSEPQDLQVPEEFQGDQVLR
169	1519	A	2049	1	945	QNLEDREVLNGVQTELLTSPTKDTLSDMTR TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI EDNSRSKREGLFHENECEVKNVNDLVDKTFA QAQDVFRQAMKSPSVLLHVLPPQNREYKES VIGSLNIFGNNDGVLKTKVPPVHGKSGLKTA NLGTGDSPETDASASLQONKSPRVPRLGGKPS SPSLSPLMGFGSNKNKKIKIDLKKGPEGLGF TVVTRDSSIHGPGPIFVNILPKGAAIKDGRLO SGDRILEVNGRDVTGRTQEELVAMLRSTKQG ETASLVIARQEGHFLPRELVMFRSQSH
170	1520	A	2050	363	1	PVATHLTILKILNSDEHAVVISSAKTLCETVKDF VAKVEKTYDKTLENVAVDAVASKCSVLNE KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV ESSSEESLGESEQLGDDVTKPSSQKA
171	1521	A	2055	139	675	IPSRPWLGRITGLDPAGFLFNGKPHQDRLDPS DAQFVDVIHSDTDALGYKEPLGNIDFYPNGG LDQPGCPKTLGGFYFKCDHQRSVYLYLSSSL

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						RESC TITAYPCDSYQDYRNGKCVSCGTSQKE SCPLLGYADNWKDHLRGKDPMTKAFDDT AEESPFCMYHYFVDITWKNVR
172	1522	A	2056	3	361	LIOHKS AVEYAQS HLSL VSMCKESHK CSEPK MEWKVKIRSDGTRYITKRPVRDRILKERALKI KEERSGLTTDDDTMSEMKGGRYWSKEERKQ HLVRGKEQRRRREFMMRIRLKLCKES
173	1523	A	2060	1	387	GTRILSMQIPFVGQFIRTS EHM AAGV FALL QAY AFLQYLRDLTKQEFQTLFFLGVS LAAG AVFLSVITLYTYGYIAPWSGRFYS LWDGTGA KIHPIASVSEHQPTTWVSFFFDLHLGCTFPA G
174	1524	A	2071	74	443	LLMGPKAKKSGSKKKVTKAERLKLQEEEE RRLKEEEEEARLKYEEEMERLEIQRIEKEKW HRLEAKDLERRNEELEELYLLERCPEAEKLLK QETKLLSQWKHYIQCDGSPDPSVAQEMNT
175	1525	A	2083	139	486	AALTWSQPFQFWPMEMQPIVTDMTVTHVW AESSTVGWLCALFRVTHVGVGATGHGVVCG RRVLCGLPLPSPAPMPIMSLPEGESRKEREVQ RLQFPYLEPGHELPAITLLAFLAAV
176	1526	A	2092	3	587	EGSVNFKFGVLFADKGQLTDDMFNSIEGSEP FQKFLNLLGDTITLKGWGTGYRGGLDTKNDTT GIHSVYTVYQGHEIMFHVSTMLPYSKENKQQ VERKRHIGNDIVTIVFQEGEESPFAFKPSMIRS HFTHIFALVRYNQNDNYRLKIFSEESVPLFG PPLPTFPVFTDQHEFRDLLVKLINGEKATLET PCI
177	1527	A	2103	44	427	GKGQVSLEGRPHRGPLCLGSWWFGSRVPGC CDGAWLAWACWVFGNDFPSPASAACSALLG CSVSTACLCVPLCSGSPAPFRRTAALQEGLR RAVSVPLTAEVSLWPALQELARCGNLAC RSDLQ
178	1528	A	2104	2	409	ALQSTLGAVWLGLLLNSLWKVAESKDQVFQ PSTAASSEGAVVEIFCNHSVSNAYNFFWYLHF PGCAPRLLVKGSQSGQGRYNMTYERFSSSL LILQVREADAAVYYCAVEVPNTDKLIFTGT RLQVFPNIQNP
179	1529	A	2111	1	312	PTRSTRPPSLFVHASAKGGEKEEGDDGHYL MRTESHTGLKKGGNANLVFMLKRNTPEPKKG SYHFDLERLRAAHILFEREQEHLAPGGHSMPL PPPLPLPACLG
180	1530	A	2116	3	366	TSIKRAIETTDVTRSGWDSSEAWQQHDVQE LCRVMFDALEQKWQTEQADLINEYQGKL KDYVRSLECGYEGWRIDTYLDIPLVIRPYGSS QAFASVVCTFHLTACVSLHRIHNSIVV
181	1531	A	2117	2	386	YGLGAHFGRLFIQAGINENDFYDGAWCAGR NDLQQWIEVDARRLTRFTGVITQGRNSLWLS DWVTSYKVMVSNDSHTWVTGKNGSGDMIFE GNSEKEIPVLNPLVPMVARYIRNPQSWFDN GSICI
182	1532	A	2123	1	493	RTKTDVYILNLAVADLLLLFTLPFWAVNAVH GWVLGKIMCKITSALYTLNFGVSGMQFLACISI DRYVAVTKVPSQSGVGKPCWICFCVWMAAI LLSIPQLVFYTVNDNARCIPFPYRLGTSMKAL IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS
183	1533	A	2140	3	561	RQAWHEAFKVRKEILTVCCLLAFICIGLIFVQ RSGNYFVTMFDDYSATLPLLVILENIACVF VYGIDKFMEDLKDMLGFAPSRYYYYMWKYI

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						SPLMLLSLLIASVVMGLSPPGYNAWIEDKAS EEFLSYPTWGLAVCASLDVFAILPVPVAFIGR RFLSIDDGAGPFCSAAYTTTGCRTPYL
184	1534	A	2145	3	538	HELTVAADRGPQPQSSVVPVTVTVLDVND NPPVFRASYRVTVPEDTPVGAELHVEASD ADPGPHGLVRFTVSSGDPGLFELDESSGTLR LAHALDCETQARHQLVVQAADPAGAHFALA PVTIEVDVNDHGAFFPLNLLSTVAENQPPG TLVTTLHAIDGDAGAFGRRLRYHL
185	1535	A	2151	2	671	LDKLLDRMENYNIFNEYILKQVAATYIKLGW PKNNFNGSLVQASYQHEELRREVIMLACSGF NKHCHQCASTLISDWISSNRNRIPLNVRDIVY CTGVSLLEDVWEFIWMKFHSTTAVSEKKIL LEALTCSDDRNLLNRLNLSLSEVVDQDAI DVIHVARNPHGRDLAWKFFRDKWKILNTRI RQKTLEFDFAEPLILAFPHILYTAIDNPPLVREH E
186	1536	A	2153	2	400	GPMCDKHSFAAEKFHAGFIDYIVHPLWETWA HLALPDAQDILYTLEDNRNWVDSMPQSPSP LDEQNRDQGLLENLHVELTLEDEDESGPEK EGEGQTYFTSSKTLGIVPQNTDSLGETGIHIC AHDKSP
187	1537	A	2158	227	442	FNCFRVASDSFLENSLLIMILPLRNATQEFIR PGAVAYTCNPSTLGGWGWITRSGVRDQPG QHGGTSP
188	1538	A	2167	3	486	AHLGGAWLTQRLSGSWAAPGPAAAKEVVA CIPQNQKMNITWRMKTSKHLQLLSFVLGAVSP AVVVPYMMVLQENGYGVEEGIPTLLMAASS MDDILAITGFNTCLSVFSSGRCARSSGSRNSKS LRTPLGTICEGDDSSIFSHLDHSSKWSSYTG HSGA
189	1539	A	2168	2	412	EFLSSNQITQLPNTTFRPMPNLRSDVLSYNKL QALAPDLFHGLRKLTLHMRANAIQFVPRIF QDCRSCLKFDIGYNQLKSLARNSFAGLFKLTE LHLEHNDLVKVNFAHFPRLISLHSLCLRRNKV AIVVSSLDW
190	1540	A	2179	64	399	MRLNQNTLLLESFGXXRPYTSEHAPTYHQW MKADELLRWTTSEPLTEHEYAMQRTWLED AYECTFIVLDAEKRAHQPGATEESCMVGDVN LFLTDLDELTLGEIEVLIAEP
191	1541	A	2190	1	469	CLDRAAGIRHERNVITYNETHTRHRGWLARR LSYVLFIERDVHKGMFATNVNTENVLNSSRV QEALAEVAAELNPDGSAQQQSKAVNKVKKK AKRILQEMVATVSPAMIRLTGWVLLKLFNSF FWNIQIHKGQLEMVKAATETNPLLLFVHR SH
192	1542	A	2197	26	157	PSKXGGIRLLLGTQLYGRFGSAIAPLGDLDLDR DGYNGEGREEFY
193	1543	A	2236	2	383	EYFPNSIWRSLFSTMDLGDIGFYTYRILQALS YTHSKGIMHRDVKPLNLCNSPRNKVILADW GLAEFYHPMRKYSVHVATRYYSPEILLDYE YYDYSLDIWA VGVILLELLTLKLHVFEQDN EQ
194	1544	A	2241	105	409	RKGVGKMPTSEGRPGQERSDWTSTYKVMGS NDSHTWVTVKNGSGDMIFEGNSEKEIPVLNE LPVPMGAR YIRNPQSWFDNGSICMRMELGC PLDPNNY
195	1545	A	2245	1	672	MGVASDWTKRIEYQPGSGSMPLFPSIHLETCD GAVSSLQIVTELQTNVYIGKGCDEITYSEKSLQ

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						KLCGASSGIDLLPSPSAATNWTAGLLVDSSE MIFKFDGRQGAIPDGIVPKNLTDQFITTMW MKHGPSPGVRAEKETILCYSDKTEMNRHHY ALYVHNCRLVFLLRKDFDQADTFRPAEFHW KLDQQALAKVDGQPGKSITRQLQEMPVTIQG ISLKPS
196	1546	A	2256	1	396	FRGTPVSGLTNRDTLAVIRHFREPRLKTVKP GKVINKDLRHYLSLQFQKSIDHKLQQVIRD NLYLRITPCTTRAPRDGEVPGVDYNFISVEQF KALEESGALLESPTYDGNFYGTPKPPAEPSPF QDPDV
197	1547	A	2259	43	594	QLAIEIGVRALLFGVVFTEFLDPFORVIOPEEI WLYKNPLGQSDNIPTRLMFAISFLTPLAVICV VKIIRRTDKTEIKEAFLAVSLALALNGVCTNTI KLIVGRPRPDFFYRCFPDGMNSEMHCCTGDP DLVSEGRKSFFSIHSSFAFSGLGFTTFYLAGKL HCFTESGRGKSWRLCAAILPL
198	1548	A	2275	3	404	TCTTVVVIPIRMLVDLSESKTISLPECATQMFF FLGFASNNCFMAAMSVDYRTAIHNPLOQYHT LMTRKICLQMMMASWMVGFLFSLCIIVTVFN LSLCLNTIQHYFCDISPVSLACNYTFYHEM AIFVLSA
199	1549	A	2315	1	375	LTQMFFIHALSAIESTILLAMAFDRYVAICHPL RHAAVLNNTVTAQIGIVAVVRGSLFFFLPLLI KRLAFCHSNVLSHSYCVHQDVMKLAYADTL PNVVYGLTAILLVMGXDRMFISLSYFLII
200	1550	A	2334	2	409	PRVRPQQRKMSFFFKTELGEKLVTKFLFETDF SDDPMLPSPDQLKKKAPFTNKKLKAHQTPVD ILKQKAHQASMQVQAYNGGNANPRPANNE EEEEDEDEYDYDYESLSDDNILEDRPENKSCH DQLQFEYKEEM
201	1551	A	2350	3	512	ISWEAQIAEIIQWVSDEKDARGYLQALASKM TEELEALRSSSLGSRTLDPLWKVRRSQKLDL SARLELQSALEAIEIRAKQLVQEELRKVKDAN LTLESKLDSEAKNRELLEEMILKKKMEEK FRADTGKMLMLCDSALFEYKYFSNECFYFLFD LIVLEAPTEFQIQY
202	1552	A	2351	1	1003	PSSYSSDELSPGEPLTSPWPAPLGAPEPEHLL NRVLERLAGGATRDSAAADILLDDIVLTHSLF LPTEKFLQELHQYFVRAGGMEGPEGLGRKQA CLAMLLHFLDTYQGLLQEEEGAGHIKDLYL LIMKDESLYQGLREDTLRLHQLVETVELKIPE ENQPPSKQVKPLFRHFRIRDSCLQTRVAFRGS DEIFCRVYMPDHSYVTIRSLASVQDILGSV TEKLQYSEEPAGREDSLLVAVSSSGEKVLLQ PTEDCVFTALGINSHLFACTRDSYEALVPLPE EIQVSPGDTIHRVEPEDVANHLTAFHWELFR CVHELEFVDYVFHGE
203	1553	A	2361	2	403	NNLNCAEPLFEQNSLNVNFTQKKTVWLIIH GYRPVGSIPLWLQNFVRILLNEEDMNVIVVD WSRGATTFTYINRAVKNTRKVAVSLSVHIKNL LKHGASLDNFHFIGGSLGAHISGFVGKIFHGQ LGRITGLDP
204	1554	A	2390	280	476	SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSQ AGSRLGAMRRCAREMDATMPAPSPCPSERV T
205	1555	A	2400	543	745	AAVALRDISWQQPYPMDFYAGSSLGFWTVN HGQDRRPHAPGRPARGVQEGSARPPSAVAC EDCSR

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206	1556	A	2406	122	485	DLSPDSREDHPQGHRRLLPKRPVRGSLMPGH THHPCPVSSSTTNDTPDQIWVSVGSLRMGTGG MGANASTSPRCWDLSSGNKKWIIQVPILASIV ESRGGLLATGVGGMCAVPRNQPLTGT
207	1557	A	2409	289	418	LWILYRHKQQVQHNHNSNRLSCRPSQEDRAT HTIMVLDKENTLS
208	1558	A	2413	64	492	VQGTGXXFIAFTEAMTHFPASPVWAGMFFL MLINLGLGSMIGTMAGITTPIDTFKVPKEMFT GGCCVFAFLVGLLFVQRSNGYFVTMFDDYSA TLPLTLIVILENIAVAWIYGTKKFMQELTEML GFRPYRFYFYMWKFVSP
209	1559	A	2417	3	877	EKERLLDEWFTLDEVPGKGLHLRLEWLTLM NASNLDKVLTDIKADKDQANDGLSSALLILY LDSARNLPYRYKTNEPVVEENFTFFIHNPKRQ DLEVEVRDEQHQCPLGNLKVPLSQLLTSEDM TVSQRFLGNSGPNSTIKMKIALRVLHLEKRE RPPDHQHSQAQVKRPSVSKEGRKTSIKSHMSG SPGPGGSNTAPSTPVIGGSDKPGMEKAQPPE AGPQGLHDLGRSSSSLLASPGHISVKEPTPSIA SDISLPIATQELRQRLRQLENGTTLGQSPLGOI QLTIP
210	1560	A	2422	35	456	REFAASDLEPFTPTDQIPSEAITQPSCIKRQRA AGNPGSLAATIDHKPCSAPLEPKIQASRNQRW GAVRAAESLTDIAEPASPQVHETPIDASQTQK VEPASKSRFTPELQAKVSHSRERALSTMDATP HHAQPORGEG
211	1561	A	2431	1	764	RRYSQKLIQHTACQLLRTPAATRIDSSNPNP LMFWLHGIQLVALNYQTDDLPLHLNAAMFE ANGGCGYVLKPPVLWDKNCPMYQKFSPLE DLDSMDPAVYSLTIVSGQNVCPNSMGSPCIE VDVLGMPLDSCHFRTKPIHRNTLNPMWNEQF LFHVHFEDLVFLRFAVVENNSSAVTAQRIPL KALKRGYRHLQLRNLHNEVLEISSLFNSRRM EENSSGNTMSASSMFNTEERKCLQTHRVTVH GVPG
212	1562	A	2436	1	411	GIRGTTGHLGCPINDPDLTTLTVSWVMEDKPI YIGNGTKKEDSLTIFAVAKRDHVS DTCGAC TDLDHNLDDKGYLTVLGEQATPTNRLGALPKG RANRTRDLELTylaERIVRLTWIPGDANNRPI TDYDCQIEHQ
213	1563	A	2445	1	1294	MSSIGCLWVSRSSQIDGLTAEKSGPEKPHGT WLMPELHPKEQLELLVLEQFLSILPEELQIWV QQHNPFESGEESVTLEDLEREFDDPGQQVPAS PQGPAVPWKDLTCLRASQESTDIHLQPLKTQ LKS WKPCLSPKSDCENSETATKEGISEEKSQ LPOEPSFRGISEHESNLVWKQGSATGEKLRSP SQGGSFSQVFTNKS LGKRDLYDEAERCLILT TDSIMCQKVPPEERPYRCDVCGHSFKQHSSLT QHQRHITGEKPYKCNQCGKAFSLRSYLIIHQ IHSGEKAYECSECGKAFNQSSALIRHRIHTG EKACKCNECGKAFSQSSYLIIHQRIHTGEKPY ECNECGKTFSSQSSKLIRHQRHITGERPYECNE CGKAFRQSSSELITHQRHSGEKPYECSECGKA FSLSSNLIHQRIHSG
214	1564	A	2461	1	615	GIPGSTISSRNIFLEDDLAWQSLIHPDSSNTPL STRLSVSVQEDAGKSPARNRSASITNLSLDRSG SPMVPSYETSVSPQANRTYVVRTETTEDERKIL LDSVQLKDLWKKICHSSGMEFQDHRVWLR THPNCIVGKELVNWLRNGHIATRAQAIAIGQ

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						AMVDGRWLDVSHHDQLFRDEYALYRPLQV LFSVYCQLECSKLIL
215	1565	A	2464	3	2932	GPGVRSQDGMADV FVHLRTAWPRCSFISGQ HGPRHGRRCVSSQDSMADV FVHLRTAWPT CSLISGQHGPGESVSYEDDDIPAPASLLHVNA AAPALTNPAPVLTAPNNTAQKEKVPSGMR QRPAGVRISSRTPDLTCAVSTHSTVPGVRISSC TPDLTCAVSHSTVPSVCISSCTPDLTCAVSTH STVPGVRISSCTPDLTCAVSTHSTVPGVRISSR TPDLTCAVSIHATVPGVRISSCTPDLTCAVSIH ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR TPDLTCAVSIHSTVPGVRISSCTPDLTCAVSIH ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH ATVPGVRISSCTPDLTCAVSIHATVPGVRISSC TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR TPDLTCAVSIHATVPGVRISSCTPDLTCAVSTH STVPGVRISSRTPDLTCAVSIHATVPGVHISSC TPDLTCAVSTHSTVPGVRISSRTPDLTCAVSIH STVPGVCISSRTPDLTCAVSIHSTVPSVHISSCT PDLTCAVSIHSTVPGVRISSRTPDLTCAVSTHS TVPGVHISSCTDLTCAVSIHATVPGVHISSCT PDLTCAVSTHTVPGVRISSRTPDLTCAVSIHS TVPGVRISSCTPDLTCAVSTHSTVPGVRISSR PDLTCAVSTHSTVPGVRISSRTPDLTCAVSIHA TVPGVHISSCTPDLTCAVSIHATVPGVRISSR PDLTCAVSIHATVPGVHISSCTPDLTCAVSTHS TVPGVRISSRTPDLTCAVSIHSTVPGVHISSCT PDLTCAVSTHSTVPGVHISSCTPDLTCAVSTH STVPGVHISSRTPDLTCAVSIHATVPSVHISSC TPDLTCAVSIHSTVPGVHISSCTPDLTCAVSTH
216	1566	A	2477	1	414	FRKSYRKGSYRCIVSEWIAEQGNWQEIQEK AVEVATVVIQFTVLRAAVPKNVSVABGKELD LTCNITDRADDVRPEVTWFSRMPDSTLPGS RVLARLDRDFLVHSSPHVALSHVDARSYHLL VRDVSKENSGYYY
217	1567	A	2480	2	460	CRTLCEGPQRFEEYELGYKAGLYEAIADHY MQVLVCQHECVRELATRPGRISPENFLPLHY DYLQFAYYRVGEYVKALECAKAYLLCHPDD EDVLDNVDDYESLLDDSIDPASIEAREDLTMF VKRHKLESELIKSAEGLGXSYTEPNYW
218	1568	A	2483	140	383	AFSSPHSPAPQFPECGFYGLYDKILLFKHDPT SANLLQLVRSSGDIQEGDLVEVVLASATFED LQIRPHALTVHSYRAP
219	1569	A	2489	3	428	SSRLVLLAGAAALASGSQGDREPVPYRDCVLQ CEEQNCSGALNHFRRSQPIYMSLAGWTCRD DCKYECMWVTVGLYLQEGHKVPQFHGKWP FSRFLFFQEPASAVASFLNGLASLVMLCRYRT FVPASSPMYHTCVAFAWVS
220	1570	A	2498	1	1297	MDGEAVRFCTDNQCVSLHPQEVDSVAMAPA APKIPRLVQATPAFMAVTILVFLVTLFVVDH HHFGREAEMLIQTFKGHMENSSAWVVEIQ MLKCRVDNVNSQLQVLGDHLGNTNADIQMV KGVLKDATTLSLQTQMLRSSLEGTNAEIQR KEDLEKADALTFQTLNFKSLENTSIELHVL SRGLENANSEIQMLNASLETANTQAQLANS LKNANAEIYVLRGHLDVNDLRTQNQVLRNS LEGANAEIQGLKENLQNTNALNSQTQAFIKSS

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						FDNTSAEIQFLRGHLERAGDEIHVLKRDLMK VTAQTQKANGRLDQTDQIQVFKSEMENVN TLNAQIQVLNGHMKNASREIQTLKQGMKNA SALTSQTQMLDSNLQKASAEIQRLRGDLENT KALTMEIQEQSRLKTLHVVTISQEQQLQRTQ
221	1571	A	2501	3	500	RVRLNNDGLSPLMMAAKTGKIGIFQHIREV TDEDTRILSRKFKDWAYGPVYSSLYDLSSLD TCGEEASVLEILVYNSKIENRHEMLAVEPINE LLRDKWKKFGAVSFYINVVSYLCAVIFTLT AYYQPLEGTPPYRTTVDYLRLAGEVITLFT GVLFFFTN
222	1572	A	2508	3	395	DAHCRKQLAMQEFMEINERLTTELHTQKQKL ARHVRDKEEEVDLMQKVESLRQELRRTER AKKELEVHTEALAAEASKDRKLREQSEHYSK QLENELEGLKQKQISYSPGVCSIEHQEITKL KTDLEKKS
223	1573	A	2544	2	412	NDPAISNFSAAVVHTIVNETLESMTSLEVTK MVDERTDYLTSLKEKTPPFHCDQAVLQCS EASSNKDMFADRLSKSIKHSIDSKSVIPNID KNAVYKESLPVSGEESQLTPEKSPKFPDSQNO LTHCSLSAA
224	1574	A	2552	401	1	GASLCFISTAFTVLTFIDSCRFSYPERPHFLSM CYNISIAIYVRLTVGRERISCDFEAAEPVLI QEGKNTGCAIIFLLMYFFGMASIIWWVILTL TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA VK
225	1575	A	2563	724	1	MSARKERREKREEEGEGEKDGEDEKEEEKE GLGEEEEKEAGKCKKKQEEKEKEKGAVYSR VARICKNDMGGSQVRVLEKHWTSLKARLNC SVPODSFFYFDVLQSIDIIQINGIPTVVGVFTT QLNSIPGSAVCAFSMDIEKVFKGRFKEQKTP DSVWTAVPEDKVPKPRPGCCAKHGLAEAYK TSIDFPDETLSEIKSHPLMDSAPPIADEPWFT KTRVRYRLTAISVDHSAAGPYH
226	1576	A	2571	449	3	EGVLFVYGNVYGDVMNFEMAAEMAQEVAP TRTVLTDDISSPIEDRDGRGVAGNFFIFKV AGAACDRGMSLEACEAVTRKANRRTYTMG VALEPCSLPQTRRHNFEIGAEEMEIGMGIHGE RGVIREKMMPADAIVDHIMDRIFS
227	1577	A	2575	3	1197	VLSDLCLFYRDEKEEGILGSILLPSFQIALLS EDHINRKYAFKAAHPNMRTYFCTDTGKEM ELWMKAMLDAAALVQTEPVKRVDKITSENAP TKETNNIPNHRVLKPEIQNNQKNKEMSKIEE KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRFESICSVTP STHDKTLGPAAEKKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIFTPSPHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHPKVK
228	1578	A	2583	3	330	LPFLGLGSVLPQGMVMASPEMNPTICSVF HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD PTMGIKPHLWWVAA
229	1579	A	2589	1	448	DDKNAQGIKRVKPTSGNAFTICKYPCGKSR ECVAPNICKCKPGYIGSNQQTALCDPDCKNH GKCIKPNICQCLFGHGGATCDEEHCNPPCQH

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						GGTCLAGNLTCTCPYGFVGPCEMVCNHRHC ENGGQCLTPDICQCKPGWYGPTCSTA
230	1580	A	2593	2	138	AVTFSVVFAYVADITQEHERSMAYGLVCMFI LYLLYLRLNAFFLR
231	1581	A	2595	185	2	SGPYTDFTPWPTEEQKLLLEQALKTYPNPPER WEKIAEAVPORTKKACIKRYKVADLRISK
232	1582	A	2596	1	391	STVTGQPRRLDLAGHQPFLELKIRANEPGA GRARRRTPTCEPATPLCCRRDHYVNFQELGW RDWILLPEGYQLNYCSGQCPTHLAGSPGIAAS FHSADVSLKANNPWGRTSWCVPTARRPLS LLYL
233	1583	A	2601	184	403	LLFSDEIIMAAPLRIADVTSLGIGGEDGRVYV YNGKETTLGDMTGKCKSWITPCPEEKVNVLQ NSIPYWERIT
234	1584	A	2614	178	335	PLTLCLPENNKPPQADAVPDKELTLPVDSTTL DGSKSSDDQKIISYLWEKTQ
235	1585	A	2616	2	896	DVLEVYGTGVASTRHEMGTLDKHKLEEDLV AKFLNVEAAMVFGMGFATNSMNPALVGKG CLILRDEVNHTSLVLGARLLGATIGIFKHNYA QSLEKLLRDAVTYGPRTTRAWKKILLVEGV YSMEGSIVHLPQIALKKKYKAYLYIDEAHSI GAVGPTGRGVTEFFGLDPHEVDVLMGFTFS FGASGGYIAGRKARILSPPACLPNTGSHSLH RLTRDLQMNEAMVALVTDRLQGWNSGEGN WDRADKFGDLVDYLRVHSHSAVYASSMSPI AEQIRSLKLIMGLDGTQ
236	1586	A	2621	1	392	NTSSFPAQSSPARPSLPHLSQHPNPLPLAS ADHPQCGRFLPLHEPEPLCPSPSLSYPTLVSS WSSPFSSHHGCPPGLYFPPTSPKTIQPPGLAQL KMLCIPPGRQQLRGAQSMFGHGAISPLLLPP A
237	1587	A	2628	398	1	DLVCKISGFRGPRDRSEAVYTTMSGRSPAL WAAPETLQFGHFSSASDVWSFGIIMWEVMAF GERPYWDMGQDVIKAVEDGFRLLPPRNCPN LMHRLMLDCWQKDPGERPRFSQIHSILSKMV QDPEPPNV
238	1588	A	2631	1	1104	WSPCSLTCGVGLQTRDVFCSHLLSREMNETV LADELRCRQPKPSTVQACNRFNCPPAWYPAQ WQPCSRTCGGGVQKREVLCKQRMADGSFLE LPETFCASAKPACQACKDDCPSEWLLSDW TECSTSCGEGTQTRSAICRMLKTGLSTVNS TLCPLPFSSSIRPCMLATCARPGRPSTKHSFHI AAARKVYIQTRRQRKLHFVGGGFAYLLPKTA VVLRCPARRVRKPLITWEKDGQHLISSTHVT VAPFGYLKIHLKPSDAGVYTCAGAPAREHF VIKLIIGNRKLVARPLSPRSEEEVLAGRKGGP KEALQTHKHQNGIFSNGSKAEKRGLAANPOS RYDDLVSRLLEQGAAPCSSSKKKK
239	1589	A	2636	1	678	MKPDNILLDEHGHVHITDFNIAAMLPRETQIT TMAGTKPYMAPEMFSSRKAGYSFAVDWW SLGVTAYELLRGRPHYHRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLKKLLEPNPDQRFPSQ LSDVQNFYPMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDVQKEFIINRE KVNRCI
240	1590	A	2639	389	3	ELLDFTTPMRKCIELLYAALTSSSTDQPKAD LWQNFAREIEEHVFTLYSKNIKKYKTCIRSKV ANLKNPRNSHLQQNLLSGTTSPEFAEMTVM

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						EMANKELKQLRASYTECIEHYLPQVIDGTL Y
241	1591	A	2640	392	3	IRLTILRCVFMRLATICVLVFTLGSKITS CDDD TCDLCGYNQKLYPCWETQVQGEMYKLMFD FIIILAVTLFVDFPRKLLVTYCSSCKLIQCWGQ QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM Y
242	1592	A	2642	405	1	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR MVL MAGAKPGMLLLCFMCCTLLSMWLSNT STTAMVMPIVEAVLQELVSAEDEQLVAGNSN TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK SPLMISQACI
243	1593	A	2646	412	2	CLAMIKGIQSSGKIIYFSSLPYVVLICFLIRAF LLNGSIDGIRHMFPTKLEIMLEPKVWREAAATQ VFFALGLGFGGVIAFSSYNKRDNCHFDVAVL VSFNFFTSVLATLVVFAVLGFKANVINEKCIT QNSETV
244	1594	A	2650	1	1271	MTTTLIGLLKTARLLRLVRARKLDTRYSEYG AAVLMLLMCIFALIAHWLACIWIYAIGNVERP YLTDKIGWLDLSLGGQIGKRYNDS DSSSGPSIK DKYVTALYFTFSSLTSVGFNGVSPNTNSEKIF SICVMLIGSLMYASIFGNVSAIQRLYSGTARY HMQMLRVKEFIRFHQIPNPLRQRL EEFQHA WTYTNGIDMNMVNTNGTCSSTSDDGHFILVS NHHQGGLIYSWDAASMQRPFNHKSLLGS TSDSNLNKYSTINKIPQLTLPSEVVKTEKNSS PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA DVLPEYKLQAPRINKFTILHYSFPKAVWDWLI LLLVITYTAIFTPYSAAFLLNDREEQKRRECGY SCSPLNVVDLIVDIMFIIDILINFRTTYVNQNEE VVSDPASV
245	1595	A	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFLDNVIMW WESLLLLTAYFCYVVFMMKFNQVEKWVVKQ MINRNKVVKVTAPEAQAKPSAARDKDEPTLP AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD PHV
246	1596	A	2660	200	506	VLVLQMNYQMLIITYVLFKVFNEFLAFEGPI LLDMRIKHLIKTNQLSQATALAKLCSDHPEIG IKGSFKQTYLVCLCTSSPNGKLIIEVSMFSFIS NYFLS
247	1597	A	2678	3	267	DAWVKNDIIFNQTERKQKISENLKHLASVRV VQKNLVFVVGLSQRLADPEVSPLVFFVILIFF VLSYLEIIFDPAQLCDSSEHIS
248	1598	A	2687	1	404	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF GAAIKSVKNPDKKS IENQVLDLSLVPLLLYSQD ENDAVAEESRQVLTICAQFLKWKLPREVYSK DPWHIKPTEAGTICRFFEKCKGKINLEQTL MYSKNPKL
249	1599	A	2692	1	440	FRRRRRRRERDCAAQGARRHCRHLAECKLV SFPIGIYKVL RNVSGQIHLITLANNELKSLTSK FMTTFSQLRELHLEGFLHRLPSEVSALQHLK AIDL SRNQFQDFPEQLTALPALETINLEENEIV DVPVEKLAAMPALRSINL
250	1600	A	2693	459	21	LLPGSLGVPILHSQPWDPSQCPRAPSTPRRL PPLGALSQALTFLSRAAKNHSQDPGKGT KPP AAPAAPPPRSSLPAPLPMGLKDKGPQAPPTIF NSPWHFATLPGALOPQLSQAAPSPIPPPCLMG ISSCPDLKLTKSSTP
251	1601	A	2694	2	404	FVFDLKL RVPGF AALLIHGASSVPGPETVRLR

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						QKRKKKAPDHSSGRKEELVTTHTVDKLETKK PVGRVLCGLSGELLHSLLP RRKTEKRALGSH RKAGFPEHPVAPEPLSNQCISKEGREQVLSEI GAGDCL
252	1602	A	2697	421	1	PKSHSGAYQCFATRKAAQTAQDFAIALEDG TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPT VTWALDDEPIVRDGSHTNQTMSDGTITISH MNVTPQIRDGGVYRCTARNLVGSAEYQARI NVRGPPSIRAMRNIT
253	1603	A	2698	65	401	ACCQWRRTLIPAKSTTVSCTISTPHHPFRGSYS FDDHITDSEALSRSSTVFTSHPRMLKRQPAIEL PLGGEYSSDVPRLSTQLSSSLG YFSTLMTG AFTNNIASSTIL
254	1604	A	2699	438	301	GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ RVRGPWEAGPGVGY
255	1605	A	2700	1	842	LQNRDSSSEGIRKKLVEAEELKEKHREAQVS AQHLEVHLKQKEQHYEBKIKVLDNQIKKDLA DKETLENMMQRHEEEAHEKKGKILSEQKAMIN AMDSKIRSLEQRIVELSEANKLAANSSLTQR NMKAQEEMISELRQKQFYLETQAGKLEAQN RKLEEQLEKISHQDHSKRNRLLELETRLREVS LEHEEQKLELKRQLTELQSLQERESQLTALQ AARALESQLRQAKTELETTAEAEIEIQALET VGLGSNIFRLKASARMSVELALSILAHF
256	1606	A	2701	2	405	FVGGPGADPPVAVMWDPRAARMDLTAYAE LLKESGNQVLKNGNPSLAIRKYDEAIQILLQL YQWGVPPRDLAVLLCNKSNAFFSLGKWNIA FVAAKECLQWDPTVYKGYRAGYSLRLHLQ PYEAARMFFEGLR
257	1607	A	2702	2	399	FVESASSRPPGCFSGDGRFWLVSEGSRRGWD FNPFSFLDPRYSVGGDENIGTVITLANILREF NPSLKGFSVGTGKETSFNALNQA VAGGRAE DLPVQARRLVLMKNDTRIHFQEDWKIITLFI GGNDL
258	1608	A	2709	1	1097	SVGARQGEARDRIIRFFPKGDLEVLQAQVERI MTRKELLTVYSSDGESEFETIVLKALVKAAG SSEASAYLDELRLAVA WNRVDIAQSEIFRGDI QWRSFHLASLMDALLNDRPEFVRLISHGLS LGHFLTPMRLAQLYSAAPSNLIRNLLDQASH SAGTKAPALKGGAELRPPDVGHVLRMLLG KMCAPRYPSGGA WDPHPGQGFGESEMYLLSD KATSPLSLDAGLGQAPWSDLLWALLNRA QMAMYFWEMGSNAVSSALGACLLLRVMAR LEPDAAEEAARRKDLAFKFEFGMGVDLFGECYR SSEVRAARLLLRRCPLWGDATCLQLAMQAD ARAFFAQDGVQSLPTQKWWGDMARR
259	1609	A	2721	1	403	VYLGAGPGLFFSNEGAKGEKANIPKMLLPR GGFSQREMVTGERSPSEEEEEEEGFGERA SCRRGLFRVRLTRVGLAAPSASRGQEGDAA PKSPVREKSPKFRFPRVSLSPKARSGSGDQEE GGLRVRLP
260	1610	A	2728	1	477	LLOGDLRYHLQQNVHFTGTVKLYICELALA LEYLQRYHIIHRDKPDNILLDEHGHVHTDFN IATVVKGAERASSMAGTKPYMAPEVFQVYM DRGPGYSYPVDWWSLGITAYELLRGWRPYEI HSVTPIDEILNMFKVERVHYSSTWCKGMVAL LRK
261	1611	A	2730	3	547	LTITDFILVLYRYRSPLVQIYEIBQHKIETWR EYLLQGCFKPLVSISPNDLSFEAVYTLIKNRH

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						RLPVLDPVSGNVLHILTHKRLKFLHIFGSLLP RPSFLYRTIQDLGIGTFRDLAVVLETAPILTAL DIFVDRRVSAALAVVNECGTHPQDERLGLGW GLGEPGSEERLFPAAITSR
262	1612	A	2733	3	431	GPEFFPGSAKLVLFDLSYNNLTQLGAGAFRSA GRLVKLSLANNLGVGHEDAFETLESLOVLE LNDNNLRSLSVAAALALPALRSLRLDGNPWL CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM ESRRISLRACRRPASRV
263	1613	A	2736	2	343	PARISGVDPVPRKATKGGENCSEFNKNWQF LWGLNGNFFKEPWGGRNNHAKGFRITW ARSSSQNNRTFQNNRNLRLQRDSQKKQGFA RLISPLVNLQSPGGLEFYQAT
264	1614	A	2738	2	245	RAMLKCLREGQPPSYNWTRLDGPLPSGVRV DGDTLGFPLTTEHSGIYVRHDTNEFSSRDH DTVDVLDPPEDSGKQVDL
265	1615	A	2752	2	388	AAGDAPLRSLQANRTFPFSDVKGDHRLV LAAVETTVLVLFVAVSLGNVLCALVLVARR RRGATACLVNLFCADLLFISAIPVLAVRWT EAWLLGPVACHLLFYVMTLSGSVTILAAV SLER
266	1616	A	2755	192	1	AFREVGGYWGLLCEHLYAIPSKTSEGNWTAK LQGYLPLQDAFHIFQDPLTGDLPWPPELILGP V
267	1617	A	2760	434	714	ASRLEKQNSTPESDYDNTPNDEPDGMGYM HRTSVPGEGLPRAEDLAGLGQQKQFTTHTPF LYFQTHKGLKSSIRSEVTCLGISQCWRKGGF
268	1618	A	2762	1	405	IACFCGQDEWSPERSTRCFRRSRFLAWGEP AVLLLLLLSLALGLVLAALGLFVHHRDSPL VQASGGPLACFGLVCLGLVCLSVLLFPQSP ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE LPLSWAE
269	1619	A	2772	3	243	TRPAEKIQYLVLFVMSHPSQAYDKLSLSDHL LIAVLNLLRREVSEHGRHLQQYFNLVFMVYAN LSKNLSFSEFCFDVSY
270	1620	A	2789	1	486	ELQSQAQCTHTKETEQLRSQQLTKQQHQQA VEQIAKAEETHSSLSQELQARLQTVTREKEEL LQLSIEGKVLQNKQAEICQLEEKLEIANEDR KHALERFEQEA VAVDSNLRVRELQRKVDGIQ KAYDELRLQSEAFKKHSLDLLSKERELNGKL RHLSF
271	1621	A	2795	1	568	KEKRVTVQLPTESIQKNQEDKLMVPRKQRE FSGSDRGKLPGSEKINQGPSMIGRKEERLITE RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN FQQTQIQTAESKAHKKLPQYNSLQEEKCLE VKGIQEKQVFSNTKDSKQETQNKSFSSVKE SQRDDGKGALNIVEFLRKREELHQLSTVKQP
272	1622	A	2797	8	523	KCMQKGKYGAMESEPCVCTEADFCDYGYE RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST GYRKVVSNCTDGVREQYTAQPKCPGKAP RGLRIVTADGKLTAEQGHNVTLMVQLEEGD VQRTLQVDFGDGIAVSYNLSSMEDGDXHV YQNXGIXRXTVQVDNSLGS
273	1623	A	2801	72	395	HPSRSNVGPRQLTVWNTSNLSDNRRKYIFS DEEQNQLGIRIHQDIPFPRRRELALRTTNG KADSLNVSRSVMQELSELEKQIQVIRQELQL AVSRKTELEEH
274	1624	A	2805	168	320	ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE IFIARNGVVGETLTHCKRV

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275	1625	A	2812	208	321	GSLATCQLSEPLLWFLRLVDTSDALKAFHD MGKIIFQ
276	1626	A	2813	41	266	AORSLHGAGDRAWVGISPTDWSPKVVELCK KYQQQTVVAIDLAGEITIPGSSLLPGHVQAY QVGPVRRNGEAGPG
277	1627	A	2817	3	410	VLQERLDNFQKRCIQLASSTEGKVDKLLMRN LFISYLHTPKHKQHEVLQAMGSILGITGEEME PLFQEEHGTATRWMTGWLEGGSKSVKPTPL GLNQQPALNGSFSEJ.FVKFLKTESLSSTLPTX LPPHNSPGKIK
278	1628	A	2821	238	457	GLSGPSCSCPHSPLPTIISRAQLETALKWRNVE VKLRLLHLLEELQMEHDIRHYDLESVPMTWD PVDQNPRLV
279	1629	A	2822	342	1	PLIPANLPAHSNPLQPLPSLPHPLPATHKFFPT TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS CRLPSRPSVSRELPPQSGPASSVPLAPTLPLDS VPSQRHPTXPPAS
280	1630	A	2825	307	77	PSMVWSYHWGVKQKRLALCVSFEEGGRRK CGQYWPLEKDSRIRFGFLTNTLTGAVGEPG VAFQCDGQRRREPTC
281	1631	A	2827	81	381	KMGTA VWPKEKEKRDKASQEGGDVLGAR QDCITPSLKS L V A T G N L L D E E T A K A P L S T V S A NTTNMDEVPRPQALS GSSV V W S G C V A S R S VILSLTSG
282	1632	A	2830	471	160	KLPXDKYELEPSPLTQVILERKSPHTCWQVVFV TSSGKYNELGYPPGYLKASTLLTCVNL FVMP YNYPVLLPLDDLDFK VHKLPKPNLKWQAFDS YLKTLPPYYL
283	1633	A	2835	462	148	VSPALS LTPTIFS YSPSPGLSPFTSSSCFSFNPEE MKHYLHSQACSVFNHYLSPTTFPRYPGLMVP PLQQMHPEESTQFSIKLQPPVGRKNRERVE SSEESAP
284	1634	A	2836	2	384	KTLPRTLDDLADGTILKVGVCSEDASKLLQ DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL KSLAETVLNFPDLKSLLLRCSNWD AETLTED QVTYAARDAQISVALFLHLLGYFFSRNSPGEK KR
285	1635	A	2843	20	271	PIRPPYYSGLDRDCSWLPLAKAWLPDVMIL VCDRVSE DGINRQQAQEWCIKHGFELVELSP EELPEEDGKCLCVRRKYGTI
286	1636	A	2845	197	278	TAEDVLTVA YEHGVNLFDTAEVYAAGK
287	1637	A	2851	2	427	FVAEVRREWAKYMEVHEKASFNSELHRAM NLHVGNLRLLSGPLDQVRAALPTALSPKDK AVLQNLKRILAKVQEMRDQVSLEQQLRELI QKDDITGSLVTTDHSQMKLFEEQLKKYDQL KVYLEQNLA AQDRVLCALT
288	1638	A	2859	2	469	FVNLGILTCIECSGIHREMGAHISRIQSLELDK LGTSELLPAKNVGNNSFNDEMEANLPSPPKP TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA KLNELLEAIKSRDLLALIQVYAEGVELMEPLL EPQQLAETALHLA VRTADQTS LHLVE
289	1639	A	2861	2	454	FVASGGPATARMSDSQFFCAEERSGHCAVV DGNFLYVWGGYVSIEDNEVYLPNDEIWTYDI DSGLWRMHLMGELPASMSGSCGACINGKL YIFGYDDKGYSNRLYFVNLRTD ETYTWEK ITDFEQPPITPRDKLSCVWYKDRLLYFG
290	1640	A	2868	1	378	FRQGQLYK VFLHGSQQGVYHSQQVGPFGSAI SPDLLLDSSGSHLYVLT AHQVDRI PVAACPOF PDCASCLQAQDPLCGWCVLQGRCTRKGQCG

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						RAGQLNQWLWSYEEDSHCLHIQSLLPQHHPRQE
291	1641	A	2870	1	385	FRYMPNNRQQLLRKRHIGNDIVTIVFQEPGALPFTPKSIRSHFQHVIVVKVHNPCITENVCYSVGVSRSKDVPPFGPPKGVTFPKSAVFRDFLLAKVINAENAAHKSEKFRAMATRTRQEYILKDLA
292	1642	A	2877	3	188	RPTRPPPTATQSPSTMDTSLKKEKSAILDLIYIPPPAVPYSPRYVAVHCHGMLVSCWCCHI
293	1643	A	2878	1	427	REKEEEVEEEEDKVVKEKEAEQEKEEDSLGAGTHPDAAIPSGERTCGSEGRSRLDLVNYFLSPEKLTAEENRYCESCASLQDAEKVVLSQGPCYLILTLRFSFDLRTMRRRKILDDVSIPLLRPLAGGRGQAYDL
294	1644	A	2879	109	245	QLCCFCFRQTTILVYILSFIGMVIFTFTDLRYIIVFVTGGVLG
295	1645	A	2880	3	320	LASSQHGLNNLSLLFSICKTCIRTMDDHHCPRANNCVGEQNHRRFFCALHCKSKHFCIEFTLNTNFFNCFPLPGAEEKSTIDAPPSLQPFLLQDSKYNTALSLSESISQ
296	1646	A	2892	209	363	SQYSHSLDYHLLQVTKNPFLLGDSNPNQGTERLQEFSSQKMDQVRGHWPVST
297	1647	A	2893	8	424	SPXTLXLDTFILLGIQDNILVLILATPPFMAGOKLYSTMGRFLDRKNPACREMAVLLANLAQGDSLAARAIAVQKGSIGHLLGFLEDSLAATQIQSQASLLHMHNPPEFTSVDMMRACRALALAKVDDNHSEF
298	1648	A	2894	310	445	FWIYFSPFFMTGYLPLGFEEFAVEITYPESEGTSGLLNLSAQVNL
299	1649	A	2898	1	492	KIKAKNLTYDLCISIFLGTSTLLVWVGVIYRILGYFQAYNVILITMQASLPKVLRFACACAGMIYLGYTFCGWIVLGPYHDKFENLNTVAECLFSLVNGDDMFATFAQIQQKSILVWLFSLRYLYYSFISLFTYMLSLFIALITDSYDTIKKQFQNGFPETDLQEF
300	1650	A	2901	1	445	PVWWNSLNGASEVTFVSVHVKDGGSPFKTDSTTVTVRFVFNKADFPKVRABEQTFMFPENQPVSLVYTTITGSSLRGEPMSYYIASGNLGNFTFQIDQLTGQVSIQPLDFEKIQKYVWVWIEARDGGVPPFSSYEKLDITVLDVNDNAPIF
301	1651	A	2902	162	433	THFICLPLGYCFPLLDKDLQLPSGFNCNDFLEEPCGWMYDHAKWLRITWASSSSPNDRTFPGKPAVSEDMKELRPACSTYFNPREFPYKL
302	1652	A	2909	2	412	GPQMLCKKIYFIWVTRSQCFEVLADIMQEV EENDHQDLVSVHIYVTLAEKFDLRTTMLYICERHFQKVLNRSFLTGLRSITHFGRPFFEFFNLSLQEVHPQVRKJGVFSCGPPGMTKNVEKACQLVNRQDRAHFM
303	1653	A	2914	291	453	KLNRWLCFFYSWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKRPSSCS
304	1654	A	2926	179	354	PGVPSQALRKAESLKKCLSVMEAKVKAQTAPNKDVQREIADLGEVGAASLPSSGPGA
305	1655	A	2938	135	438	GMGYLHAKGILHKDLKSKNVFYDNGKVVITDFGLFSISGVLAQRREDKLRIQNGWLCHLAPEIIRQLSPDTEEDKLPSKHSDVFAFGTTIWEYLHAREWP
306	1656	A	2944	2	329	VRWNSCVNCSAFNGASLSTSLGESSGCLWEIGKWLSCSLLSFPPLAVLIITFCIVTVLGREALTKGALWAVFLLAGSALLCAEVTGVIWRQPE

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						SKTKLSFKVSSSA
307	1657	A	2950	2	411	NYLCLAKNSAGSAMGKTRLVVQVFPVIENGL PDLSTTEGSHAFLPCKARGSPENITWDKDGQ PVSGAEGKFTIQPSGELLVKNLLEGQDAGTYT CTAENAVGRARRRVHLTILVLPVFTTLPGDRS LRLGDRLWLR
308	1658	A	2951	1	407	PTRPVRVFDNEFDAESQRKRTTSVSKMERM DSSLPEEEDEDEKEAINGSGNAENRERHSESS DWMKTVPSYNQTNSSMDFRNYMMRDETLEP LPKNWEMAYTDTGMIYFIDHNKTTTWLDP RLCKKAKAPEDC
309	1659	A	2954	2	179	QDFLTTLTTEPTGLLYVGAREALFAFSMEALE LQGAVRGGAVGGSRAQRARPRGAVLG
310	1660	A	2959	1	419	QDMMERAIDTFVGHDDVEPGSYVQMFFPYPC YTRDDFLFVIEHMMPLCMVISWVYSVAMTIQ HIVAEKEHRLKEVMKTMGLNNAVHWVAWFI TGFVQLSISVTALTALIKYGOVLMHSHVVITW LFLAVYAVATIMFCF
311	1661	A	2963	3	465	MKPQMPGLGAPNGYGPGRGRAGVPGGPERR PWVPHLLPFSSPGYLGVMAQKPGAGEGGMK PQKPGRLRGTLPQKSGHGHENGPWPGPCNA RVAPMLLRLPTPGVPSDKBGGWGLKSQPPS AVQNGKLPQHQPNGYGGAEPGFNGGLEPQ KI
312	1662	A	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM HTGGCSPKTKPHKEECIVPTPCYKPEKLPV EAKLPWFQQAQEEGAASVEEPSFPEAWS ACTVTCGVGTQVRVRCQVLLSFSQSVADLPI DECEGPKPA
313	1663	A	2969	2	430	VVADNCRQGYLDALRFLERRGLTKEPVLWT LVSKEPPAPADGNWDAGCDQRRKGGLSLNW KVPHVQVKDVPNFQELSPLEAALKKACTRD PSRWARFWHSGPGQVLTLYLLPCTLPFEYIYF RSRRLVVWLPDVPADLWWMQ
314	1664	A	2971	422	33	LDXSHNALQRLRPGWLAPLQRLALHLDHNE LDALGRGVFVNASGLRLDLSSNTLRALGRH DLDDLGALEKLLLFNNRLVHLDEHAFHGLRA LSHLYLGCNELASFSDHLHGLSATHLLTDL SSNRM
315	1665	A	2973	1	525	ITVSTHSGSPFGLPEQSQWLWVRAALDREA QELYILKVMAYSGSKAELGQQTGTATVRVSI LNQNEHSPRLSEDPFLAVAENQPPGTSVGRV FATDRDSGPNGLRTYSLQQLSEDSKAFRIHPQ TGEVITLQTLTREQQSSYQLLVQVQDGGSP RSTTGTVHVAVLDLNDNT
316	1666	A	2978	2	400	ELVVELVSAGKSGPERNTYEVQVVTGNVPA GTDANVYLTITYGEEYGDTERPLKKSDESKN FEQQQTDTFTYIDLGALETKIRIRHDNTGNR AGWFLDRIDITDMNNEITYYPCQRWAVEE DDGQLSRE
317	1667	A	2981	3	440	VLNCQGRPTRPVRINGDGOEVLVLAESDNVR LGCYVLDPDYGPNGLDIEWMQVNSNPAH HRENVFLSYQDKRINHGSLPHLQHRVFAAS DPSQYDASINLMNLQVSDTATYECRVKKTMT ATRKVITVQARPAVPMCWTEGQ
318	1668	A	2995	119	414	LPEKEFPIRKSSSLKVTKCLFTEQPKPIILRFA ENYDARLLRIDIANLTLREQVQELFNKTYGKQ RRTPGEGHVAADVREVAGFPVPAEGISGETIH
319	1669	A	2999	2	332	GFFAYTYGRLVVVEDLHSGAQHWSGHSAGI

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						STLALSHSAQVLASASGRSSTTAHCQIRVWD VSGGLCQHIFPHSTTVLALAFSPDDRLLVTL GDHDGRTLALWGTGIL
320	1670	A	3000	693	322	IDESTGLIITVNYLDYETKTSYMMNVSAITDQA PPFNQGFCSVYITLLNELDEAVQFSNASYEAA ILENLALGTEIVRVQAYSIDNLNQITYRFDAY TSTQAKALFKIDAITVRGWGQGAFFPI
321	1671	A	3001	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPQPC GWGQSSDLLSRIDLDELMMKKDEPLDFPDILE GFEYAFNEKGQLRHIKTGEFVFVNYREHLHR WNQKRYEALGEIITKYVVELLEKDCNSKKVS
322	1672	A	3007	192	447	ERVNSLFPGRGDSQCACCPSPVWVFLETGF LFPWFLQVEVIKAYMQGEVEFEDGENGK DGAASPRNVGHNIYILAHQLARH
323	1673	A	3019	18	245	KELLFYHLIVNNINFFNTRYAKIHIPHASVSEH QPTTWVSFFFDLHLVCTFPAGLWFCIKNIND ERVFGKRGF
324	1674	A	3020	523	797	LCYFSARYHQKIFGILYIFILSAINRKPEPNLFI YLFIFFEMESHSTHAGVQRHNLNSLQPLPPG FKRFSCLCFLSSWNRYRGAPPGANF
325	1675	A	3022	2	156	NDFLPLYFGWVLTKKSSSETLRKAGQVFLEEL GNHKAFFKELRQCRWQVGAL
326	1676	A	3023	38	172	KMVRGSKKLISFFPGGPGYGLAGRDPSKGLAT FCLNKEALKDEFE
327	1677	A	3027	1	385	LTLEFLLLPAASELAHGKRLACCIVDHKLPEC GFYGLYDKILLFKHDPTSANLLQLVRSSGDIQ EGDLVEVVLASATFEDFQIRPHALTVHSYRA PAFCDHCGEMLFGLVLRQGLKCDGCGCLNYHK RC
328	1678	A	3030	13	569	ITRPTISCQRPGPLAAGMLPYTVNFKVSART LTGALNAHNKAAVDWGWQGLIAYGCHSLV VVIDSITAQTLQVLEKHKADVVKVWAREN YHHNIGSPYCLRLASADVNGKIIVWDVAAGV AQCEIQEHAKPIQDVQWLWNQDASRDLLAI HPPNYTVLWNADTGTKLWKKSADNLSFSF D
329	1679	A	3038	90	744	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAED GNIEYKKLVNPSQYRFEHLVTQMKWRLQEG RGEAVYQIGVEDNGLLVGLAEEEMRASLKT HRMAEKVGADITVLREREVDYDSMPRKITE VLVRKVPDNQQFLDLRVAVLGNVDSGKSTL LGVLTOGELDNGRGRARLNLFRHLHEIQSGR TSSISFEILGFNSKGEVHGNGTQWGTLMG W
330	1680	A	3040	3	397	LCSTLLLLTIPSWVLSQITLKESGPTLMKPTET LTLCTFSGFSLNTSGVGVAWIRQPPGKALE WLALIWDDDKRYSPLNDRLTIKDTSRNQ VVLTMNMGFVDTATYYCAQFARGAGSN WFDPWGQ
331	1681	A	3043	3	1509	AGIRHEAPPTTSNRHRRQIDRGVTHLNISGLK MPRGLAIDWVAGNVYWDSDGRDVIEVAQMK GENRKTLSGMDPEHAIVVDPLRGTMVWSD WGNHPKIETAAMDGTLRETLVQDNIQWPTG LAVDYHNERLYWADAKLSVIGSIRLNGTDPI VAADSKRGLSHFFSIDVFEDYTYGVYINNRV FKIHKFGHSPLVNLTGGLSHASDVVLYHQHK QPEVTNPCRKKCEWLCLLSPSGPVCTCPNG KRLDNGTCVPVSPPTPPDAPRPGTCNLQCFN GGSCFLNARRQPKCRCQFRYTGDKCELDQC

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						WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC TQQVCAGYCANNSTCTVNQGNQPCRCCLPG FLGDRCCYRQCSCGYCENFGTCQMAADGSRQ CRCTAYFEGSRCEVNKCSRCLGACVVNKQS GDVTCNCIDGRVAPSLTCVGHCSNGGSC MNSKMMPECQCPHMTGPRCEEHVFSQQQP GHILASLIP
332	1682	A	3045	3	952	TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG AVDEEVGDYFPEFLDMLEESPLKMTLPWGT LSSLRLQCRSQSDDGPIMWVRPGEQMIPTAD MPKSPFKRRRSMNEIKNLQYLPRTSEPREVL EDRTAHADHVGQGFWDQSTAAVGVLKAV QFGEWSDQPRITKDVICFHAEDFTDVVQRLQ LDLHEPPVSQCQVWVDEAKLNQMRREGIRY ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW HIRLKQYHPVVEATQNTESNSNMDCGLTGKR ELEVDSCQVRKTESEEAETIQLLTASSSFP PASE
333	1683	A	3046	497	167	SACSTGPELPGRATRSLTRPANQKCGCDGRL YYDGCAMIAMNGSVFAQGSQFSLDDVEVLT ATLDLEDVRSYRAEISSRNLAVSAPVDTCVG CSSKTWKVAPFVRAWWRP
334	1684	A	3053	37	276	VITDLEEQLNQLTEDNAELNNQNFYLSKQLD EASGANDEIVQLRSEVDHLRREITEREMQLTS KQVRRVNVKVVRSLEDF
335	1685	A	3054	2	846	WDAWGDWSDCSRTCGGGASYSRLRCLTGR NCEGQNIRYKTCNSHDCPPDAEDFRAQQCSA YNDVQYQGHYEWLPRYNDPAAPCALCKH AQGNLVVELAPKVLDTGTRCNTDSLDMCISG ICQAVGCDRQLGSNAKEDNCGVCAGDGSTC RLVRGQSKSHVSPEKREENVIAVPLGSRSVRI TVKGPAHLFIESKTLQSKGEHSFNSPGVFVV ENTTVEFQRGSERQTFKIPGLMADFIKTRY TAAKDSVVQFFFYQPIHQWRQTDFFPCTVT CGGG
336	1686	A	3058	54	347	VVGKQEAGAHSDSCCLLHTPPRLTPAHSRKA LRNSRIVSQKDDVHVCMICLRAIMNYQVSRG AWDWRLGSPACPHWGLHKLPLRWDPLSLYP VLCWGT
337	1687	A	3059	2	709	ILTSLVELTRFETLTPRFSATVPCWVEVQQE QQRRHPQHLHQHHGDAQAHTRTWKLQT DSNSWDEHVFELVLPKACMVGHVDFKFVLN SNITNIPQIQVTLKKNAPGLGKVNGLRLCPF LEDHKEDILCGPVWLASGLDLSGHAGMLT SPKLVKGMAGGKYRSFLIHVKA VNERGTEI CNGGMRPVVRLPSLKHQSNKGYSLASLLAK VAAGKEKSSNVKNENTSGTRK
338	1688	A	3060	85	384	KAFYNYHVELELLQMLVTGGVSSQLEQHLDK DKVYGVADSCSLLSGRNRCKLGLSLHETIL SDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDE EELNP
339	1689	A	3063	236	362	CFLCSGDFMVMTIFFNVSRRFYGYAFQNYV PSSVTTMLSWV
340	1690	A	3065	3	1249	DLWQFTPLHEAASKNRVEVCSLLSYGADPT LLNCHNKSAIDLAPTQPKERLAYEFKGHSL QAAREADVTRIKHLSEMVNFKHPQTHETA LHCAAASPYPKRKQICELLRLKGANINEKTKE FLTPLHVASEKAHNDVVEVVVKHEAKVNAL DNLGQTSLHRAAYCGHLQTCRLLLSYGCDPN

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						IISLQGFALQMGNNVQQLQEGISLGNSEA DRQLLEAAKAGDVETVKKLCTVQSVNCRDIE GRQSTPLHFAAGYNRVSVVEYLLQHGADVH AKDKGGLVPLHNACSYGHYEVAELLVKHGA VVNVADLWKFTPLHEAAKGYEICKLLQ HGADPTKKNRDGNTPLDLVKDGDTDIQLLR GDAALLDAAKKGCLARVKLSSPDNVNCRD TQGRHSTPLHLAKG
341	1691	A	3070	1	547	GVLIPSFQNLFAADILAGIESVTSEHNYQTLIA NUNYDRDSEEEVINLLSYNIDGILSEKYHTI RTVKFLRSATIPVVELMDVQGERLDMVEGFD NRQAADFDMVCTMLEKRVHKLILYLGSKDDT RDEQRYQGYCDAMMLHNLSPLRMNPRAISSI HLRMQLMRDALSANPDLDGVFCTN
342	1692	A	3073	463	3	RINRCRKPDSADILVPGDTISLIGTTSRLIDYNE IDDNRVTAEEVDILLREGEKLAPVMAKTRILR AYSGVRPLVASDDDFSGRNVSRGIVLLDHAE RDGLDGFITTTGGKLMTYRLMAEWATDAVC RKLGNTRPCTTADLALPGSQEPKVP
343	1693	A	3075	250	1	LLIYLAIAPVAMSALAGVKSQVQVRIRAAQS LGASRAQVLFVILPGALPEILTGLRIGLVG WSTLVAAELIAATRGLGFM
344	1694	A	3076	2	138	LYFDAYLQSLQVAAISTFCCLLIGYPLAWAV AHSKPSTRNILL
345	1695	A	3078	469	3	LKIRGQRIELGEIDRVMQALPDVEQAVTHAC VINQAAATGGDARQLVGYLVQSGLPLDTSA LQAQLRETLPFHMVPVLLQLPLIANGKL DRKALPLPELKAQAPGRAPKAGSETTIAAFS SLLGCDVQDADADFFALGGHSLAMKLAT
346	1696	A	3082	404	2	QNITSKDLVRLDPQTVPIELQLVLSFNHMI ERIEDVFTQSNFSADIAHEIRTPITNLITQTEI ALSQSRSQKELEDVLYSNLEELTRMAKMVSD MLFLAQADNNQLIPEKKMLNLAHEVGKVF QFEALPE
347	1697	A	3084	3	340	NELTFKEAEISKLYTKVHPAYRTLEKRALE DEKAKLNGRVLTAMPKTQQEIVRLTRDVEGQ QVYMQLLNKEQELKITEASTVGDVRIVDPAIT QPGVLKPKKGLILGAI
348	1698	A	3086	723	10	TQAMVWQQKACAEDDPQLSGRHWLHAATL YNIAAYPHLKGDDLAQAQALSNRAYEEAA QRLPGTMRQMEFTVPGAPITGFLHMPKGDG PFPTVLMCGGLDAMQTDYYSLYERYFAPRGI AMLTIDMPVSGFSSKWKLTQDSSLLHQHV LALPNVPVVDHTRVAAFGRFGANVAVRLAY LESPRLKAVACLPVVHTLLSGLKCCQQVPE MYLDVLASRLGMHDASTKSSTRENH
349	1699	A	3087	2	249	RIRSSDPEITLAGTPLHAYLIGMTLICAGFSV GFGVAMSQALGFFSLRAGVASSTLGIAQVCG SSLWIWLAADVVGIGAWNM
350	1700	A	3099	3	424	EAPETPQSPQPGPSSPISLSAEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVSPNCNTVQEKTFN KDTVIVSEPSDEESQGLPTMARRNDISELE DLSGMEDLK
351	1701	A	3108	2	404	IKKNHIGYQLLHRRALFEKRTLSDYALIFG MFGIVVMVETELSWGAYYKAPLYSLALKCL ISLFTILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD GLDLP

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352	1702	A	3110	341	2	AQLAEVCPPTLLTTNTSSITAAAEIKNPER VAGLHFFNPAPVMKLVEVVSGLATAAEVVE QLCELTSWKGQPVRCSTPGFTVNRVARPY YSEAWRALEEQAPEVI
353	1703	A	3111	3	188	HFSLFRIAFVFLTYMTVGLPLPVIPLFVHHEL GYGNTMVGIAVGIQFLATVLTGRYAGRLA
354	1704	A	3116	367	225	WQLFILNGTTLNIGETDTESCVNGWVYDRSS FPFSNMTEVRGLVFLS
355	1705	A	3117	101	53	VINLVYI.ISSPRPELKPVDKESEVVMKFPDGF EKFSPPILQLDEVDFYYPKHVIFSRSLVSADL ESRICVVGENGAGKSTMLKLLGDIAAPVIRGI RHAHRNLKIGYFSQHHVGAAGT*TFACGNL LGTQVFLGRPEEYRHLQGFMGISGELGHA SSLPACLGQKEAEVAFCDGLLPCPNFLAILA DEPTNHLGHGRAIEALGPCLOTISGVGVILVS HE*SALSRLVCRELVWC*GRSTSPF
356	1706	A	3121	137	466	RGGRDWGEHNRQLEEHQARAWQGMADAG AASREHARWQGTGLAPGTRVAVAPTVCVQGL PQERSVCRPFSSRWREGPVWALGAGAHGKP RWGGVRCVVRGGRWFTPAFH
357	1707	A	3124	1249	229	MLEAPGPSDGCELSNPASRVSCAGQMLEVQ PGLYFGGAAVAEPDHLREAGITAVLTVDS EPSFKAGPGVEDLWRLFVPALDKPETDLLSH LDRCVAFIGQARAEGRAVLVHCHAGVSRV AIIAFLMKTDQLPFEKAYEKLQILKPEAKMN EGFEWQLKLYQAMGYEVDTSATYKQYRLQ KVTEKYPELQNLQELFAVDPTTVSQGLKDE VL YKCRKCRRLFRSSILDHREGSGPIAFAH KRMTFSSMLTTGRQAQCTSYFIEPVQWMESA LLGVMDGQLLCPKCSAKLGSFNWYGEQCSC GRWITPAFQIHKNRVDEMILPVLGSQTGKI
358	1708	A	3127	816	139	EVETLGPRTPGP/EAQSPTPGSCPGWQEPSPGP TPPP*LSGPGPGQAPVLGKLLPDPEETPAGKTP LGKHFWWGLPVTSAFSPGAAA*FGGALSPP GGDL/GHMLLQGPSPFRLQQQ*QTPPGSHSP PTANREINPGAAAADTRSCWGHKRSWRGW RGLAPWRLGFGSPGIP*PAPAGIP/GRPTWEGG KGAGGKPSETLTRSPFVWRGKRSANGFLSW VQILQ
359	1709	A	3132	3	191	HEHLLLLLVCFLVKSQGVNDNEEGFSSARG HRPLDKKREDAPNLRPALADITVCDYRAQIA *AASTPKRAASIAHNAVSCR*AQIA
360	1710	A	3134	1	286	REPPRPALLFF*DRVSLCCPGWNAVVSQSLT AAPTQVQ/SDSPITPSSWDYRHHVPEYANFL *RQGFPMPLRLVSNWAQTVHPPRPVKVLDL QA
361	1711	A	3135	56	1449	PVPAPRVSPSARGAPGRFRLPGVRGRHS/WA AD*RGSRM/PPRAPAPSTGP/APGGKKVGR VPEDPDAYEPRCSAL*V*PTHVTSQFCDP*N GQIRSYFTVLLRGLNETMLVK/PLCREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMMWMLCLAAQQ APGLPHRTSIRPGWRRLTEPAWARRHRRPW GQRGAVRPPPQAAPPPSHQGRRTNIDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASORLPEVIYGVVTLFTPEAGT F/LIPSPT*MSPALVIQFPVPTQMGLRISGLPR QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RNQSPLGNDTLSSGLPMGPRRQVWPLARVG GHSSPREPQVLKKPLWGQTDIAGVGSASLYP DNL
362	1712	A	3136	1270	274	RVGMVLGTREVG DSTPPSPPLYPFTGNEFVQ HNTWQLSRVYPSDLRTDSSNYPQELWNAG CQM/V*GGSRDWEEGVEEQVGNKFSSDGR VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS LKEGLEGLHGESCSFLLGPSVAMNMQTAGL EMDICDGHFRQNGGCGYVLKPDFL.RDIQSSF HPEKPISPFKAQTLNQNVISVQQLPKVDKKE GSIVDPLVKVQIFGVRLDTARQETNYVENNG FNPHYWGQTLCFRVLGPDPFMLRFKMDYDW KSRNDLLGKTPCPGT CMQGYRHHLLSKDG ISLRPASIFYICIQEGLEGDES
363	1713	C	3139	60	248	MFAGSYGKSMFSSKVLNCLPKWRYHFVIA PAMNESPLAPHLHQHLVFSVFQVLTILIGV**
364	1714	A	3140	57	418	SAFKTLQLPAFSLYFDLGSLLKLLRIHTSIVK NHKVESPRTMSPG*DPQSFLQIPQPRPQLRV GLTSGLIQHFSPPSCQFLLRGPPFPQPPLGI SGASLCPVLSPPR*PLQPSLL
365	1715	A	3145	122	413	LLPYPSLFVFLRQCHFVTRLECNGVVSACHN LHLPGSSDSPASAS*VAGTTGVCHHTRLIFVF LV*TGPHYVAQAGLELLTA*SVPQLPKVVGL QA
366	1716	A	3150	247	2	VGEKLHDIRFGNDFDMTPKAQATKEKIDKLN FIKKKLCIEGYY/NREPQNGRKIFANYVSDK GLMATIYEELLKLSNKLIIQ
367	1717	A	3152	3	2367	QKLKQNPQKRAHVEDGGSRSKQGNEQSKKT PIEKSDFAAATHPRAFYLSKPDETPNWMSD SGTGLTYWKLEEKDMHHSLLPETLEKTFISLSS TDVSPNQVLTLDPTLHMKPQKQISGIQPHGLP NALDDRISSPDSVLEPSMSSPSDIDSFSQASN VTSQLPGFPKYPSHTKASPVDSWKNQTFQNE SRTSSSTFPSVYTITSNDISVNTVDEENTVMVAS ASVSQSQLPGTANSVPECISLTSLEDPVLSKIR QNLKEKHARHIADLRAYYESEINSLKQKLEA KEISGVEDWKITNQILVDRCGQLDSALHEATS RVRTLENKNNLLEIEVNDLRERFSAASSASKI LQERIEEMRTSSKEKDNTIIRLKSRLQDLEBAF ENAYKLSDDKEAQLKQENKMFQDLLGEYES LGKEHRRVKDALNTTENKLLDAYTQISDLKR MISKLEAQVKQVEHENMLSLRHNSRIHVRS RANTLATSDVSRKWLIPGAEYSIFTGQPLDT QDSNVNDQLEETCSLGHRSPLEKDSST/GSSST SLLIKKQRETS DTPIMRALKEDEGKIFKNWG TQTEKEDTSNLL*/INPRQTETSVNASRSPEK CAQQRQKRLNSASQRSSSLPPSNRKSSTPTKR EIMLTPVTVAYSPKRSPKENLSPGFSHLLSKN ESSPIREKTYSEKATDNHVNHSCEPVPNGV KKVSVRTAWEKNKSVSYEQCKPVSVTPQGN DFEYTAKIRTLAETERFFDELTKEDQIEAAL SRMPSPGGRI TLQTRLNQVKCLSLNLL
368	1718	A	3163	2	2350	EFKSGGCGAGLVAAGAVLVLYPASRAGERT RVPGSPAPSSPLHSPGACGTEVDMDFQRSPL LEVKGNIELKRPLIKAPSQPLSGSLRKRRPDQ MEDGLEPEKKRTRGLGATTKITTSHPRVPSLT TVPTQTGGTTAQKVSCKTGPRCSTAIATGLK NQKPVPAVPVQKSGTSGVPPMAGGKKPSKRP AWDLKGQLCDLNAELKRCRERTQTLDQENQ

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						QLQDQLRDAQQVVKALGTERTTLEGLHAKV QAQAEQGGQELKNLRACVLELEERLSTQEG VQELQKKQVELQEERRGLMSQLEEKERRLQT SEALSSSQAEVASLRQETVAQAALLTEREER LHGLEMERRRLHNQLQELKGNIRVFCRVPRV LPGEPTPPGGLLLFSPGGGPPDPPTRLSLSRSD ERRGTLGAPAPPTRHDFSFDRVFPFGSGQDE VFEEIAMLVQSALDGYPCIFAYGQTGSGKTF TMEGGPGGDPQLEGLIPRALRHLFSVAQELSG QGWYTSFVASVVEIYNETVRDLLATGTRKGQ GGECEIRRAGPGSEELTVTNARYVPVSCEKEV DALLHLARQNRAVARTAQNERSSRSHSVFQL QISGEHSSRGLQCGAPLSLVDLAGSERLDPGL ALGGERERLRETQAINSSLSTLGLVIMALSN KESHVPYRNSKLTLYLLQNSLGGSAKMLMFV NISPLEENVSELSNLSRFASKVEPSVLFGTAQS NRKWKTDPDLVCVCVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGCFIGWRAPCPRAIK
369	1719	A	3165	365	12	GYTSQGRWIDIERGPLTANTESLHNNFNALP GYRKIE*I*TYKKN*INFGGVLLNIVKISILS/K IYRFDAIPVKILTRFFINLDKILKFLVKTKIAK NRIKTFYIMRRKKLGDS
370	1720	A	3170	393	42	GASISPSAVIDGVEGLKPMQEQEAQAGPCLD *HMAPEQWVAPRRLRLIFSVLHALIAAAAA QSSAEEDPRN*GQSSDQAPNQGLIVTVH RVHVPLGAAATVPVHRSHFPR
371	1721	A	3173	770	510	GNGGCGLSQIPPSHLGAFSRGSLLSRGDPRGP PPHPVIFVFVVEIGQFTVLARMVVIS*PCDPP ALASQSGITGVSHLARPQNLVYF
372	1722	A	3180	381	76	RVLHHDNVPAHSSPQKREISQEFQLEIRHLP*S PDLAPSGCFLFLNLKNIFK/GTHFSLVDNVKK TVSTWLH/SQNAQFYKDRNLNGWYHCLQKCL QHY*AYVEK
373	1723	A	3181	410	14101	RREVAGPEGKGLLLASAHTMLTPPLLLLLPL SALVAAIDAPKTCSPKQFACRDQITCISKGW RCDGERDCPDGSEAEICPQSKAQRCQPNB HNCLGTELCVPMRLCNGVQDCMDGSDGEP HCRELQGNCSRLGCQHHCVPFLDGPCTYCNS SFQLQADGKTCKDFDECSVYGTCSQLCTNTD GSFICGCVGYLLQPDNRCKAKNEPVDRPP VLLIANSQNLATYLSGAQVSTITPTSTRQTTA MDFSYANETVCWVHVGDAAQTQLKCARM PGLKGFVDEHTINISLHHVEQMAIDWLTGN FYFVDDIDDRIFVCNRNGDTCVTLLDLELYNP KGLALDPAMGKVFFTDYGOIPKVERCDMDG QNRKTLVDSKIVFPHGITLDLVSRLVYWADA YLDYIEVVDYEGKGRQTHQGLIEHLYGLTVF ENLYATNSDNANAQKQTSVIRVNRFNSTFY QVTRVDKGGALHIYHQRQPRVRSACEN DQYKPGGCSDICLLANSHKARTCRCSGFS LGSDGKSCCKPEHELFLVYGKGRPGIIRGMD MGAKVPDEHMIPENLMNPRALDFHAETGFI YFADTTSYLGROKIDGTERETILKDGHNVE GVAVDWMGDNLVWTDGPKKTISVARLEK AAQTRKTLIEGKMTHPRAIVVDPLNGWYMW TDWEEDPKDSRRGRLEAWMDGSHRDFVT SKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI LLNGTDRKIVYEGPELNHAFGLCHHGNYLFW TEYRSGSVYRLERGVGGAPPTVTLRSERPPI

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						FEIRMYDAQHQVGSNKRVRNAGCSSLCL ATPGSRQCACAEDQVLDADGVTC LANPSYVP PPQCQPGEFACANSRCIQERWKCDGNDCLD NSDEAPALCHQHTCPDRFKCENNRCPNRW LCDGDNDCGSEDES NATCSARTCPPNQFSC ASGRCPISWTCDLDDCGDRSDESASCA YPT CFPLTQFTCNNGRCININWRCDNDNDCGDNS DEAGCSHSCSSTQFKCNSGRCIPEHWTCGD NDCGDYSETHANCTNQATRPFGGCHTDEF QCRLDGLCIPLRWRCDGDTDCMDSSEKSC GVTHVCDPSVKFGCKDSARCISKA WVCDDG NDCEDNSDEENCSLACRPPSHPCANNTSVC LPPDKLCDGNDDCGDGSDEGELCDQCSLNN GGCSHNCSVAPGEGIVCSCPLGMELGPDNHT CQIQSYCAKHLKCSQKCDQNKFSVKCSYEG WVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLH KGDYSVLVPGLRNTIALDFHLSQSALYWTDV VEDKIYRGKLLDNGALTSFEVVIQYGLATPEG LAVDWIAGNTYWVESNLDQIEVAKLDGTLRT TLLAGDIEHPRAIALDPRDGILFWTDWDASLP RIEAASMSGAGRRTVHRETGSGGWPNGLTV DYLEKRI L WIDARSDATYSARYDGS GHMEVL RGHEFLSHPFATLYGGEVYWTDWRTNTLA KANKWTGHNVTVVQRTNTQPFDLQVYHPSR QPMAPNPCEANGGQGPCSHLCLINYNRTVSC ACPHLMKHLKDNNTTCYEFKKFLLYARQMEIR GVDLDAFYNYIISFTVPDIDNVTVLDYDARE QRVYWSDVRTQAIKRAFINGTG VETVVSADL PNAHGLAVDWVSRNLFWTSYDTNKKQINVA RLDGSFKNAV VQGLEQPHGLV VHPLRGKLY WTDGDNISMANMDGSRNLTLLFSGQKGPVGL AIDFPESKLYWISSGNHTNRCNLDGSGLEVID AMRSQLGKATALAIMGDKLWWADQVSEKM GTC SKADGSGSVLRNSTLVMHMKVYDESI QLDHKGTNPCSVNNGDCSQLCLPTSETTRSC MCTAGYSLRSGQACEGVGSFLLYSVHEGIR GIPLDPNDKSDALVPVSGTSLAVGIDFHAEND TIYWVDMGLSTISRAKRDQTWREDVVTNGIG RVEGLAVDWIAGNTYWDQGFVIEVARLNG SFRYVVISQGLDKPRAITVHPEKGYLFWTEW GQYPRIERSRLDGTERRVVLVNVISWPNGISV DYQDGKLYWCDARTDKIERIDLETGENREV LSSNNMDMFSVS VFEDFTYWSDRTHANGSIK RGSKD NATDSVPLRTGIGVQLKDIKVFNRDR QKGTNVCAVANGGCQQLCLYRGRGQRACA CAHGMLAEDGASCREYAGYLLYSERTILKSI HLSDERNLNAPVQPFDEPHMKNVIALAFDY RAGTSPGTPNRIFFSDIHFQNIQINDDGSRRT IVENVGSVEGLAYHRGWDILYWTSYTTSTIT RHTVDQTRPGA FERETVITMSGDDHPRAFVL DECQNL MFWTNWNQHP SIMRAALSGANVL TLIEKDIRTPNGLAIDHRAEKL YFS DATLDKIE RCEYDGS HRYVILKSEPVHPFGLAVYGEHIF WTDWVRRAVQRANKHVGSNMKLLRVDIPQ QPMGIIAVANDTNSCELSPCRINNGCQDLCL LTHQGHVNCSCRGRI LQDDLTCRAVNSSCR AQDEFECANGECINFSLTCDGVPHCKDKSDE KPSYCNRRCKKTFRQCSNGRCVSNMLWCN GADDCGDGSD EIPCNTACGVGEFRCDGTGTC IGNSSRCNQFVDCEDASDEMNC SATDCSSYF

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						RLGVKGVLFQPCERTSLCYAPSWVCDGAND CGDYSDERDCPGVKRPRCLNYFACPSGRCP MSWTCDEKDDCEHGEDETHCNKFCSEAQFE CQNHRCISKQWLCDSDDCGDGSDEAAHCE GKTCGPSSFSCPGTHVCVPERWLCDDGDKDCA DGADESIAAGCLYNSTCDDREFMCQNRQCIP KHFCVCDHDCADGSDSEPCBYPTCGPSEF RCANGRCCLSSRQWECDEGENDCHDQSDAPK NPHCTSPHKKCNASSQFLCSSGRCAEALLCN GQDDCGDSSDERGCHINECLSRKLSGCSQDC EDLKIGFKCRCRPGFRLKDDGRTCADVDECS TTFPCSQRCINTHGSYKCLCVGEYAPRGDGP HSCKAVTDEEFFLIFANRYLRKLNLDGSNY TLLKQGLNNAVALDFDYREQMIYWDVTQTQ GSMIRRMHLNGSNVQVLHRTGLSNPDGLAV DWVGGNLYWCDKGRDTIEVSKLNGAYRTVL VSSGLREPRALVVDVQNGLYWTDWGDHSL IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTE RIYWADAREDYIEFASLDGSNRHVLSQDIPH IFALTLFEDYVYWTDWETKSNRAHKTGTN KTLISTLHRPMDLHVFFHALRQDPVNPFPK VNNGGCSNLCLLSPGGGHKCACTNFYLGSD GRTCVSNCTASQFVCKNDKCIPFWWKCDTE DDCGDHSDEPPDCPEFKCRPGQFQCSTGICTN PAFICDGDNDQDNSDEANCDIHVCLPSQFK CTNTNRCIPGIFRCNGQDNCGDGEDERDCPE VTCAPNQFQCSITKRCIPRVWVCDRNDNCVD GSDEPANCTQMTGCVDEFCKDSGRGIPARW KCDGEDDCDGDGSEDEPKBCDERTCEFYQFRC KNNRCVPGRWQCDYDNDGDNDSDEESTPR PCSESEFSCANGRCIAGRWKCDGDHDCADGS DEKDCTPRCDMDQFQCKSGHCIPLRWRCD DADCDGSDDEACGTGVRTCPLDEFQCNNT LCKPLAWKCDGEDDCGDNNDENPEECARFV CPPNRPFRCKNDRVCLWIGRQCDGTDNCGD GTDEEDCEPPTAHTTHCKDKKEFLCRNQRL SSSLRCNMFDGCGDGSDEEDCSIDPKLTSCAT NASICGDEARCVTEKAAYCACRSGFHTVPG QPGCQDINECLRFGTCSQLCNNTKGHLCS ARNFMKTHNTCKAEGSEYQVLYIADDNEIRS LFPGHFHSAYEQAFQGDSEVRIDAMDVHVKA GRVYWTNWHTGTISYRSLPPAAPPTTSNRHR RQIDRGVTHLNISGLKMPRGIAIDWVAGNVY WTDSGRDVIEVAQMKGENRKTLSGMDIEPH AIVVDPLRGTMYSWSDWGNHPKIETAAMDGT LRETIVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSKRGLSHPPSIDV FEDYIYGVTYNNRVFKIHKFGHSPLVNLTTGG LSHASDVVLYHQHKQPEVTNPCRKKCEWL CLLSPSGPVCTCPNGKRLDNGTCVPVPSPTTP PDAPRPGTCNLQCFNGGSCFLNARRQPKCRC QPRYTQDKCELDQCWEHCRNGGTCAASPSG MPTCRCTGFTGPKCTQQVCAGYCANNTCT VNQGNQPCRCCLPGFLGDRQYRQCSGYCE NFGTCQMAADGSRQCRCTAYFEGSRCEVKN CSRCLEGACVVNKQSGDVTNCNTDGRVAPS CLTCVGHCSNGGCTMNSKMMPECCQCPHIM TGPRCEEHVFSQQQPGHIASILPLLLLLVL VAGVVFYKRRVQGAQGFQHQRTMNGAM NVEIGNPTYKMYEGGEPDDVGGLLDADFAL

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						DPDKPTNFITNPVYATLYMGHGRHSRLASTD EKRELLGRGPEDEIGDPLA
374	1724	A	3187	191	1815	CLELASAGKPIESKALSLLAPAPTMTSLMPG AGLLPIPTPNPLTTLGVSLSSLAGAIPAAALDPNI ATLGEIPQPLMGNVDPKIDEIRRTVYVGNL NSQTTADQLEFFKQVGEVKFVRMAGDET QPTRFAFVEFADQNSVPRALAFNGVMFGDRP LKINHSSNAIVKPPMTTPQAAAKELEEVMKR VREAQSFISAAIEPGWLHSTSLCNDFLGCF*RR RMYRE*APCTICGTFFHLCLINWDL*LF*AYTA K*FFPPRVWKEQ*KKRRVRSRSHTRSKSRSSSK SHSRKRKSQSKHRSRSHNRSRSRQKDRRRSK SPHKRKSRERRKSRSRSHSRDKRKDTREKI KEKERVKEKDREKEREREKEREKEKERGKN KDRDKEREKDREKDKEKDREKEREKEHEKD RDKEKEKEQDKEKEREKDSKEIDEKRKKDK KSRTPPRSYNASRRSRSSSRERRRRSRSSRS PRTSKTIKRKSSRSPSRSRNKKDKKREKERD HISERRERERSTSMRKSSNDRDGKEKLEKNST S
375	1725	A	3192	415	101	AHSSHQTRAILQEFQWDIIRHPPLSPNLALSG FFPNLKKSLRGTHFSSVKKVITLTLWLNQDP WF/FFYP*SPDLQIPSSFRNGLNDWYHHSQKC PDLGAYVKK
376	1726	A	3199	931	418	GV*WCDLGSPQPPPGFKQFCLGRSSSWDYR HVPHPANFVFLLETGFLHAGQAGLAGDPFAS ASQSAGITGVSHTPWPNHILIFYACLVRSKRI K
377	1727	A	3201	274	1285	KTGYTSRGSPLSPQSSIDSELSTSELEDDISIM GYKLQDLTDVQIMARLQEESLRQDYASTSAS VSRHSSSVSLSSGKKGTCSDQEYDQYSLEDEE EFDHLPPQPRLPRCSPFORGIPHSQTFSSIREC RRSPSSQYFPSNNYQQQQYYSPOAQTPDQQP NRTNGDK/PPKYYA*PSPDAKYNCH**QHSSP VTVRNSQSFDSSLHGAGNGISRIQSCIPSPGQL QHRVHSVGHFPVSIRQPLKATAYVSPTVQGSS NMPLSNGLQLYSNTGIPTPNKAAASGIMGRS ALPRPSLAINGSNLPRSKIAQPVRSFLQPPKPL SSLSTLRDGNWRDGCY
378	1728	A	3202	112	1789	VPGVTSRPSVLRGDHLFALLSSETHQEDFIT YKGFVHKVIEDRVKLSFSMSLLSRFVGW* PFKVNFY/TFNRQPLRVQHRAELTGRWLLW PMLFPVAPRDVPLPSDVKLKLYDRSLESNP EQLQAMRHIVTGTRPAPYIIFGPPGTGKTVT LVEAIKQVVKHLPKAHILACAPNSNGADLLC QRLRVHLPSIYRLLAPSRDIRMVPEDIKPCCN WDAKKGEYVFPKAKKLQEYRVLITLITAGR LVSAQFPIDHFTHFIDEAGHCMFESLVAIAG LMEVKETGDPGGQLVLAGDPRLQGFVLRSP TQKHGLGYSLERLLTYNSLYKKGPDGYDPO FITKLLRNYRSHPTLDIPNQLYYEGELQACA DVVDRERFRCRWAGLPRQGFPIIFHGMGKD EREGNSPSFFNPEEAATVTSYLKLLAPSSKK GKARLSRPSVGVISPYRKQVEKIRYCTIKLDR ELRGLDDIKDLKVTCCSTVTPCLPCAPTCLP ETSSSFHSSPRPRPTAALNRARALPEPLTPGD SNLRVWDGIRKPACLTNTSCHS
379	1729	A	3206	432	130	PKAAPSVXLWFPFL*GSFKPTKGHTXCVXIK *LSTREAXDSXPGRIAXXRQGGKVETTTAL

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						XXQSNKGTTRASSYXEPDAXEQWKFPHKKLQLPGXTHE
380	1730	A	3207	187	507	GGTGHHPARPPLSGVGGCQCSHSPWTAGSPEQRDHPAPHKQIEAGQLPGPAWGG*KGPAAXLLPGPGGGPGPVASLEAQAASSGVTPNGGGRTYPTTFSSGE
381	1731	A	3225	1	840	GTRPGHLPAPSDGFCV/HL*SIPSWGSP*GESL/EMQLITSLGLQEFDIARNVLELIYAQTLVWIGIFFCPI.I.PFIQMMI.FIMFYSKNISLMMNFQPPSKAWRASQMMI'FFIFLLFFPSFTGVLCILAITIWRKPSADCGPFRGLPLFIHSIYSWIDTLSTRPGYLWVVWYRNLIGSVHFFILTLIVLITYLYWQITEGRKIMIRLLHEQINNEGKDKMFLIEKLIKLQDMEKKANPSSLVLERREVEQQGFHLHGEHDGSLDLRSRRSYQEGNPRA
382	1732	A	3238	256	38	LLMIKVSSTCFSCHLHHHHHHHHRRHHQHGHNSLFFSLKSSNSSTLPVYLSYNILVFSKCLVFDFLFSNACL
383	1733	A	3241	1542	343	KGAPSFVRLYQYPNFAAGPHAALANKSFFKADKVTMLWNKKATAVLVIASDVKDGASYYG EQTLHYIATNGESAVVQLPKNGPIYDVVWNS SSTEFCAYVGMPAKATIFNLKCDPVDFGTG PRNAAYYSPHGHLVLAGFGNLILQI*AD/IMK VWNVKNYKLISKPVASDSTYFAWCPDGEHIL TATCAPRLRVNNGYKIWHYTGSLHXYDVP NAELWQVSWQFFLDGIFPAKTITYQAVPSEVP NEEKKVATAYRPPALRNKPITNSKLHEEPPQ NMKPPQSGNDKPLSKTALKNQRKHEAKKAAK QEARS DKSPDLAFTPAQSTPRNTVSQSISGDP EIDKKIKNLKKKLKAEQLKEQAATGKQLEK NQLEKIQKETALLQELEDLELGI
384	1734	A	3242	3	678	IRSPAARSPGLETTPTCLLFVIAAIAAVFVDSAIPRLTQHRPQDGSFFYTLDPLYLPGQCAPPQPLSQCARRVHGEKLRRTFGPRHRGAGTAKMSASLVRATVRAVSKRKLQPTRAAITLTPSAVN KIKQLLDKDPKHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVVVFIEKKAQLTLLGTEM DYVFDKLSSEFVFNPNKGTGCGGESFNI
385	1735	A	3243	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEEILPEPGSEITPVASEALAEHLHGALLRGPMEGYLPGPPLGPEGGEETTTTTTTTTTITVTSPVLCNNNISEGEGYVESPDLGSPVSRITLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAPRLANSSMLGEGQVLRSPTRNLLLHPQSPRVPRGGGFRIHYQAYLLSCGFP RPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGETIINA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRLHLHFERVSLDEDNDRMLMVRSGGSPLSPVITYDSMDDDVPERGLISDAQSLYVELLSETPANPLLLSLRFEAFEDRCFAPFLAHGNVTTTDPYRPGALATFSCLPGYALEPPGPPNAIECVDPTPEHWNDTEPACKAMCGGELSEPAGVVLSPDWQSYSPGQDCVWGVHVQEEKRILLQVEILNVREGDMLTLFDGDGPSARVLAQLRGQPQRRLLSSGPDLTLOFQAPPFPNPGLGQGFVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGTVLTYQCEPGYELLGSDILTQWDLWSAAPPACQKI

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						MTCADPGEIANGHRTASDAGFPVGS HVQYRC LPGYSLEGAAMLTCYSRDTGTPKWS DRV PKC ALKYEPCLNPGVPENGYQTL YKH HYQAGESL RFFCYEGFELIGEVTTTCVPGHPSQWTSQPPLC KVTQTIDPSRQLEGGNLALAILLPLGLVIVLG SGVYIYYTKLQKSLFGSGSHSYSPITVESDF SNPLYEAGDTREYEVSI
386	1736	A	3250	5725	3984	GTSTVTMATKKHFSILNLLGMLLKKDNQDT RKLLMTWALEVAVVMKKSETYAPLFC LPSP HKFCKGLLADTLVEDVNICLQACSSLHALSSS LPDDLQRCVDVCRVQLVHRGTCIRQAFGKL LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP SNTFHPQDFSD/VISFIL YGN SHRTGKDNWLE RLFYSCQRLDKRDQSTIPRNLKTD AVLWQW AIWEAAQFTVL SKLRTPLGRAQDTFQTIEGIR SLAGHTLNPQDQVSQWTTADNDEGHGNNQL RL VLLQYLENLEKLMYNA YEGCANALTSP KVIRTFLYTNRQTCQDWL TRIRLSIMRVGLLA GQPAVTVRHGFDLLTEMKTTSLSQGNELEVSI MMVVEALCELHCPEAIQGI V WSSSIVGKHL LWINSVAQQAEGRF EKASVEYQEHL CAMTG VDCCISSFDKSVLTLASAGCKSASLKHCLNGE SRKSVLSKPTDSSPEVINYLGNKACECYISTA DWAAVQEWQNAIHDLKKSTSSTSLNLKADF NYIKLSSSFESGKFVECTEQLLELPGENINLLA GGSKEKIDMKKILRNM
387	1737	A	3255	380	76	MDIFLYNCKYQVQTEI*NSIQHIMASKKLSRF LKYVHNL*AENYKTLMK*INEDLNKQRDPY S*TARLNKMSIPTKTIFRFKATYIKIPATYFIET NMQ
388	1738	A	3260	685	428	PQWLGLQVYALPPANFVFFVEMRSTILAQTG FELLDSSDLPASASKSAGITCMSHHARTLSLK *WPFLSATQEKFC*PASEGVAV
389	1739	A	3269	1	332	LDGYHTPIYMLNRIPLAAL*ISDQTHALTI LTRLETQMINADYQNKLTLDVLLTTDREVYE PFNLTYNCLHIHQRLGAYDLG*V*Q/KLAHV PVQV*HGFDPEAMFR
390	1740	A	3270	2	372	GRCHDNQNGKSDGPDQAQAEACGGESTYQEL LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH SPRGVKKVHKFVNKGEKGIMVL AGDTLGIGV YCLLPCCMC*DRKLT YAHIPSTTDLGAGAGY
391	1741	A	3273	1	187	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ HVETFFQAEELTRSQEGMKLGENFLMFAMPP DDSKESKGK*FFQEMLDIMKAISDMMGKCTY PVLKEDAPRQH VETFFQVGINQKSRGHEVRR KFPDVCHAPR
392	1742	A	3281	901	521	FFFGDGVSPCRQAGV*WHDLSLQNLPPGFK RFSYLSLPSSWDYRHVLPQANFCIF/M*RRG FTMLARMVSI*PRDLPALASQAGITGVSHH APPQMDFTFALLCFALKGCLPRQKEGTLNLI
393	1743	A	3283	385	3	RNRSVVPEFVLLGLSAGPQTQTLLFVLFVIC LLTVMGNLLLLVINADSLHTPMYFFLGQL SFLDLCHSSVTAPKLLNLLSEKKTISVEGCM A*VFFVFATGGTESSLAVMAYDRYVAIRTR G
394	1744	A	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYHLGKC LDNCPGLEANNHTMECVSI VHC EVSEWNP WSPCTKKGKTCGFKRG TETR VREI IQHPSAKG NLCPTNETRKCTVQRKKCQKGERGKKGRE

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						RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN KQQQ
395	1745	A	3286	1	340	RVLYVPSMGFCILVAHGWWKISTKSVFKKLS WICLSMVILTHSLKTFHRNWDWESEYTLFMS ALKVNKNNAKLWNNVGHAELEKNFERAL KYFLQATHVOPDDIGAHMNVGR
396	1746	A	3293	1	172	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL IAFMKQRRMGLNDFIQKIANNYSACKQ
397	1747	A	3295	12	401	AEPACGASSCTPPSLRSSSSQSVGLRPGRL WSEACAF*AAAPQGPASPCGLPSGFPRVW AQCCPPGGALRFPEGLGVLSPRRCPQVSRGS GLSAVPQEVPSGFLGPGLRACQEAPSRFLRA GLT
398	1748	A	3300	1912	2768	KQRRWQNIQRKGPKRYIVIAGNSQSHQPMIFS MLRKLKPVTCRDVLPFIRAICIEBIGCWMQSY STSFLTDSYLKYIGWTLHDKHREVRVKCVKA LKGLYGNRDLTARLELFTGRFKDWMVSMIV DREYSVAVEAVRLILLKKNMEGVLMVDVCE SVYPIV*ASN*GLASAVGEFLYWKLFYCEI RTMGGREQRQSPGAQRITFFQLLSFFVESKSH SVTQAGVQWQPSAHRDLCLPGSSNSHVSASR VAGIAGAHRTWLIYVFFSWRQGFVLAGL VSNS
399	1749	A	3301	536	2391	LRSYGCKAPSRISHLHKVFLFLPSLLMGYSE SPPITDSWAPPISLTHHVLSQSPLSSNCWI CLSTHTQ*FTALPADLLTWTQSNVSLHISYLA PFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS GRAVALLHLIASGLTSIQINTASSKPPIWGYL STQTSFISPPFLCLSRTPYPAHATMVGGVQPQ SLCGLIFTL/RTPCRPSILHPNYKIISTSAWQKV LCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAAN SALYVSSLGPPGKNVTIPSPVTGT*QPPHRS N/RLTVDKDNFFLSPKPNLSHLQPSQTPYQAL TGAALAGSYPIWENENTLSWLPFTFTYNFCLST PSLFFLCDTN*YLCLPANWSGTCTLVFQAPTI NILPPNQTLISVEASISSSPIRNK WALHLITLLT GLGITAALGTGIAGITTSITSYQTLFTLSNTVE DMHTSITSLQRQLDFLVGVILQNWRLDLLT TEKGGTCIYLQECCFCVNESGIVHIAVRRLLH DRAAEL*HQVADSWWQGSLLRWIPWVAPF LGPLIFLFLLLMIGPCIFNLVSRFISQRLNCFIQ ASMQKHIDNIFHLCHV*YQSLRGNHSEAPEPR P
400	1750	A	3303	2	453	THWRHSSGVPGSTTARRRRRELEIATSDNQE YYNRLCOEVTNRERNDQKMLADLDDLNRK KYLEERLIELLRDKDALWQKSDALEFQKLS AEERWLGDTAEANHCLDCKREFSWMVRHHC RICGRIFYCCNNYVLSKHGGKKERCC
401	1751	A	3304	1	626	MAPQHSSLDDKVPQASTVCFEQDILQHSQ CTEHKDSLWPGGARSQPFGAHNRLSPDSCP EKIVLRALKDSRAGMPEQDKDPGVQENPDD QRRVPQGTGDAPSAFRPLWDNGGLSPFVSRP GPLERDLHAQRSEVTYNQRSQSSWMSSFPKR NAFVSPYSSMGQAQ/PLPKTNPIGESCCWEG LSLSTQILG*QKPSKYPSLCKR
402	1752	A	3305	1678	172	MELPSGPGPERLFDHRLPGDCFLLLVLLLYA PVGFCLLVRLFLGIHVLVSCALPDSVLRFF VVRTMCAVLGLVARQEDSGLRDHSVRVLISN HVTFFDHINIVNLLTTCSTVSEAEASATGRFP

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						GAQLKAPLSPLAFRMEDEALPLTPILYPTCQ FFFFIIFLNIFLLAFSSPGSQPLLNSPPSFVCSWR GFMENNGRGELVESLKRFCSTRLPPTPLLLF PEEEATNGREGLLRSSWPFISIQDVVQPLTLQ VQRTLVSFVSDASWVSELLWSLFVPTVY QVRWLRPVHRQLGEANEEFALRVQQLVAKE LGQTGTRLTPADKAEHMKRQRHPRLRPQS AQSSFPSPWVLSS/SDVQTGQTLGFREFKESF CPHYAIGVFIPERFPWPKTGCKTLTHLL*G GPYSFSCPEADHPRGT*VPTQQASGLPSFFSYG PARGGV*HPSAQQLTFAKSSWARAGRAL QERKQALYAYARRRFTERRAPGGLD
403	1753	A	3307	44	447	DPSPSLLAVALGLRAGERTSRGPGSSPSGGIS GGASAGLASSPECACGRSHFTCAVSALGECT CIPAQWQCDGNDNCGDHSDEDCILPTCSPL DFHCDNGKCIIRSWVCDSDNDCEDDSDEQD CPRECEDE
404	1754	A	3311	409	1	PRHGWGRRVLGRDRPRLQKVKKSVKAIYIPG QDHVQNEEYARVLDKFGSNFLSRDNADLGT AFVKFSTLTK*LSALLKNLLQGLSRNVIFTLDS LLKGDLDKGVKDLKKPFDKA WKDYETKFAK IEKEKREREW
405	1755	A	3322	12	458	AAVVENPWDDPRVPRVRIFTWEDCLAGQA KVLCDNSYGVITDWSPKAFIRLTSQSVNG HPASKENDQMVDTIKNTKVPWWTYGDME PRPQMIRPAVGAKHKELWKILMALKKIKWE GKYTKPSQYNPNYMLELAHNSVW
406	1756	A	3324	1	426	LSMLSTISTEHLRSLVLPWYWCCHCPHLSAV MCVLLWALSLLQSLFWMFCSFLSDVSDN WCQILDFTAVWLIFLNLVLCGFTLVLLVRIC GSQKMLPLRLYVITILLTGLVFLFCSPLSIQ*F LLYWIEKDLDDL
407	1757	A	3328	213	1841	SGDLSPAELMMLTIGDVIKQLIEAHEQKDDID LNKVKTKTAAKYGLSAQPRLVDPAAVPPQY RKVLMPKLLAKPIRTASGIAVAVMCKPHRC PHISFTGNICVYCPGGPDSDFEYSTQSYTGYP TSMRAIRARYDPFLQTRHRIEQLKQLGHSVD KVEFTVMGGTFMALPEEYRDYFIRNLHDALS GHTSNNIYEAVKYSERSLTKCIGITETRPDYC MKRHLSMDLTGCTRLGIGVQSVYEDVARD TNRGHTVKAACESFHLAKDSGFKVVAHMMMP DLPNVGLERDIEQTEFFENPAFRPDGLKLYP TLVIRGTGLYELWKSGRYKSYSPDLVELVA RILALVPPWTRVYRVQRDIPMLVSSGVEHG NLRELALARMKDLGIQCRDVRTREVGIQEH HKVRPYQVELVRRDYVANGGWETFLSYEDP DQDILIGLLRLKRCSEETFRFELGGGVSVREL HVGYSVVPVSSRDPTKFQHQGFGLMMEEA ERIAREEHSGKIAVISGVGTRNYRKIGYRL QGPYMKMLK
408	1758	A	3335	3	467	AIASPRAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESEADLQNDVTDGYLLRVI*VAFIT ERTNQI/REVFNKLIPDSIGKDIEKACQSIPLH DDFARKVKMLKKPKFELRKLMEHHEGSS
409	1759	A	3338	7	1252	PRWRNSARDEILLSPQNYIYQWLNGSLHGL WNLASLFSNLCLFVLMPPAFFLESEGFAGLK KGIRARILETLGMLLLALLILGIVWVASALID NDAASMESLYDLWEFYLPYLYSCISLMGCLL

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						LLLCTPVGLSRMFTVMGQLLVKPTILEDLDE QIYITILEEEALQRPTKWAVFIRW/KYNIMELE QELENVKTLLKTLERRKKASAWERNLVYPA VMVLLLIETSISVLLVACNILLVDETAMPK GTRGPGIGNASLSTFGFVGALEIILIFYLMVS SVVGFYSLRFFGNFTPKDDTTMTKIIGNCVS ILVSSALPVMSTRITGITRFDLLGDFGRFNWL GNFYIVLSYNLLFAIVTTLCLVRKFTSAVREE LFKALGLHKLHLPNTSRDSETAKPSVNGHQK AL
410	1760	A	3339	127	1433	GSHRFSLASPLDPEVGFYCDIPTMRTLNFLL WLALACSPVHTTSLKSDAKKAASKTLEKSQ FSDKPVQDRGLVVDLKAESVLEHRSYCSA KARDHFAGDVLGYVTPWNSHGVDVTKVFG SKFTQISPVWLQLKRRGREMFVETGLHDVDQ GWMRAVRKHAKGLP*CLGSLRTGLTMISG/ YVLDSEDEIEELSKTVVQVAKNQHFDFVVE VWNQLLSQKRVGLIHMILTHLAEALHQRALL ALLVIPPAITPGTDQLGMFTHKEFEQLAPVLD GFSLMTYDYSTAHPQGNAPLSWVRACVQV LDPKSKWRSKILLGLNFYGM DYATSKDAREP VVGARYIQTLKDHPRPMVWDSQVSEHFVEY KKSRSGRHVVFYPTLKSQVRLELARELGVG VSIWELGQGLDYFYDLL*VGIAASAVDVFFSK PWSE
411	1761	A	3342	74	2701	VATRKLAKGFTQFAKMTGKTKTSKFKFFK FKGFSGFNLPRSFITLRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQAEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPVEPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLRDSLTSGLDYVLCRWNRNALHFKIN KVVVKAGESYTHIQYLFQESFDHVPALVRY HVGSRKAVSEQSGAIYCPVNRFTPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSLSYSDPDS GHYCOLQPPVRGSREWAATETSSQARSYGE RLKELSENGAPEGDWKTFTVPIVEVTSSFPN ATFQSLIPRDNRPLEVGLLRKVKELLAEDVA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGURKLRDLLERFHTMSIML AVDILGCTGSAEERAALLHKTQILAAELRGT MGNMFSFAAVMGALDMAQISRLEQTVVTLR QRHTEGAILYEKKLPFLKSLNEGKEGPPLSN TTFPHVLPITLLECDASAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLWGSQGASSQA RRYEKFVKVLTALSHKLEFVRSSEL
412	1762	A	3347	1	898	IDRAAECRTKPLPMAVSIRGNADSVACLVL VLYLIKRLVACAAVFYGFVHMKIYPETYI LPTLHLLPDRDNDKSLRQFRYTFQACL*ELL KRLCNRTALMFVAVAGLTFALSFGFYEYG WEFLEHTYFYHLTRDIRHNFSFYFMYLT AESKWSFSLGIAAFLPQLILLSAVSFAYYRDL VFCWFLHTSIFVTFNKVCTSQYFLWYLCCLPL

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						VMPLVRMPWKRAVVLLMLWFIGQAMWLAP AYVLEFQGKNITFLFIWLAGLFFLLNCSILIQII SHYKEEP LTERIKYD
413	1763	A	3361	3	474	PIPVRWNSLEGRLLRGYEQHANDGKDYSISRN *DLRSWTAADMAAQITKRKWEAEFEAEQIKA YLEGTCVER/LRTHLENGKETLQLTEQSSQPTI PIVGIVAGLVLLGAVVTGAVVSAVMCRKKNS GHFLPTDRVSYSEAASSDHAQGSVDVSLTACK V
414	1764	A	3363	1488	453	HQILELKKKILKTYNPDYDEDLVQEASSEDVL GVHMDKDTERRDIEMKRQLRRLRELHLYST WKKYQEAMKTSLGVPQREDEGSLGKPLCP PEILSETLPGSVKKRVCPSSEHLEEFIAEHL EASNQSLTVAHADAGTQTNQDLEDLEEHP GQTVSEEADEVHMMEGDPDTLAELLIRDVLQ ELSSYNGEEEDPEEVKTSLGVPQRGDLEDLE EHVPGQTVSEEADEVHMMQVDPATLAKSDL EDLEEHPQTVSEEADEVHMMQVDPATLA KQLEDSTITGSHQQMSASPSAPAEAEATEKTK VEEVKTRKPKKKTRKPSKSKSRWNVLKCWD IFNIF
415	1765	A	3369	431	315	IPWSWVGRLSVRKMSILF*LTYNYNAILNKTP PSFSPSL
416	1766	A	3373	42	651	RQEKMLGEIGASGVLRSMLEKRRKQNMKG NGNVTLTPLLPAVQCGCHLQPAGRSPLPSSHS APGLCSPLHPLQPPQEAETCPSTLQGREKAA PGQGRPLCSLWAGGAGAPGERGAEGRGPSD QAPDPKSGPWLFPPLGAPAEVRLHNVPHNL RRPFLP*ARGK*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH
417	1767	A	3382	2	2061	EAQDFRACGPDAGGRFAARDAPQNSLRFPFS SPP/GWPGQLRLPRVPGSELRCGKPERGRLP ASPPGKIRGWPPGSKRPLGLGRSFPFGFAPRT WRPEARGPSVQSLPPIFSPQSAQTAR*RP KNAAGRCGGA/RGPRLSLGPPPPPPAPALPAR ASAGAGAAAAALAVGGVRGAGGARGTGGY GHCSGR/PTGRTGPGPQGPMPMPARPR*ASIS TRGSRRGPGSRPARAAAFRAGDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP RIGPGWDCALLPSGPSPRAVGCAPETWDP SPRRGTSPVPSVRLRSEANPRLGLPALLNSY PLKGPGLPPPWPRTQTGHVITVQPSGSCIEH SKSLD/RGPWGAPPWGPSSSLCSPKLATAGP PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC SMDHANRITKGPVPTSNCFSHIPGAGDGCSD HSSCEGHFDLHAGREMPAAPGLSELRVRFT VGCGGLASGISSASVGLSPNRAGGPGQGDW EMYPVSWQTQESGGQG/SPKTGR*VGMLQA GAGSLQGGTGDGVWGLWEDGP/RG*DSPLPS GTGTEP*TPTTSPFPQPSGVYPSRATLLPMP Y*ALGPSANKSEKPLLSFLYRGLCCRIQLA KGIGQLSEIPLLNVEAFWSMWVITYFRK
418	1768	A	3398	304	2121	EEEEEEEDDDDDNNEEEFECCYPPGMKVQV RYGRGKNQKMYEASIKSDVEGGEVLYLVH YCGWNVRYDEWIKADKIVRPADKNVPKIKH RKKIKNKLDEKDKDEKYSKNCPPALGPN PFFQTNPISWKWYPKLDLTDKNSDTAHIKSI EITSILNGLQASESSAEDSEQEDERGAQMDMN NGKEESKIDHLTNNRNDLISKEEQNSSSLLEE

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						NKVHADLVISKPVSKSPERLRKDI E V L S E D T D Y E E D E V T K K R K D V K K D T T D K S S K P Q I K R G K R R Y C N T E E C L K T G S P G K K E E K A K N K E S L C M E N S S N S S D E D E E E T K A K M T P T K K Y N G L E E K R K S L R T T G F Y S G F S E V A E K R I K L L N N S D E R L Q N S R A K D R K D V W S S I Q G Q W P K K T L K E L P S D S D T E A A A S P P H P A P E E G V A E E S L Q T V A E E S C S P S V E L E K P P P V N V D S K P I E E K T V E V N D R K A E F P S S G S N F S A * I P L P Y L H L N R L H Q S L * Q K G S R Q Q S S V T V S E P L A P N Q E E V R S I K S E T D S T I E V D S V A G E L Q D L Q S E R E * L A S R F * C Q C E L K Q * * S A R T R T S * K S L Y R S E K S E R C S G R R K F I K K A E K K P * S N S G K Q Q K E G K
419	1769	A	3399	206	463	Q R E C L S I H I G Q A G I Q I G D A C W E L Y C L E H G I Q P N G V V L D T Q Q D Q L E N A K M E H T N A S F D T F F C E T R A G K H V P R A L F V D L E P T V I D G I R
420	1770	A	3408	1010	685	R R L S F F F * I W S S V L V T Q A R V Q W R D L G S P Q P L P P G F K R F S C L S L P S S W D Y R H P S P R P V N F / H V F L V V M G F H H V G Q A G L E L L T S G D L P A L A S Q S A R I T G V N H C A Q P R G H F H
421	1771	A	3409	355	1326	A D S N L I E S C W Q E L G L G P W G G D W R V E Q V G A S A S L R F P R E V C S I R F L T A V S L L S L F L S A F W L G L L Y L V S P L E N E P K E M L T L S E Y H E R V R S Q G Q Q L Q Q L Q A E L D K L H K E V S T V R A A N S E R V A K L V F Q R L N E D F V R K P D Y A L S S V G A S I D L Q K T S H D Y A D R N T A Y F W N R F S F W N Y A R P P T V I L E P H V F P G N C W A F E G D Q G Q V V I Q L P G R V Q L S D I T L Q H P P P S V E H T G G A N S A P R D F A V F L L S F F T H Q G L Q V Y D E T E V S L G K F T F D V E K S E I Q T F H L Q N D P P A A F P K V K I Q L S N W G H P R F T C L Y R V R A H G V R T S E G A E G S A Q G P H
422	1772	A	3412	2	421	E F D A Q P S I G A L V V F K R P * A T T G S D P G P K R G M N Y L V S C S M R S P E S G K G E P G T A R D Y T P M G R P P P P V P S V S P G P L P G S L A I A P H S P E P H P W E Q Q P P R G Q A R S P P G G W L G S A T / R V R R P H N H P / R G H / H S P V D T A G A P A S P G P D V C E
423	1773	A	3420	91	706	D A Q R A I Y S S V G P A V S L R Q R Q Q D G A V K E S G R / R G G V R S F S R A A A A M A P I K V G D A I P A V E V F E G E P G N K V N L A E L F K G K K G V L F G V P G A F T P G C S K T H L P G F V E Q A E A L K A K G V Q V V A C L S V N D A F V T G E W G R A H K A E G K V R L L A D P T G A F G K E T D L L D D S L V S I F G N R R L K R F S M V V Q D G I V K A L N V E P D G T G L T C S L A P N I I S Q L
424	1774	A	3421	4	7688	R Q V T R V G T R V L G S T T A A V F L S V E D D N D N A P Q F S E K R Y V V Q V R E D V T P G A P V L R V T A S D R D K G S N A V V H Y S I M S G N A R G Q F Y L D A Q T G A L D V V S P L D Y E T T K E Y T L R V R A Q D G G R P P L S N V S G L V T V Q V L D I N D N A P I F V S T P F Q A T V L E S V F L G Y L V L H V Q A I D A D A G D N A R L E Y R L A G V G H D F P F T I N N G T G W I S V A A E L D R E E V D F Y S F G V E A R D H G T P A L T A S A S V S T A L D V N D N N P T F T Q P E Y T V R L N E D A A V G T S V V T V S A V D R D A H S V I T Y Q I T S G N T R N R F S I T S Q S G G L V S L A L P L D Y K L E R Q Y V L A V T A S D G T R Q D T A Q I V V N V T D A N T H R P V F Q S S H Y T V N V N E D R P A G T T V V L I S A I D E D T G E N A R I T Y F M E D S I P Q F R I D A D T G A V T T Q A E L D Y E D Q V S Y T L A I T A R D N G I P Q K S D T T Y L E I L V N D V N D N A P Q F L R D S Y Q G S V Y E D V P P F T S V L Q I S A T R D R S G L N G R V F Y T F Q G G D D G D G D F I

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						<p>VESTSGIVRTLRLDRENV AQYVLRAYAVDK GMPPARTPMEVTVTVLDVNDNPPVFEQDEFD VFVEENSPIGLAVARVATDPDEGTNAQIMY QIVEGNIPEVQLDIFSGELTALVDLDYEDRPE YVLVIQATSAPLVSRATVHVRLDRNDNPPV LGNFEILFN NYVTNRSSSPFGAIGRVPAHDP DISDSLTYSEFERNELSLVLLNASTGELKLSR ALDNNRPLEAIMSVLVSDGVHVSVAQCALRV TIITDEMLTHSITLRLLEDMSPERFLSPLLGLFIQ AVAATLATPPDHVVFNVRQDTPDAPGGHILN VSLSVGQPPGPGGGPPFLPSEDLQERLYLNR LLTAISAQRVLPIDNCLREPCENYMRCSV LRFDSAPFIASSSVLFRPHVPGGLRCRCPPGF TGDYCETEVDLCYSRCPGPHGRCRSREGGYT CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT CVNLLVGGFKDCPSGDFEKPQCQVITRSFP AHSFITFRGLRQRFHFTLALSFKTERDGLLL YNGRFNEKHDFVALEVIQEQVQLTFSAGEST TTVSPFVPGGVSDGQWHTVQLKYNNKPLL QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS VLGNYSCAAQGTQGGSKSLDLTGPLLLGG VPDLPEFVRMRQFVGCNRNLQVDSRHIDM ADFIANNGTVPGPCAKKNVCDSKTCHNGGTC VNQWDAFSCCEPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLPISQPYLSLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHHAQLALGAJGGP GHAILSFYQQQRAEGNLGPRHLHGLHLSNITV GGIPGPAGGVARGFRGCLQGVVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCANSY CSNDWDSYSCSDPGYYGDNCTNVCDLNP EHQSVCTRKPSAPHGYTCBPNNYLGPHYCET RIDQPCPRGWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSPTCLLCDCYPTG SLSRVCDPEDGQCCKPGVIGRQCDCRDNPF AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHCDHRGWLPNNLF NCTSIITSELKGFAERLQRNESGLDSGRSQQ ALLLRNATQHTAGYFGSDVKVAYQLATRL AHSTQRGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQTEGGTAWLLQHYEAYAS ALAQNMRYTLYSPFTVTPNIVISVVRDLKGN FAGAKLPRYEALRGEQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRRHPELS GEAVASVITYRTLGLLPHNYDPDKRSLRVPK RPIINTPVVSISVHDDEELLPRALDKPVTQFR LLETERTKPICVFNHNSILVSGTGGSARGC EVVFRNESHVSCQCNHMTSFAVLMDVSRRE NGEILPLKLTLYVALGVTLAALLTFFFLTLL RILRSNQHGIRRLTAALGLAQLVFLGQNA DLPFACVIAILLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRFYMLGWGVPAFTTG LAVGLDFEGYGNPDFCWLSYDITLWSFAGP VAFVSMVSFLYLAARASCAAQRQGEFKKG PVSGLQPSFAVLLLSATWLLALLSVNSDTLL FHYLFATCNCIQGPFIFLSYVVLKSKVRKALK LACSRKPSDPALITKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTSRSGKSQSPYIFLLR EESALNPGAQGPPGLGGIPGR/LCFLGRFKDQ HDS*TRDFDSDLSEDDQSGSYASTHSSDSEE</p>

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EEEEEEEEAAFPGEQGWDSL LGPGAERLPLHS TPKDGPGPGKAPWPGDFGTAKESSGNGAP EERLRENGDALSRGSLGFLPGSSAQPHKGIL KKKCLPTISEKSSLLRLPLEQCTGSSRGSSASE GSRGGPPSRPPRQSLQEQLNGVMPIAMSIKA GTVDEDSGSEFLFFNFLH
425	1775	A	3429	155	1417	GEPAVQSCDCGCTQRSCPWLLVAPGLLSSSSS RAASVREADAPLPASIHVVSQSGRPEGSL GSAECLPGDPLGARRATRAHSPVGPPLSLPA AGTAVKRGLQPG*GA/GATSTPGTGAATGGL CGPAWAAPS AVGPCCCPSSITPSQMRARP SLGCLPSWASVPGTEHPPGPQGPGPS*DLCSV* KREFQRPWAGMVILHRISAADPARAPGPD NLQSALQQPATGCSEPAAYVSPPIGLWGA**P EYG*PQHSLPG*TAPADR*PAGIKDRVYSNSI YELLENGQRAGTCVLEYATPLQTLFAMSQYS QAGFSREDRLQAKLFCRTLEDILADAPESQN NCRLIA YQEPADSSFSLSQEVLRHLRQEEKE EVTVGS LKTS AVPSTSTMSQEPPELLISGMEKP LPLRTDFS
426	1776	A	3431	1662	369	AIWLSWLQHDLLPTPTQVAIDFTASNGDPR SSQSLHCLSPRQPNHYLQALRAVGGICQDYD/ SVGESGAGGNRQGLAQRIPLQLPSDKRFP AFGFGARIPPNEFVG*MRGKEGDGGRVSQAE KAGPHCSRLALTGSHDFAINFDPENPECEGK RGDFHLRPLPADTLHTGAOTPLPRAQLPVPST HPRPVFNEISGVIASYRRCLPQIQLYGPTNVAP IINRVAEPAQREQSTGQATKYSVLLVLT DGV VSDMAETRTAIVRASRLPMSIIVGVGNADFS DMRLLDGDDGPLRCPRGVPAARDIVQFVFR DFKDVSPPGPFR LK DSSASHPPKSDLRLPPFD VLLRTREPSWPP*SPTSPSDDPASITLPLTPNHI TVPTLAAAPSALAKCVLAEVPRQVVEYYASQ GISPGAPRCPCLATTPSPSP
427	1777	A	3446	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA ASRPEASGDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPQLPQPPPAQPLLPQPPPPPPPPPP GPAAVEEPLHRPKKELSA TKKDRVNHCLTIC ENVAQSVRNSPEFQKLLGIAMELFLLCSDDA ESDVRMVADECLNKVIKALMDSNLRLQLEL YKEIKKNGAPRSLRAALWRFAELAHVLPQK CRPYLVNLLPCLTRTSKRPEESVQETLAAA VP KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVEDEHSTLLLGVLTLRLVPLLQQQV KDTSLKGSFGVTRKEMEVS PSAEQLVQVYEL TLHHTQH QDHNVTGALELLQQLFRTPPEL LQTLTAVGGIGQLTAAKEESGGRSRS SIVELI AGGGSSCSPVLSRKQKGVLLGEEEALED DS ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSQVSAVPSDPA MDLNDG TQASSPISDSSQTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIGDIGQSTDDDS APLVHCVRLLSASFLLTGKKNVLVPDRDVRV SVKALALSCVGAAVALHPESFFSKLYKVPLD

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						<p>TTEYPPEEQYVSDILNYIDHGDQPVRGATAILC GTLICSLSRSRPHVGDWMGTIRTLTGNTFSL ADCIPLLRKTLKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQIIDVLTNRSSYWLVRTEL LETLAEIDFRLVSFLEAKAENLHRGAHHYTG LKLQERVLNNVVIHLGDEDPVRHVAAASL IRLVPKLFYKCDQGGADPVVAVARDQSSVYL KLLMHETQPPSHFSVSTITRIYRGYNLLPSITD VTMENNLSRVIAAVSHELITSTRALTFGCCE ALCLLSTAFPVCIWSLGWHCVPPLSASDES KSCTVGMATMILLSSAWFPLDLSAHQDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPLSPIRRK GKEKEPGEQASVFLSPKKGSEASAASRQSDTS GPVTTSSKSSSLGSFYHLPYLLKLDVLRKATHA NYKVTLDLQNSTEKFGLRSLDVLSQLLEL ATLQDIGKCVIEILGYLKSCFSREPMATVC VQQLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA SLRNMVQAEQENDTSQWFDVLQKVSTQLKT NLTSVTKNRADKNAIHNRILFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYIEVGQFRESEAIIPNIF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRTGNKADAGKE LETQKEVVVSMILLRIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADHILPMLAKQQMH DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLSQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEKQIKNLPEETFSRFLQLVGILLEDIVT KQLKVEMSEQHTFYCQELGTLMLCLIHIFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNL ARSMITTHPALVLLWCQILLVNHTDYRW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLVDRLLCTFFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQY LQSSGLAQRHQRLYSLDRFLSTMQDLSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFOPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVS KLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNPKAISEEEEEVDNTQNPKYI TAACEMVAEMVESLQSVLALGHRNSGVPA FLTPLLNRNIIISLARLPLVNSYTRVPPLVWKL WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYR INTLGWTSRTQFEETWAILLGVLVTQPLVME QEEPPPEEDTERTQINVLAVQAITSVLVSAMT VPVAGNPVAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIAHHLYQAWD PVPSLSPATTGALISHEKLLQINPERELGSMS YKLGQVSIHVS WLGNISITPLREEEWDEEEEE</p>

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						ADAPAPSSPTSPVNSRKHRAVVDIHSCSQFL LELYSRWILPSSSARRTPAILISEVVRSLLVVS DLFTERNQFELMYVTLTTELRRVHPSEDEILAQ YLVPATCKAAAVLGMDKAVAEPVSRLLESTL RSSHLPSRVGALHGILYVLECDLLDDTAKQLI PVISDYLLSNLKGIAHCVNIHSQQHVLVMCAT AFYLIENYPLDVGPEFSASIIQMCQVMLSGSE ESTPSIYHCALRGLERLISEQLSRLDAESLV KLSVDRVNVHSPHRAMAALGLMLTCMYTG KEKVSPGRTSDPNPAAPDSESVIVAMERSVL FDRIRKGFPCEARVVARILPQFLDDFFPQDIM NKVIGFELSNQQPYQPMATVVYKVFQTLHS TGQSSMVRDWVMLSLSNFTQRAPVAMATWS LSCFFVSASTSPWVAAILPHVISRMGKLEQVD VNLFCVLATDFYRHQIEEELDRRAFQSVLEV VAAPGSPYHRLTCLRNHVHKVTTTC
428	1778	A	3449	3	430	NSRPSPSAALVEVLLRSGSTFPHTVSGGWAA WGPWSSCSRDCELGFRVRKRTCTNPEPRNGG LPCVGDAAEYQDCNPQACPVRGAWSCWTS WSPCSASCGGGHYQRTSCTSPAPSPGEDICL GLHTEALCATQACPEGWS
429	1779	A	3464	583	3	DALDRRYLERCHPAAGGWVGE*ALCOKT/ RFSGVLEPPLPSLKDGGRFPAWT*RSCKSLR AAFTSQFFPSRRSRASPGSAPGNGQNLTEQHP CPGSCDPQVLSASWM*VEHRSKFRPPP*NSTI PPES/RS*QGGTVQTGHSSGREAGSWRARGR NAGRR*KGGGKIGTKQGA VRARKECRGEMA SGETDSE
430	1780	A	3473	2802	270	FRMRIFLHCPWNQQMWKIWNLLETSLSCKA HLSIQKLLKERIQQLPVFKHRDSIVETLKRHR VVVVAGETGSGKSTQVPHFLLLEDLLNEWE ASKCNVCTQPRRISAVSLANRVCELGCENG PGRNSLCGYQIRMESRACESTRLLYCTTGV LLRKLQEDGLLSNVS/HMFTVDEVHERSVQS DFLLILKEILQKRSDLHLILMSATVDSEKFST YFTHCILRISGRSYPVEVFHLEDIEETGFVLE KDSEYQCKFLEEEVITNVTSKAGGIKKYQE YIPVQTGAHADLNPFFYQKYSSRTQHAILYMN PHKINLDLIELLAYLDKSPQFRNIEGAVLIFL PGLAHIQQLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAAFLLPPPQVRKIVLATNIAETGITI PDVVFVIDTGRTKENKYHESSQMSSLVETVFS KASALQRQGRAGRVRDGFCEFRMYTRERFEG FMDYSVPEILRVPLEELCLHIMKCNLGSPEDF LSKALDPPQLQVISNAMNLLRKIGACELNEPK LTPLGQHLAALPVNVKIGKMLIFGAIFGCLDP VATLAAVMTEKSPFTTPIGRKDEADLAKSAL AMADSDHLTTYAYLGWKKARQEGGYRSEI TYCRNFLNRTSLLTLEDVKQELIKLVKAAGF SSSTTTSWEGNRASQTLSPQEIALLKAVLVA GLYDNVGGKIYTKSVDTVTEKLACIVETAQ GK AQVHPSSVNRDLQTHGWLLYQEKIRYARVY LRETTLTTPFPVLLFGGDIEVQHRERLLSIDGW IYFQAPVKIAVIFKQLRVLIDSVLRKKLENPK MSLENDKILQITELIKTENN
431	1781	A	3474	1	441	FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ PCPPAPAPSRPSLGSGLQORVPAALATAAQEL PATLGGDGGKPALTAGEAALPGLHRSGVPAA AARC*PCT/SRPT*STLSPTQAAWWCRPSRRQ QRGEASTGGASGRRCGSCFQV

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432	1782	A	3478	416	23	QLRRLTLPNFKTY/YSS*IEIAWH**KNMQID QWFRRESPEIDLCKYS*LSFDKEAKA/KWKE CSLFNKWC/YKNWM/LHVQKKRI*VQTLHPS QKLKSKWIKDLNVECRITKLLDQEYPGDLGY SRALNSGSR
433	1783	A	3504	1876	552	CLAPCSPQPEKNGMQPLLLLPPLLYQQLLHS SLGAPGESTLLVRTSKLLVGLGLQLLVWLLL QTRSLALLQLHLTSSAPLLAAPTAVCSCSRCS APRSRCVARPAARTGLPTAPASSPAPAASPA PAASPAPAESTA/PQPLLLPKP/PPAPGAPPPRP GAPPPRPAASPSPAASPAASPVLTASPPPLP AASPSPAASPAASPVLTASPPPLPAASPSPA ASPAPPAASPVLTASPPPLPAASPALAASPVHT ASPPVHVASPPVHTASPPVHVASPPVHTASPP VHVASPPVHTASPPVHVASPPVHVASPPVHV ASPPVHTASPPVHVASPPVHTASPPVHVASPP VHTASPPVHVASPPVHVASPPVHVAYPPVHV ASPPVHVASPPVHVASPPVSCSGDSTSDCFPP QPGA/VFPHSLAPSLGGWSHLVAALP
434	1784	A	3516	142	590	GGVNRPRSETEQVKTPVLISWDRHPPRP SFFVFLV*TGFTALARMVLISWPCDLPTSASQ SAGITGVRHHA/RLLYFEQESHVTAQAGWVQ WHNLGSLQPLSLEDRLSPGVLGCSALCRSGV RTKFGINMVTSRERGTTPLPKEG
435	1785	A	3529	1	3161	MSLVRAALEALDELDFGVKGGQSVIHVLA DEVQHCQSILNSSLPRASTSKEVDASLLSVVS FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLKKGKNGVPLLPPELYSVPPDRVDEEYQNPHT VDRVPMGKLFHMWQSLYILGSLMAEGFLA PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTTKITAPVSILAETEEKTIL KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF LPFLNSVSGCNRMKLSGRPYRHMVGLGTSK LYDIRKTIFTFTPFIDQQQFYALDNKMIVE MLRTDLSYLCRWMTGQPTTTFPISHMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLTTSCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHLLAHTAPHKLAPTSQKGGDLRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ SGEVDFKALVLQKETSSLQEQADILYMLYT MKGPDWNTELYNERSATVRELLTELYGKVG EIRHWGLIRYISILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLYEALTQLIDEA SEGDMSSILTQEMVYLAMYMRTPQGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATEGL MNLSPSAMKNLLHHILSGKEFGVERSVRPTD SNVSPAISIHEIGAVGATKERTGIMQLKSEIK QSPGTSMTSSGSPSA YDQSSKDSRQGW QRRRLD GALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMPGEIKFSVHVESVL NRVPQPEYRQLLYEAIL/VLTMLADIENHSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKD PASGICITLLYDSAPSGRFGTMTYLSKAAATY VQEFPLPHSICAMQ
436	1786	A	3546	73	393	CP*LTWELLEVKAEVLQDSDLGRYSTPSSCL EQPDSCRPHYGRSFYALEEKHVIFSLDVGETDN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KGKGTIRGI*TFKGRKGGTYQREHDANPLA PXSARSCWVRKG
437	1787	A	3554	5157	2939	AVRAEPGLEELSSGLRAHSPSATTVCEPEAQG SASGCRYAAHPHWGLGGAAAAGGSWEPPQPP RPVCEPAGRGKPHPPAAPRSPLPGSRRRPHA AQPGARARTSPPPASARNMAARPAATLAWSL LLLSSALLREGCRARFVAERDSEDDGEEPVV PESPLQSPITVLVAVLARNAAHTLPHFLGCLER LDYPSKSRMAIWAATDHNVDNTTFIFREWLLK NVQRLYHYVEWRPMDEPESYPDEIGPKHWP TSRFAHVMKLRQAALRTAREKWSYDILFIDV DNFLTNPQTLNLLAENKTIVAPMLESRLYS NFWCGITPKGFYKRTPDYVQIREWKRTGCGP VPMVHSTFLIDLRKEASDKLTFFYPHQDYTW TFDDIIVFAFSSRQAGIQMYLCNREHYGYLP LKPHQTLQEDENLHVQIEAMIDRPPMEPSQ YVSVVPKYPDKMGFDEIFMNLKRRKGQGGD RWLRTLVEQIEVKIVEAVDQKALNTSQLKA LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV WKEVIDRELEKTLVIEDDVRFEHQFKKMLMK LMDNIDQAQLDWELIYIGRKRMMQVKEPEKA VPNVANLVEADYSYWTLYVISLEGAQKL GANPFGKMLPVDEFPLVMYNKHPVAEYKEY YESRDLKAFSAEPLLIYPHTYTGQPGYLSDE TSTIWDNETVATDWDRTAWKSRKQSRISYN AKNTEALPPPTSLDTPSRDEL
438	1788	A	3563	130	527	IFNSSLFCRVFLRWSTFLVAQARVQ*C NLSSLQPLPPGFK*FSCLSPPRS*D YRRPPRPA NFLYF**RQGTVLGQAQLELLT/S/GDPPTS SQSAGITGVSHRAWVPVHAISTHISLVKTRPSLT TLG
439	1789	A	3565	446	1834	LLQPAMRKSPGLSDCLWAWILLSTLTGRSY GQPSLQDELKDNTTVFTRILDRLLDGYDNRL RPGLGERVTEVKTDIFVTSFGPVSDHDMETI DVFFRQSWKDERLKFKGPMTVLRLNNLMAS KIWTPDTFFHNGKKSVAHNMTMPNKLRLITE DGTLLYTMRLTVRAECPMAGFRDPMDDAH ACPLKFGSYAYTRAEEVVEWYREPARSVVV AEDGSRLNQYDLLGQTVDSGIVQSSTGEYVV MTTHFHLKRKIGYFVIQTYLPCIMTVLSQVSF WLNRESVPARTVFGVTTVLTMTLSISARNSL PKVAYATAMDWFIACVAFVFSALIEFATVN YFTKRGYAWDGKSVVPEKPKVKDPLIKKN NTYAPTATSYTPNLARGDPGLATIAKSATIEP KEVKPETKPEPKKTFNSVSKIDRLSRIAPFL FGIFNLVYWATYLNREPQLKAPTPHQ
440	1790	A	3568	1	350	STSSCFPAAAAAIMREIVHLQAGQCGNQIGAK FWEVISDEHGIDPTGTYHGSDQLQLERINVYY NEATGEAPVPSPTALRGPRGCLG*RPPVPAG GKYVPRAVLVDMEPGTMDSV
441	1791	A	3569	2	1751	FVAVAGAVSGEPLVHWCTQQLRKTFGLDVS EEIIQYVLSIESAEIIEYVTDLLQNEGKKQG FIEELITKWQKNDQELISDPLQCFKKDEILDG QKSGDHLKGRKKGRNRQEVAFTEPDTTAE YKTFPDLAKAQENSNSVKKTKFVNLYTREG QDRLAVLLPGRHPCDCLGQKHKLNNCLICG RIVCEQEGSGPCLFCGTLVCTHEEQDILRGDS NKSQKLLKKLMSGVENSGBKVDISTKDLLPH QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQVI

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						DDESDYFASDSNQWLSKLERETLOKREBELR ELRIIASRLSKKVITDFAGRKILEEENSLAEYII SRLDETIQAIANGTLNQPLTKLDRSSEPLGVL VNPNNMYQSPQWVDHTGAASQKKAFRSSGF GLEFNSFQHLRIQDQEFQEGFDGGWCLSVH QPWASLLVRGIKRVGRSWYTPHRGRLWIAA TAKKPSPQEVSELQATYRLLRGKDVEFPNDY PSGCLLGCVLDLCLSQKQFKEQFPDISQESDS PFVFICKNPQEMVVKFPIKGNPKJWKLDISKIH QGAKKGLMKQNKAV
442	1792	A	3576	1	2019	MPRSHTGERLCEGKEGSQCAENFSPNLSVTK KTAGVKPYECTICGKAFMRLSSLTRHMRSH AIRANEKPYKCKEKGRAFLSLQILSKHERSH TGEKPYCKQCGKTFIYHQPFQRHERTHIGEK PYECKQCGKALSCSSSLRVHERIHTGEKPYEC KQCGKAFSCSSSIRVHERHTGEKPYACKEC GKAFISITSVLTHMITHNGDRPYKCKECCGA FIPPSFLRVHERIHTGEKPYCKQCGKAFRWS TSIQIHERIHTGEKPYKCKEKGKSFSAFPAFRV HVRVHTGEKPYKCKEKGKAFSRISYFRIHER HTGEKPYECKKCGKTFNYPLDLKHKRNHTG EKPYECKEAKTFISLENFRHMITHHTGDGPY KCRDCGKVFIFFSALRTHERTHTGEKPYECKQ CGKAFSCSSYIRIHKRTHHTGEKPYECKEKG AFIYPTSFQGHMRMHTGEKPYKCKEKGKAFS LHSSFRIRHTRIHNIEKPLEC*Q/CGKAFSVSTS LKKPMRNAQSDRKL Y/KCEK*EKVFNSNRCP QSCENSH*REKSCQCK*YRKRDTR*FMYSQV PHNHVSVSNGPYR/CGSPIRL YNT*NISINRNL VAVVTP*CSLTFKCLWCWCKRAALS VV*/IVQ DSGRGRWLTPVIPALWEAKAGGSRGQEIKTIL ANTVKPHLY
443	1793	A	3578	287	114	DFYERKFQFIEGHKQIVNKWRDLLCSWKRK LSIIKKSVLQNNL*FSAASMRFKQVFF
444	1794	A	3582	3335	1909	HLFFSLFLAAMAMTGSTPCSSMSNHTKERVT MTKVLTLENFYSNLIAQHEEREMRQKLEKV MEEGLKDEEKRLRRSAHARKETFLRLKRT RLGLEDFESLKVIGRGAFGEVRLVQKKDTGH VYAMKILRKADMLEKEQVGHRAERDILVEA DSLWVVKMFYSFQDKNLNLYLMEFLPGGDM MTLLMKKDTL TEEETQFYAETVLADSIHQ GFIHRDIKPDNLLLSKGVKLSDFGLCTGLK KAHRTEFYRNLNHSLSDFTFQNMNSKRKAE TWKRNRRQLAFSTVGTDPYIAPEVFMQTGYN KLCDWWSLGVIMYEMLIGYPFCSETPOETY KKVMNWKETLTFPPEVPISEKAKDLILRCCCE WEHRIGAPGVVEIKSNSFFEGVDWEHIRERPA AISIEKSIDDTSNFDEFPESDILKPTVATSNHPE TDYKNKDWWFINYTYKRFELTGARGAIPSYM KAAK
445	1795	A	3584	1	6169	RTRGIEKRFAYSFLQQLIRYVDEAHQYILEFD GGSRGKGEHFFPYEQEIKFFAKVVLPLDQYFK NHRLYFLSAASRPLCSGGHASNKEKEMVTS FCKLGVLRHRISLFGNDATSVNCLHILGQT LDARTVMKTGLESYKSALRAFLDNAEDLE KTMENLKQGFTHTRNQPKGVTQIINYTTVA LLPMLSSLFEHIGHQHGFEDLILEDVQVSCYRI LTSYALGTSKSIYVERQRSALGECLAAFAGA FPVAFLETHLDKHNTYSIYNTKSSRERAALSLP TNVEDVCFNPISLEKLMEEIVELAESGIRYTO

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						MPHVM EVILPMLCSYMSRWWEHGPENNPER AEMCCTALNSFHMNTLIGNIIKITYNNLGHDE GAWMKRLAVFSQPIINKVKPQLLKTHFLPLM EKLKKKAATVVSEEDHLKAEARGDMSEAEL LILDEFTTLARDLYAFYPLLIRFGDYNAKWL KEPNPEAEELFRMVAEVFTYWSKSHNFKREE QNFVVQNEINNMSFLITDTKSKMSKAAVSDQ ERKKMKRKGD RYSMQTSLIVAALKRLLPIGL NICAPGDQELIALAKNRFSLKDTEDVDRIRS NIHLQKLEDPAIRWQMALYKDLPNRTDDTS DPEKTVERVLDIANVLFHLEQKSKRVGRRHY CLVEHPQRSKKA VWHKLLSKQRKRAVVACF RMAPLYNLPRHRAVNLFLQGYEKS WIETEEH YFEDKLIEDLAKPGAEPPEDEGTRVDPILHQ LILFSRTALTEKCKLEEDFLYMAADIMAKS CHDEEDDDGEEEVKSFEEMEMEKQKLLYQQ ARLHDRGAEMVLQTISASKGETGPMVAAT LKLGIALNGGNSTVQKMLDYLKEKDKVGP FQSLAGLMQSCSVLDLNAFERQNKAEGLGM VTEEGSGEKVLQDDEFTCDLFRFLQLCEGH NSDFQNYLRTQTGNNTTVNIISTVDYLLRVQ ESISDFYWYYSGKDVIDEQGQRNFSKAIQVA KQVFNTLTEYIQGPCTGNQQSLAHSRLWDAV VGFLHVF AHMOMKLSQDSSQIELLKELMDLQ KDMVVMLLSMLGNVYNGTIGKQMVMDMLV ESSNNVEMILKFFDMFLKLDLTSSDTFKEYD PDGKG VIFKRDFHKAMESHKHYTQSETEFL SCAETDENETLDYEEFVKRFHEPAKDIGNVA VLLTNLSEHMPNDTRLQTFLAESVLNYPQ FLGRIEIMGSAKRIERVFEISESSRTQWEKPQ VKESKRQFIFDVVNEGGEKEKMELFVNFCD TIFEMQLAAQISEDLNERSANKEESEKERPEE QGPRMAFFSILTVRSALFALRYNLTLMRMLS LKSLKKQMKKVKKMTVKDMVTAFFSSYWSI FMILLHFVASVFRGFFRILCSLLGGSLVEGA KKIKVAELLANMPDPTQDEVRGDGEEGERKP LEAALPSEDLTDLKELEESDLSDFGLDLKR EGGQYKLI PHNPNAGLSDLMSPVPMPEVQE KFQEQKAKKEEKEEKEETKSEPEKAEGEDGE KEEKAKEDKGKQKLRLHTRHYGEPEVPESA FWKKIAYQQKLLNYFARNFYNNMRMLALFV AFAINFILLFYKVSTSSVVEGKELPTRSSENA KVTSLDSSSHRIIVHYVLEESSGYMEPTVRIL PILHTVISFFCIIGYYCLKVPLVIFKREKEVARK LEFDGLYITEQPSDDIKGQWDRLVINTQSF NNYWDKFVKRKMVDKYGEFYGRDRISELLG MDKAALDFSDAREKKKPKKDDSLSAVLNSID VKYQMWKLG VVFTDNSFLYLAWYMTMSVL GHYNNFFFAAHLDIAMGFKTLRTLSSVTH NGKQLVLTGGLAVVYLYTVVAFNFRKF YNKSEGDTPDMKCDDMLTCYMFHMYGV RAGGGIGDEIEDPAGDEYEYRIIFDIIFFFVI VILLAIQGLIIDAFGELRDQQEQVKEDMETKC FIGIGINDYFDTVPHGFETHILQEHNLANLYF FLMYLINKDETEHTGQESYVWKMYQERCWE FFPAGDCFRKQYEDQLN
446	1796	A	3592	1	355	AGLELLNSDDPPALASQSAGITGVTRTPSLFF* DTVLLCCSGWSAVAPSRLTAALFS*AQAVCL SLPRSWDYRRW/PPHPANFCIFCRDE/SLA/ML PRLVSNSTWQAILLPRPKMLGLQV

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447	1797	A	3598	1202	1070	LFVGGGPGICPEGASGFAPGAPAPRVGVDAEVGR*V*GAAASQGA/GSLRPRPTGPHGPAWLQVWGA AAVCAGPAM*/AVRAKRGPAG*EPNSPWRSGVLAARAVGAGPWP*P*PGCS*ARGPSSRSAPGLASGPAAPLLQGVHSSAGPLLCYI NGTLALGLKP**AWGWGEWRPKG
448	1798	A	3604	3115	557	FRKGGGGPKDFGAGLKYNSRHEKVNGLEE GVEFLPVNNVKKVEKHGPRWVVLAAVLIG LLLVLLGIGFLVWHLQYRDVVRQKVFNNGYM RITNENFVDAYENSNSTEFVSLASKVKDALKL LYSGVFPFLGPYHKESAVTAFSEGSVIAYYWSE FSIQHLVEEAERVMAEERVMMLPPRARSLS FVVTSVVAFPTDSKTVQRTQDNSCSFGLHAR GVELMRFTTPGFPDSFPYAHARCQWALRGD ADSVLSLTFRFDLASCDEGRHLVATVYNTL SPMEPHAILVQLCGTYPPSYNLTFHSISQNVL LITLITNTERRHPGFATFFQLPRMSSCGGRL RKAQGTFSFPYYPGHYPNIDCTWNIEVPNN QHYKVRFFKFFYLLEPGVPAGTCPKDYVEING EKYCGERSQFVVTNSNKTIVRFHSDQSYTDT GFLAEYLSYDSSDPCPGQFTCRTRGCRKELR CDGWADCTDHSDELNCSCDAGHQFTCKNKF CKPLFWVCDSLNDCGDNSEQGCSCPAQTF RCSNGKCLSKSQCCNGKDDCGDGSDEASCP KVNVTCTKHTYRCLNGLCLSKGNPECDGK EDCSDGSDKDCDCGLRSFTRQARVVGTD ADEGEWFWQVSLHALGQGHICGASLISPNWL VSAAHCYIDDRGFRYSPTQWTAFLGLHDQS QRSAPGVQERRLKRIISHPPFNDFTFDYDIAL ELEKPAEYSSMVRPCLPDASHVFPAGKAIWV TGWGHITQYGGTGALILQKGEIRVINQTCEN LLPQQTTPRMMCVGFLSOGVDSCQGDSSGFL SSVEADGRIFQAGVVSWDGCAQRNKPGVY TRLPFRDWIKENTGV
449	1799	A	3618	2	613	FVSGSPWRMDGSTERLEARRPAGRLPWSSRQ EMTRRPSLMAGRQHGWSAQQSATVANPVPG ANPDLLPHFLGEPEDVYVKNKPVLLVCKAV PATQIFFKCNGEWVRQVDHVIERTDGSGLP TMEVRINVSRRQVEKVFGLEEWQCVAWS SSGTTKSQKAYIRIA YLRKNFEQEPLAKEVSL EQGIVLPCRPPGIPPAE
450	1800	A	3620	1	2676	MEPSLGQGMDLTCTPFGVSPACGAQASWSIFG ADAABVPGTRGHSQQEAAMPHPIDEPPGE PQAAQSPAGQGPPTAGVSCSPTPTVLTGDA TSPEGETDKNLANRVHSPHKRLSHRHLKVST ASLTSVDPAGHIIDL VNDQLPDISEEDKKKN LALLEEAKLVSERFLTRRGRKSRSSPGDSPA VSPNLSFASPTSSRSNSLTVPPTPEGDEADV SPSHPGEFNVPKGLADRKQNDQRKVSQGR LAP RPPPVKSKELAEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQGPVSELGKQLLKTG WEGSFLPRSPQDAAGVGPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLRLGLSWDSGP EE PGPRQLQVLAKLPLAEEERKRFAGKAGGLAK APGLKDFQIQVQVPRMQKLTKLREEHLMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRLRVHRSPLPGSAPP LTEKEVENVQVLSAFAFRNDSYTTLESRLNQA E RERNLTEENTEKELENFKASITSSASLWHHCE HRETYQKLLEDIAVLHRLAARLSSRAEVVGA

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						VRQEKRMASKATEVMMQYVENLKRTYEKDH AELMEFKKLANQNSSRSCOPSEDGVLRTARS MSLTLGKNMPRRRVSVAVVPKFNALNPGQ TPSSSSIPSLPALSESPNGKGSPLVTSALPALLE NGKTNNGDPDCEASAPALTLSCLEELSQETKA RMEEEAYSKGFQEGGLKKTKEQLDLKEEEEQ KSESPPEEPVEETEEEEKDPRSSKLEELVHFL QVMYPKLCQHWQVITWMAAVMLVLTVVV GLYNSYNSCAEQADGGLGRSTCSAAQKDSW WSSGLQHEQPTAQ
451	1801	A	3623	504	198	QLIQHQTVHTGRKLYECKECGKAFNQGSTLI RHQRIHTGEKPYECKVCGKAFRVSSQLKQHQ RIHTGERFPYQCKELKGRGAEMLA VLAVKEQ NRTPVNYGK
452	1802	A	3628	2	195	MTCLHSAKAFFHY*SSCSFSCEEGFALIGPEVV QCTALGVWVTAPAPVCIQVQCQHLALNEG MG*DYPTAFAYGSSCKYECHTVYRVRGLD MLHSRGCYLWNGHFTT*EASCEPLRPCH*S V*CSFSCEEGFALIGPEVVQCTALGVWVTAP VCIQVQCQHLALNEGTMG
453	1803	A	3637	662	142	IQAKGLGIWHVPNKSPMQHWRKGSLLRYRT DTGFLQTLGHNLLGIYQKYPKYGEGKCWT DNGPVPVYDFGDAQKTASYSPYQGREFT AGFVQFRVFNNERAANALCAGMRVTGCNTE HHCIGGGGYFPEASPOQCGDFSGFDWSGYGT HVGYSSSREITEAAVLLFYR
454	1804	A	3641	1	362	TQVHPAMLGLDELGRSGCGHCTQADLRFGD AAGRDPGQDNDNRNTAEPAPPPPRVMAAAA ALRAPAQSSVTFEDVAVNFSLEEWLLNEAQ GCLYHDVMLETLTLISSLOKVLILNCDLS
455	1805	A	3646	2	414	AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT
456	1806	A	3656	396	8	QIVSFNSYLTLYTKNNLKSMDLNVNTEMIK LLELKNHNLG*AKFFLN*IQKALIKRKILHW P/LIKIK/SFCSLSDTIKKMKRQTTVWEQTFIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F
457	1807	A	3660	14	1961	SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGKLTNSSKEPKF TKCRSPERETFSCHWTDEVHHGKTNLGPQLF YTRRNTQEWTEWKECPDYVSAGENSICYFN SSFTSIWIPYCIKLTSGNGTVDEKCFVSDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLVYVTLPMQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQRIKMLILPPVPVKI KGIDPDLLEKGLLEVNILAIHDSYKPEFHS DDSWVEFIELDIDEFDEKTEESDTRLLSSDH EKLHINLVKDGDSGRTSCEPDILETDFNAH DIHEGTSEVAQPQLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIAEKNKPPPLPTEGAE STHQAHHQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGQKNKAGMSQCDMHPMEMVSLCQENF LMDNAYFCEADAKKCPVAFPHIKVESHIQFS LNQEDIYITTESLTATAAGSPAGTGEHVPGSEM

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						PVPDYTSIHIVQSPQGLILNATALPLPDKEFLS SCGYVSTDQLNKIMP
438	1808	A	3663	154	462	TRAPASGRSGAGLALSANAPDSGGHPGATEG PAGSLAHASGSARGTWRVRGRSGSHGWERTV GAGGCANFVPALHSCASAPRGTRVSALGPK TGSSPLSSPKG
459	1809	A	3664	902	135	LGKYNTSMALFDFVLHNSTGEIRYITEDDVIQ SQNALGKYNTSMALFESNSFEKILESFPYYVD LNQTLFVQVSLHTSDPNLVFLDTCRASPTSD FASPTYDLIKSGCSRDETCVYPLFGHYGRF QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRC NQGCVSRSKRDISSYKWKTDLSIGPIRLKRDR SAANGNSGFQHETHAEETPNQPFNSVHLFSFM VLALNVVTATITVRHFVNQRADYQYQKQLQ NY
460	1810	A	3670	850	557	LGILMSPQVEAGEI*ALLTPPPGCMQFSPLTL/P K*WVSPGLTP/PPPEVPSVFLVEPGLPHAGQA GLDLLTSGDPPASTSQSARTTDVSHRAQPLAI S
461	1811	A	3671	2472	2099	IGVLAFETGSCSVTRLYCIGIIMPHCSLDLAGS/ TSAFRIAGTTSVHHHPQLTFFFFWIETGSHCV VQTGL*LLALSNPPALASQIAGISGMSHRAWP GLVLYSLEFSLLCASQSLIMLFTCYNE
462	1812	A	3672	394	110	VKPVNGESKRD*GADTQTCEGEADEQLQTN CYYD/STKSFFYISCG*KRKPTWAENRRUNA KMFGLPHLSNDPWGYEEREVIGFHRSRVSRG HGS
463	1813	A	3673	348	1	QRNPFSAGHPQRPPTSGSQSELLAQPRLRPGR KSSFSRDQDVW*SQAVPKRQ*QRNPFSAGHP QRPPTSGSQSELLAQPRLRPGRKSSFSRDQDV WPGOKPRPSQQHQMCASPTLGQRSPFALEP VPAYHGGRDPPASARPSVGPVKPRAAPAGG GWRRIKPKSSTK
464	1814	A	3676	2253	320	PVIQRCSQPYGFSLLISFFLKCVSETSQPPSR KVFQLLPSFPTLTRSKSHESQLGNRIDDVSSM RFDLSHGSPQMVRDGLSVTHRFSTKSWLS QVCHVCQKSMIFGVKCKHCRLKCHNKCTKE APACRISFLPLRLRRTESVPSDINNPDVRAAE PHFGTLPKALTKEHPPAMNHLDSNNPSSSTT FSTPSSPAPFPTSSNPSSATTPPNPSPAGQRDSR FNFPSCA/YFIHHR/QQFIFDISAFHAAPLPE AADGTRLDQPKADVLEAHEAEAEPEAGK SEAEDDEDEVDLPSSRRPWGPISRKASQTS VYLQEWDPFEQVELGEPGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPHLAITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIHKMGY LHAKGIVHKDLKSRNVFYDNGKVVTDFGLF VIGISGVVPEGRRENQLKLSHDWLCYLAFETVR EMTPGKDEDLPPSKAADVYAFGTWVYELQ ARDWPLKNQAAEASIWQIGSGEGMKRVLTS VSLGKEVSENLSACWAFDLQERPSFSLMD MLEKLPKLNRRLSHPGHF*KSADINSSKVVPFR FERFGLGVLESSNPKM
465	1815	A	3679	8	803	IPSPAWWNSTWADTFSLLLALAVALYLYGY WACVLQTHRAFCASNTEDLETVNNHIKHYRP QAPLLAVGISFGGILVLNHLAQARQAAGLVA ALTLSACWDSFETTRSLLETPLNSLLFNQPLTA GLCQLVERLSY/E*DLQARTIRQFDERYTSA

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						FGYQDCVTTYKAAASPRTKIDAIRIPVLYLSAA DDPFSTVCALPKQAAQHSPYVALLITARGGHI GELEGLLPWQHWMYMSRLLHQYAKAIRQDPE GLPDLRALLPSEDRNS
466	1816	A	3684	3	307	SSQYTVQSKTKIFL*AAREKQ/RHTCRRFSIRLS ANISSQTGEARGQWPSVFKVLKEKKLSTKKS FGQK*GRVRKTFDPKQK/LREFDTRPTIQEML TGVLLQ
467	1817	A	3687	2465	837	ELFTPLIAAHQLYNYVADHASSYHMKPLRMA RPGGPEHNEYALVSAWHSSGSYLDSEGLRHQ DDFDVSLLVCHCAAPFEEQGEAERHVLRLQF FVVLTSQRELFRLTADMRRFRKPPRLPPEPE APGSSAGSPGEASGLILAPGPAPLFPPLAAEVG MARARLAQLVRLAGGHCRDRLWKRLFLE PPGPDRLRLGGRLALAELELEA VHAKSIGD IDPQLDCFLSMTVSWYQSLIKVLLSRFPQSCR HFQSPDLGTQYLVVLNQKFTDCFVLVFLDSH LGKTSLVTVFREPFPVQPDSESPFAQLVSTY HHLESVINTACFTLWTRLL*GSGLDH*MSLFL ESWAYQIACQROD*PALLGPRASQTLSDTKG FVTMS*GSAAPAWQOEPPSPNTHSH*PIQDSR ESGQPRGLPFPFWGTFFGPPGRVSGVHTGWQ TPPRAPLPESCPLPLTTVSHLCPLSLRVFTSHL DITAGHSHRDDTWVPIPALPLKHLRPPSSPFA LGPWVSHPLMRVWQKLSHLHSPNGTGFSMG GKQQRN
468	1818	A	3691	960	499	QTCRKDKRAIYPHFQNE*MNEIKAI*SGTGGI QCFHSQNDSAFFFLFLETEFCSAATVQWVH DFLSMQPPPPGFKQFTCLSLSSWNYRRPPPF PGNF*FLVKTGFPHVGGTGFELLTSSDLAPLA SQNGGITGMSPCA WPFPPPPPPFLC
469	1819	A	3714	4747	495	MAYSWQTDPNPNESHEKQYEHQEFVFNQP HSSSQVSLGFDQIVDEISGKIPHYESEDENTFF VPTAPKWDSTGHSLNEAHQISLNEFTSKSREL SWHQVSKAPAGFSFVLPKPQNTNKECSWG SPIGKHGADDSRFSILAPSFTSLDKINLEKEL ENENHNHYHIGFESSIPTNSFSDFMPKEENK RSGHVNIVEPSLMLLKGSLLQPMWESTWQK NIESIGCSIQLVEVPQSSNTSLASFCNKVKKIR ERYHAADVNFNSGKIWSTTTAFPYQLFSKTK FNIHIFIDNSTQPLHFMPCANLYVKDLIAELH FCTNDQLLPKDHILSVWGSEEFQNDHCLGS HKMFQKDKSVIQLHLQKSREAPGKLSRKHEE DHSQFYLNQLEFMHIWVSRQCLLTIRKY DFHLKYLLKTQENVYNIIEEVKKICSVLGCVE TKQITDAVNELSLILQRKGENFYQSSETSAGK LIEKVTELSTSIYQLINVYCNFSFYADFQPVNV PRCTSYLNPLPSHLSFTVYAAHNIPETWVHR INFPLEIKSLPRESMLTVKLFGIACATNNANLL AWTCLPLFPKEKSLGSMFLSMTLQSEPPVEM ITPGVWDVSQSPVTLQIDFPATGWEYMKPD SEENRNLEELPKCEKIHARLSQKQTPLLSE EKKRYLWFYRFYCENNENCSLPLVLGSAPGW DERTVSEMHTILRRWTFQPLEALGLLTSSFP DQEIRKVAVQQLDNLNDELLEYLPQLVQAV KFEWNLESPLVQLLLHRSLSQIQVAHRL YWL LKNAENEA YFKSWYQKLLAALQFCAGKALN DEFSKEQKLKILGDIGERVKSASDHQRQEV KKEJGRLEEFFQDVNTCHPLNLPALCIKGIDH DACSYFTSNALPLKITFINANLMGKNISIFKA

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						GDDLRLQDMLVLQLIQVMDNIWLQEGLDLMDQ MIIYRCLSTGKDQRLVQMVPDAVTLAKIHRH SGLIGPLKENTIKKWFSSQHNHLKADYEKALR NFFYSCAGWCVVTFILGVCDRHNDNMLTKS GHMFHIDFGKFLGHAQTFGGIKRDRAPFITS EMEYFTTEGGKQNPQHFQDFVELCCRAYNIR KHSQLLNLWLAEMMLYAGLPESLGRQDLKY VYNLRLPQDITDLEATSHFTKKIKESLECFPVK LNNLIHTLAQMSAISPAKSTSQTTPQESCLLST TRSIERATILGFSKSSNLYLIQVTHSNNETSL TEKSFEQFSKLHSQLQKQFASLTPEFPWW HLPFTNSDHRRFRDLNHVMEQILNVSEVTN SDCVLSFFLSEAGQQTVEESSPVYLGEKFPDK KPKVQLVISYEDVKLTILVKHMKNIHLPDGS PSAHVEFYLLPYPSEVRRRRTKSVPKCTDPT NEIVVYDEVTELOQGHVLMMLIVKSKTVFVGA NIRLCSVPLDKEKWYPLGNSII*PLLLFSSFGM KSLEKDEFVGGMLLSNPIW
470	1820	A	3718	430	75	SHGSISILNLHQGCVFPLSLPAQGLRCYRCLA VLEGASCSVVSCPFLDGVCVSQKVSVCWQ*/ CPWGARAEGRLSAVVDSQISOCKGDLCAV VLAAGSPWALCVQLLLSLGSVFLWALL
471	1821	A	3723	891	494	LRQSLNSVPQAGVQWRDSSLQAPPPFTPLS CLSLPSSWDYRRLPPCLANFLYF**RRGFTML ARMVLIS*PRDPPASASQSTEITGGSHRAQHP TDSRDHSERSVKKSHEVISELRMKVIKCKVAF SKNPI
472	1822	A	3734	443	251	GFIET*NFCVSKDTSKKLS/RLPTKWKNVFAN *ISDKGLVSRICQELLRLHDAEQVSSTAQLSL
473	1823	A	3746	3	500	THASGGARSAGWAGRGVRAGTEAGRGGIF LTLILRTRDLPAGMSEGVDLIDYADEEFNQ DPEFNNIDQIDLDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNKTPAILYTYSLRNRRRA AVYVGSFSSWWTTDQQLIQVRSIGVYDVGEV KFAENRAK
474	1824	A	3753	2	5262	RPLFAREGGIYAVLVCMEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSFLDAQ MTREIFASIDSATRPOSESLLLTVPAAVILMLN TEGCSSAARNGLLLNLLCNHHTLGDQIITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLNR YSEPPGSPAERALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLKRL QQETQPFLLLRITLDAPGPNKTLILLSVLVIT RLLDPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCGAKEI LSKVLDKHSQAQLLGCCELRLDLYTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINP FFDVFLRHLCOGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPPTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFG DSTSCIGTELNTVNVMPASRVILLENLNRFW PIQIRIKRCQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL GKTCWEALVSPLVQNTSPDAEGVSALGWLL DQYLEQRETSRNPLSRAASFASRVRLCHLL VHVEPPPGSPSEPSTRPFSKNSKGRDRSPAPSP VLPSSSLRNITQCWLSVVQEQVSFLAAAWR APDFVPRYCKLYEHLQRAGSELFGPRAAFML

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						ALRSGFSGALLQSSFLTAAHMSEQFARYIDQ QIQGGLIGGAPGVEMLGQLQRHLEPIMVLG LELATTFEHFYQHYMADRLLSPGSSWLEGAV LEQIGLCFFNRLPOLMLQSLSTSEELQRQFHLF QLQRDKLFLEQDEEEKRL*EEEEEEEEEEA EKELFIEDPSPAISILVLSRCWPVSPCLYLHP RKCLPTEFCDALDRFSSFYSSQSNHFVLDMG PHRRLLQWTWLGRAELQFGKQLHVSTVQMW LLLKFNQTEEVSVETLLKDSLSPELLLQALV PLTSGNGPLTLHEGQDFPHGGVLRLEHPPQ RSGEALWLIPPQAYLNVKDEGRTLEQKRN LSCLLVRLKAHGEKGLHIDQLVCLVLEAWQ KGNPPGTLGHTVAGGVACTSTDVLSCLHLL GGQYVKRRDDRQILMYAAPEPMGPRGQA DVFPFGSQSETSKPSPEAVATLASQLPAGRT MSPQEVGLMKQTVRQVQETLNLEPDVAQH LLAHSHWGAEQLLSYSEDPEPLLLAAGLCV HQAQAVPVRPDHCPVCVSPGLGDDDLPSLCC MHYCKSCWNEYLTTRIEQNLVLNCTCPAD CPAQPTGAFIRAIIVSSPEVISKYEKALLRGYVE SCSNLTWCTNPQGC DRILCRQGLGCGITCSK CGWASCFNCSFPEAHYPASCGHMSQWVDDG GYDGMVSVEAQSKHLAKLISKRCPSQAPIE KNEGCLHMTCAKCNHGFCWRCLKSWKPNH KDYNC SAMVSKAARQEKRFQDYNERCTFH HQAREFAVNLNRNRSIHEVPPRSFTFLNDA CQGLEQARKVLAYACVVSFYSDAEYMDVV EQQTENLELHTNALQILLEETLLRCRDLASSL RLLRADCLSTGMELLRRIQERLLAILQHSAD FRVGLQSPSVEAWEAKGPNMPGSPQASSGP EAEEDDEDDEDVPEWQDEFEELDNDSFS YDESENLDQETFFFGDEEDEDDEAYD
475	1825	A	3754	1093	96	GTSRNQHSFKTHA*RSS/WPQPPLFLPPLQFQ ATGRRRRRTTQRTAALLTDGTTKTGAAW SRRPSLCWPSRTTGAPGAK*AVLVRSAPTITN PPNPQSPTGAAGKLAPGNRAG/SEPSSQEP DGTTRPASITGVAQSPATPATPSLCLHVPAP SRGQTLGVRTTGRASRLTVDRSRLSWPGRSA RSGGGRWRPNAPGRWRAP*SWEPGSWTE PWRWFFPAAESPFRCTYCTNHVSPAGPARPS HVYIIRATINSISHPLCRAQSSPWEAAGVWRR PAQPAFTSDVINLLRKPRVKRHDLIYQFLGN TLWEEGRQRPPELQPAR
476	1826	A	3758	901	521	FFFNGVSPCPQAGV*WHDLSLQNLPPGFK RFSYLSLPSSWDYRHVPPROANFCIF/M*RRG FTMLARMVSIS*PRDLPALASQSAGITGVSHH APPQMDFTFALLCFAPKGCLPRQKEGGTLNLI
477	1827	A	3761	843	575	GVISAHCNRL/CHLPGSSNSPASASQVAGTIG ARTIPS*IFVLVETGPHHVSQDGLDLLNFVI RPRRLKVLGLQACTRARLPSPLKEL
478	1828	A	3763	267	1240	HLLSFHLWSASLDCLEQLSQRHVKGMLLGP PPVNESTKPSPPWKLTPPMCSIPPVFPKSGS PTTSWS/PSGHSKLEVERAQTGFCLHYCP*P GVTDNITSLHYIPFRLSGLVCFPAH*FPSY WTGHSFASQAWLRQVPEVSKHLQCPAESLL TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWQGPESPLPEASSAPPPTLGTLPVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE QTPITQSTNGPLPSPCHHEHPLSSVEGEAPPA

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						EGSDHIG
479	1829	A	3766	2	2152	YSPIRLLEVCVPLPKIFIKRQAPLKVSLLQDLK DFFQKVSQVYVAIDERLASLKTDTFSKTRREEK MEDIFAQKEMEEGEFKNWIEKMQARLMSSS VDTPQQLQSVFESLIAKKQSLCEVLQAWNNR LQDLFQQEKGRKRPSVPPSPGRLRQGEESKIS AMDASPRNISPGLQNGEKEDRFLTTLSSQSST SSTHLQLPTPEVMSEQSVGGPPELDTASSSE DVFDGHLGSTDQVKEKSTMKAFANLLPG NSYNPIPPFPDPDKHYLMYEHervPIAVCEKE PSSIAFALSCKEYRNALEELSKATQWNSAEE GLPTNSTSDSRPKSSSPIRLPEMSGGQTNRTE TEPQPTKKASGMLSFFRGTAGKSPDLSSQKRE TLRGADSAYYQVGQTGKEGTENQGVPEQDE VDGGDTQKKQLINPHVELQFSDANAKFYCRL YYAGEFHKMREVILDSSEDFIRSLHSSPWQ ARGGKSGAIFYATEDDRFILKQMPRLVQSF LDFAPHYFNITNAVQQRPTALAKILGVYRI GYKNSQNTEKKLDLLVMENLFYGRKMAQ VFDLKGSLRNRNVKTDGTGKESCDVLLDENL LKMVRDNPLYIRSHSKAVLRSTSHSDSHFLSS HLIIDYSLVGRDDTSNELVVGIDYIRFTWD KKLEMVVKSTGILGGQG*MPTVVSPELYRTR FCEAMDNYFLMVPDHCOTGLGNC
480	1830	A	3777	251	3	QCGSAGTLIHY**ECKMVQLLWKTIV*QFLI KLN\KDPATLTDVYPNEVKNYVRTKTYTQMF I/ANFIMAKSWKQPTHPVST
481	1831	A	3779	333	3	EAAIROPEPNILDVNOIFKDLAMIIHDQGDID SIEANAESSEVLVERAPQLQRPAYYQKKS KKMCLVVLVQTAILICERIM*VVYTTKWSPPI VLPVSCFQGGQKFN
482	1832	A	3780	2	371	TGGRQGGNDHTSITEKPSRDFNRHLITQNI*M PNQDMKSSNSLIRKVOIKPTILYHHIFTRKA KMKTTIDKTKYR*GFKAITLIHCSQDCKLQ*S /L*ENHFMIFPKAEQHITYDITIPFLR
483	1833	A	3787	43	448	LMKDLSPYVMETHYLNRNLNER/RSMWRHIG KLPNTKDQEKILKAIRGREVIQGS/RQQYRR PAAFSAAEKARRLWCS/VFNIERRNL/CEYPTK LSFNKGEMTFSDKTEFTTNRPSLKMLLKDR QEEGKMF*KEKCFKRKE
484	1834	A	3798	1	727	FFFFETESRSVAQAGVQWCNLSLQALPPGF SHSPASASRVAGTTGTRH*ARLIFYFSRDGVS PC*PGWS*SPDLVIRPPARLPKCWDYRREPRP A*FFVFLVEIQGFTMLARMVSIS*PQ/CDLPAS VSQNAGITGVSHCAWPCLFHCFGGFFEMESC SVAQAEVQWHLRLSLQAPPPGFTPFSCSLSPG SWDYRRPPRPANFACFSRDGVSPC*PGWSRS PDLVIRPPRPKVLGLQA
485	1835	A	3802	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLPPGF KQFSCSLSPSSWD*RVPTSRPAKF/CVIF*DG SHCQPGWSAVVQPLH
486	1836	A	3811	378	98	RYD*SSQSENIPQKEFLKYP*CTATLGMNRN MSIMKKKSIFSAEFYKVSPLSLLVHLLAIEWG FHIEIQLTIHQHFLNYELESDFVHIVEYM
487	1837	A	3814	771	320	FDPDWTRAAGIRHEKKPKALAYRRENSPGDL PPPLPPPEEASWAL/GAEGSRQHVLPGAGA QWGEESGPGRAPGSPAGAPPR*RGLAPNSRP SFLSRGQGTSTCSTAGSNSSRGSSSRGSRGPG RSRSRSQSRSSQSRPGQKRREEPR

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488	1838	A	3818	1	781	FRACLELIPYAPILSWTACPPAMAGPRGLLP LCLLAFCLAGFSFVRGQVLFKGC DVKTTFTVT HVPCTSCAAIKKQTCPSGWLRELDPQITQDCR YEVQLGGSMVMSGCRKCRKQVQKACCP GYWGSRCHECPGGAETPCNGHGTCLDGMDR NGTCVCQENFRGSACQECQDPNRFPGDCQSV CSCVHGV CNHGPBGDGSCLCFAGYTGPCHD QELPVWQELGFPQNNPRLRKAPNCKCLPG*H RNLIAITPNPCRP
489	1839	A	3822	934	669	FFFSEMSRSVTRLECSGAISHLRLGSSNSP ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG QDGLDLL/NLMIHPRPKVLGFQA
490	1840	A	3825	79	9748	GCQSCWPAWFLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFYLRPRAPFIAPVLSGA ASRFEASGDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPQLPQPPQAQPLLPQPQPPPPPPPPPP GPAVAEPLHRPKKELSATKKDRVNHCLTIC ENIVAQSVRNSPEFQKLLGIAMELFLCSDDA ESDVRMVADECLNKVIALMDSNLRLQLEL YKEIKKNGAPRSLRAALWRFAELAHVLRPQK CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP KIMASFGNFANDNEIKVLLKAFIANLKSSSFTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVEDEHSTLLILGVLTLRLVPLLQQQV KDTSLKGSFGVTRKEMEVSPEAEQLVQVYEL TLHHTQHGDHNVVTGALELLQQLFRTPPEL LQTLTAVGGIGQLTAAKEESGGRSRSQSIVELI AGGGSSCSPVLSRKQKGVLLGEEEALEDDSD ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDITEQPRSQHTLQADSVDLASCDLTSS ATDGDDEEDILSHSSSQVSAVPSDFAMDLDNDG TQASSPIDSSQTTEGPDASVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLKNNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIGDQSTDDDS APLVHCVRLSASFLLTGKKNVLPDRDVRV SVKALALSCVGAVALHPESFFSKLYKVLPLD TTEYPPEQYVSDILNYIDHGDQPVRGATAILC GTILCSILSRSPHVGDWMTIRTLTGNTFSL ADCIPLLRKLKDESSVTCLACTAVRNCVM SLCSSSYSELGLQLIIDVLTNRNSSYWLVRTEL LETLAIEDFRLVSFLEAKAENLHRGAHHTGL LKLQERVLNNVVIHLLGDEDPVRVHVAASL IRLVPKLFYKCDQGAQDPVAVARDQSSVYL KLLMHETQPPSHFSVSTITRIYRGYNLLPSITD VTMENNLSRVIAAVSHELITSTTRALTFGCCB ALCLLSTAFPVCIWSLQWHCGVPPLSASDES KSCVTGMA TMILTLSSAWFPLDLAHDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRLVPMVEQLFSLKLVNIC AHVLDDVAPGPAIKAAPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASASRQSDTS GPVITTSKSSSLGSFYHLPSYKLHDLVKATHA NYKVTLDLQNSTEKFQGGFLRSALDVLSQLLEL ATLQDIGKCVIELGYLKSCFSREPMMATVC VQQLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAIHNLHRLFEPLVIKALKQ

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						YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYIEVGQFRESEAIPIFF FLVLLSYERYHSKQIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMILLRIQYHQVLEMFILVLQ CHKENEDKWRLSRQIADILPMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGLAILRLVLSQSTED IVLSRIQELSPSPYLISCTVINRLRDGDSTILE EHSEGGKQIKNLPEETFSRFLQLVGILLEDIVT KQLKVMSEQQHTFYCQELGTLMLCLHIFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNL ARSMITTHPALVLLWCQILLVNHTDYRW AEVQQTPKRHSLSSTKLLSPQMSGEEDSDLA AKLGMCMREIVRRGALLFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEV LQSSGLAQRHQRLYSLLDRFLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQFELPAEP AAYWSKLNLDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAQPG EQLLSPERRTNTPKAISEEEEEVDPTNQPKYI TAACEMVAEMVESLQSVLALGHKRN SGVPA FLTPLLRNIIISLARLPLVNSYTRVPLVWKL WSPKPGDGFGTAFPEIPVEFLQKEVFKEFTYR INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPEEDTERTQINVLAVQAITSVLVSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSLSPATTGALISHEKLLLQINPERELGMS YKLGQVSIHSVWLGNISITPLREEEWDEEEEE ADAPAPSSPTSPVNSRKHRAGVDIHSQSFL LELYSRWILPSSSARRTPAILISEVVRSLVVS DLFTERNQFELMYVTITELRRVHPSEDEILAQ YLVPATCKAAAALVGMMDKAVAEPVSRLESTL RSSHLPSRVGALHGVLYVLECDLLDDTAKQL IPVISDYLLSNLKGIAHCVNIHSQQHVLVMCA TAFYLIENYPLDVGPEFSASIIQMGVMLSGS EESTPSIIYHCALROLERLLSEQLSRDAESL VKLSVDRVNVHSPHRAMAALGLMLTCMYT GKEKVSPGRSDPNPAAPDSSESVIVAMERVS VLFDRIRKGFPCEARVVARILPQFLDDFFPPQ DIMNKVIGEFLSNQOPYPQFMATVVYKVFQT LHSTGQSSMVRDWVMSLSNFTQRAFPVAMA TWSLSCHFVSASTSPWVAAILPHVISRMGKLE QVDVNLFCVLATDFYRHQIEELDRRAFQSV LEVVAAPGSPYHRLTCLRNHVHVTTTC SNPPASASRVAGITGVHQHAWLIFVFLVEMEF HHVGQAVLKLISGDLVPSASQSA VAFSPMIMPDLFYFRDPPEEIEKEE*AAAEKVEE FQSEWTA VV/P/EFTATQSEVADWFKDMQVP SVPIQQPFTEDWST*PIMNDWSATSTAQTTE WVRITTEWP
491	1841	A	3826	469	302	SNPPASASRVAGITGVHQHAWLIFVFLVEMEF HHVGQAVLKLISGDLVPSASQSA
492	1842	A	3836	392	88	VAFSPMIMPDLFYFRDPPEEIEKEE*AAAEKVEE FQSEWTA VV/P/EFTATQSEVADWFKDMQVP SVPIQQPFTEDWST*PIMNDWSATSTAQTTE WVRITTEWP

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493	1843	A	3838	19	380	TPSDMNRAFETDTQSIGENRSPSEPDYFERK KFKRS*EKAHIRYKIDQPEDIPKIEFI.CKHSK CTATLSMRNMSLMKKKCSFSEFLAFFPSLL VCHLLAIKLGIFYIEIHLTTFNNTF
494	1844	A	3845	2	352	FFFLRRSL/DSVAQAEQWLIELGLLQAPPPGF KPISLPAQLPSSWDYGRPPPCANFCIF/M*RRG FTVLARMVLIS*PCDPPTLASQGTAITGMSYH ARPQDIDFLYAHQGRWCWRL
495	1845	A	3847	1774	40	DIFFRRAKEGMGQDEAQFSVEMPLTGKAYL WADKYRPRKPRFFNRVHTGFENKYNQTHY DFDNPPPKIVQGYKFNIFYPDLDKRSTPEYFL EACADNKDFAILRFHAGPPYEDIAFKIVNREW EYSHRHGFRCCQFANGIFQLWFHFKRYRYRR* RPWGTAGRCPRGHSKGASVKLVVTPGFLSGL QGRGFTSHLRPHLSFARPOFPPI*KGHH*AC HGELRRHWDRLA*GPDATEGALGASFEHEG GQQPPADLTQADTLHRFSARLGGAHRACPK RRPFRVLWRWARGAWAWRCQAREKQETQG QPCHITGHPLGREAEPAAGAAPALAHRRPF ARTGSTEPGPCWRPIRHCRRDPLWPTLCARD WPPTHPVLAGGVHFAAG/IGGCVEVPVSVN VMGTKSH*AVLPPPPSTGPGGQGLEPGWGLE KGEGLPPGIPPPGLLTGPWASMRPVTPSFAHIR TVAPSHSPFSGOEGRGPHGCHSPGR/SGFAGR LVLQHPTGTSPTAKRKVPFPGPEGHPTSPVT SPRPPTAPPRHPASSGNSSVCFSKKTCRWEKK SFVLMELAYWQDRMFF
496	1846	A	3849	830	442	AKSPLPLG*IQWRNLGSLKRLPLPGFK*FTCLG LLSSWDYRSLPPRPVNFILVELGFHHVDQAG LKLLTSSALPALASQSAEITGMSHRIWFLPLLR RPPVIRIRAPPQRLPFNLITSLKALSPNMAITF
497	1847	A	3859	2	393	ALRKTRRDGIARTGAQPAASWKGTTNNYPWR LEMAGRPGSQEQSKDRGTGSLPPSPQRPLGPS PEGAGSPPPPGIPRGGGSSSEGP/PQLLFVPR RFPAPKKGLPSDTPHSAKPTPHLILGGEDSQ VPIL
498	1848	A	3860	253	634	KNASTVYSSQGDPKSFFFLRWSLALVAQAG EQ*RDLSLQPPPPGFK*PSCLSLPSSWD/YRCP LPCLANF*FLVETGFHHVQADLKLLTSGDP PTSASESAGITGVSHRAWPRIHFLYWKTFLL
499	1849	A	3863	423	263	APSQISVAFLYAA/DKLFKEI*KKIPFILAS/DKI KIGINLTKEVKYLYTENYITLMKEIK/DTDKW KDILY*WIGKINI*KMSTPPKAIYRFNAIPTKIP MTFTEIEKSIKFIWNHKKPNTQSNIEQKE*S FCSILLWVFGGFLWFHMFMDFSISVKNVIGI LVGIALNL
500	1850	A	3865	2	15246	LPRGCLWCLQRSPTPARPQSPRPARSPLEPLF DLRPWASDLDIMGDAEGEDEVQFLRTDDEV VLQCSATYVLEQLKLCLEAGFGNRLCFLEP TSNAQNVPPDLAICCFVLEQSLSVRALQEML ANTVEAGVESSQGGHRTLLYGHAILLRHAH SRMYLSCLTTSRSMTDKLAFDVGLQEDATGE ACWWTMHPASKORSEGEKVRVGDDIILVSYS SERYLHLSTASGELQVDASFMQTLWNMNPIC SRCEEGFVTGGHVLRLFHGHMDECLTISPADS DDQRRLLVYYEGGAVCTHARSLWRLEPLRIS WSGSHLRWGQPLRVHVTGGQYLALTEDQG LVVVDASKAHTKATSFCSRISKEKLDVAPKR DVEGMGPPEIKYGESLCFVQHVASGLWLTYA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						APDPKALRLGVLKKKAMLHQEGHMDALS TRCQQFESQAARMIHSTNGLYNQFIKSLDSFS GKPRGSGPPAGTALPIEGVILSLQDLIIFYEP EDLQHEEKQSKLRSLRNRQSLFQEEGMLSMV LNCIDRLNVYTTAAHFAEFAGEEAAESWKEI VNLLYELLASLIRGNRSNCALFSTNLDWLVS KLDRLLEASSGILEVLVLCVIESPEVLNIIQENHI KSIISLLDKHGRNHKVLVDVLCSLCVCNGVAV RSNQDLITENLLPGRELLLTQNLINVTIRPN IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGNGV GDDLYSYGFDGLHLWTGHVARPVTSPGQHL LAPEDVISCCLDLSVPSISFRINGCPVQGVFESF NLDGLFFPVVSFSAGVKVRLLGGRHGEFKF LPPPGYAPCHEAVLPRERLHLEPIKEYRREGP RGPHLVGPSRCLSHDTDFVPCPVDTVQIVLPPH LERIREKLAENIHFWALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLPEPERNYNLQMSGETL KTLALGCHVGMADKAEADNLKKTLPKTY MMSNGYKPAFLDLSHVRLTPAQITLVDRLAE NGHNVWARDRVGQGWYSYSAVQDIPARRNPR LVPYRLDEATKRSNRDSLQAVRLLGYGY NIEPPDQEPSQVENQSRCDVRIFRAEKSYTV QSQRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVFNGHRGQRWHLGSEPPGRPW QPGDVVGCMDLTENTITFTLNGEVLMSDSGS ETAFREIEIGDGLPVCSLGPGQVGHNLGQD VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVS RVDTGTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRRSAGGWSEAENGKEGTAKGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLKA KKVAMMTQPPATPTRLRLPHDVPADNRDD PEIILNTTTYYSVRVFAGQEPSCVWAGWVT PDYHQHDMFSLSKVRVVTVMGDEQGNV HSSLKCSNCYMWVGGDFVSPGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFFAVFVLPTHONVIOFELGKQKNIMPLSA AMFQSERKNPAPQCPRLEMQLMPVSWSR MPNHFLQVETRAGERLGWAVQCQEPLTMM ALHIPEENRCMDILELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLLHLE DAHLPGPLRAGYYDLISIHLESACRSRSM SEYIVPLTPETRAITLFFPGRSTENGHPRHGLP GVGVTSLRPPHFPFPCFVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGQHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQILKMIPEVFTEEEEEDEEEEGEEDEE EKEEDEEETAQEKEDKEKEEEAAEGEKEEG LEEGLLQMKLPESVKLQMCHELLYFCDQELQ HRVESLAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPEQINMLLQFKDG TDEEDCPLPEEIRQDILLDFHQDLLAHCGIQLD GEEEPPEETTLGSRLMSLLEKVRVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLHRYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE TVMEVMNVVLGGGESKEIRFPKMVTSCCRFL

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						<p>CYFCRISRQNRSMFDHLSYLLENSGIGLGM QGSTPLDVAAASVIDNNELALALQEODLEKV VSYLAGCGLQSCPMLVAKGYPDIGWKPCCGG ERYLDLFRFAVFVNGESVEENANVVVRLLR KPECFGPALRGEGGSGLLAAIEEAIRISEDPAR DGPGRDRRRREHFGEEPENRVHLGHAIMS FYAALIDLLGRCAPEMHLIQACKGEALRIRAI LRLVPLEDLVGHISLPLQIPTLGKDGAIVQPK MSASFVPDHKASMLVFLDRVYGIENQDFLLH VLDVGFLPDMRAAASLDTATFSTTEMALAV NRYLCLAVLPLITKCAPLFAGTEHRAIMVDS MLHTVYRLSRGRSLTKAQRDVIEDCLMSLCR YIRPSMLQHLRLRLVFDVPILNEFAKMLKLL TNHYERCWKYYCLPTGWANFGVTSEELHL TRKLFWGIFDSLAKKYPDEL YRMAMPCLC AIAGALPPDYVDASYSSKAEEKATYDAEGRNF DPRPVETLNVIDEKLDSEFINKFAEYTHEKWAF DKIQNNWSYGENIDEELKTHPMLRPYKTFSE KDKEIYRWPIKESLKAMIAWEWTEKAREGE EEKTEKKKTAKISQSAQTYDPREGYNPQPPDL SAVTLSRELQAMAEQLAENYHNTWGRKKKQ ELEAKGGGTHPLLVPYDTLTAKEKARDREKA QELLKFLQMNGYAVTRGLKDMELDSSSIEKR FAFGFLQQLLRWMDISQEFIAHLEAVVSSGRV EKSPHEQEIKFFAKILLPLINQYFTNHCLYFLS TPAKVLGSGGHASNKEKEMITSLFCKLAALV RHRVSLFGTDAPAVVNCLHILARSLDARTVM KSGPEIVKAGLRSFFESASEDIEKMVENLRG KVSQARTQVKGVGQNLTYTTVALLPVLTTLF QHIAQHQPDDVILDDVQVSCYRTLCSYSLG TTKNTYVEKLRPALGECLARLAAAMPVAFLE PQLNEYNACSVYTTKSPRERAILGLPNSVEEM CPDIPVLERLMADIGGLAESGARYTEMPIVIE ITLPMCLSYLPRWWERGPEAPPSPALPAGAPP CTAVTSDHLNSLLONILRIIVNNLGIDEASWM KRLAVFAQPIVSRARPELLQSHFPTIGRLRKR AGKVVSEEEQLALEAKAEAEQEGELLVRDEFS VLCRDLYALYPLLIRYVDNNRAQWLTEPNPS AEELFRMVGEIFTYWSKSHNFKREEQNFFVQ NEINNMSFLTADNKSMAKAGDIQSGGSDQE RTKKKRRGDRYSVQTSIVATLKKMLPIGLN MCAPTDQDLITLAKTRYALKDTDEEVREFLH NNLHLQKGKVEGSPSLRWQMALYRGVPGREE DADDPEKIVRRVQEVSAVLYLDQTEHPYKS KKAVVWHKLLSKQRRRAVVACFRMTPLYNLP THRACNMFLESYKAAWILTEDHSFEDRMIDD LSKAGEQEEEEVEEEKPDPLHQLVLFHSRT ALTEKSKLDEDLYMAYADIMAKSCHLEEG GENGEAEVEVSFEKQMEKQRLLYQQARL HTRGAAEMVLQMISACKGETGAMVSSTLKL GISILNGGNAEVQKMLDYLDKDKKEVGFFQS IQALMQTCSVLDLNAFERQNKAEGLGMVNE DGTVINRQNGEKMADDEFTQDLFRFLQLLC EGHNNDFFQNYLRTQTGNTTTINIICTVDYLL RLQESISDFYWYYSKGVIEEQGKRNFASKAM SVAKQVFNSLTYIQGPCTGNQQLAHSRLW DAVVGFHVFHMMMKLAQDSSQIELLKL LDLQKDMVMVLLSLLEGNVVNGMIARQMV DMLVESSSNVEMILKFFDMFLKLDIVGSEAF QDYVTDPRGLISKKDFQKAMDSQKQFSGPEI</p>

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						QFLLSCSEADENEMINCEEFANRFQEPARDIG FNVAVLLTNLSEHVPHPRLHNFLELAESILE YFRPYLGRIEMGASRRIRYFEISETNRAQW EMPQVKESKRQFIFDVVNEGGEAEKMFVVS FCEDTIFEMQIAAQISEPEGEPEDEDEGAGA AEAGAEGAEEGAAGLEGTATAAAGATARV VAAAGRALRGLSYRSLRRRVRLRLRTAREA ATAVAALLWAAVTRAGAAGAGAAAAGALGL LWGSFLGGGLVEGAKKVTVTTELLAGMPDPT SDEVHGEQFAGPGGDADGEGASEGAGDAAE GAGDEEEAVHEAGPGGADGAVAVTDGGPFR PEGAGGLGDMGDTTPAEPPTPEGSPILKRKL VDGVEEELPPEPEPEPEPELEPEKADAENGK EEVPEPTPEPPKKQAPSPPPKKEAGGEFWG ELEVQRVKFLNYLSRNFYTLRFLALFLAFAIN FILLFYKVS DSPGEDDMEGSAAGDVSGAGS GGSSGWLGAEGEAEAGDEEDENMVYFLEES TGYMEPALRCLSLHLTLVAFLCIIGYNCLKVP LVIFKREKELARKLEFDGLYTEQPEDDDVKG QWDRLLVNTSPSPSNYWDKFKVRKVLDDKHG DIYGRERIAELGMDLATLEITAHNERKPNPP PGLLTWLMSSIDVKYQIWKFGVIFTDNSFLYL WYVMVMSLLGHYNNFFFAHLLDIAMGVKTL RTILSSVTHNGKQLVMTVGLLAVVVYLYTVV AFNFFRKFYNKSEDEDEPDMKCDMMTCYL FHMVVGVRAGGGIGDEIEDPAGDEYELYRVV FDITFFFFVIVILLAIQGLIIDAFGELRDQEQV KEDMETKCFICIGISDYFDTTPHGFETHLEE HNLANYMFFLMYLINKDETEHTGQESYVWK MYQERCWDFFPAGDCFRKQYEDQLS
501	1851	A	3869	467	665	VIVAIYQLIFDKGAKTIQ*PFQQLALCKRMK LGPCFTPCGKINSEWIRELSVRVKTIKHLEIGV N
502	1852	A	3888	1042	724	SGMQWRDLTLPQLPFRFKQFSCSLPGSWD YRHAPLLTNF*FLVEMGFCYVGQAGRKLL ASSDQSALASQSAGITGISTAGPPFFFLNFEA GSCSVAQAGVQ
503	1853	A	3891	1773	1193	EVDSQSGVQ*QAPGSLQLQTPGLK/VSCLLSR QDYRSSLPHLASCCYYYYY/VFL*RRGLTTL VQGGKLKLPSSNPFASAP*TAGITGMSHCAGP HFN*MFVKISCIRE*F*HTRIYDIFLILFFKET WVLLCYPGWQIPGLKFPSSCLRLSSWDHRC APPCPASFFIFHVDVSPPCGLVSITFKMLLL L
504	1854	B	3896	279	70	MVSKSKSILMSYNHVELTFSMDMKMPEAFRR TQKHTIYLIPYQVIFWSTGKDAMRSFMMFFY QKEYYENQ*
505	1855	A	3899	2	1396	EPGVPTKKTWFDKPDFNRTNSPGFQKKVQFG NENTKLELRKVPPELNNISKLNEHFSRFGTLV NLQVAYNGDPEGALIQFATYEEAKKAISSTEA VLNNRFKIVYWHREGSTQQLQTTPKVMQPL VQQPILPVVKQSVKERLGPVPSSTIEPAEQS ASSDLQVLSTLLA*QKQCIIQLL/WKAAQKT LLVSTSAVDNNEAQKKQKQKALQDVRKR KQEILEKHETQKMLISKLEKNKTMKSEDAE IMKTLEVLTKNITKLKDEVKAASPGRCPLPSI KTKTQMQLKELDTLDLYKKMQAGEEVTEL RRKYTELQLEAAKRGILSSGRGRGIHSRGRGA VHGRGRGRGRGVPGHAVVDHRPRALEIS

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						AFTESDREDLLPHFAQYGEIEDCQIDSSSLHA VITFKTRAEAEAAVHGARFKGQDLKLAWN KPVTNISAVETEEVEPDEEBQREIIIA
506	1856	A	3911	1952	919	DAELSGTSLSLVLTQCCKRIKDTVQKLASDHK DIHSSVSRVGKAIKDNFDSDISVGDGCWQA DSQRLLEVMVEHFRQGMLDVAEELCQES GLSVDPQSKEFFVELNRILEALKVRVLRPALE WAVSNREMLIAQNSSLEFKLHRLYFISLLMG GTTNQREALQYAKNFQPFALNHQKDIQVLM GSLVYLRQGIENSPLYVHLLDANQWADICDIFT RDACALLGLSVESPLSVSFSAGCVLPALINIK AVIEQRQCTGVWNQKDELPIEVIDLG*KSAGY HSIFACPILRQQTDDNPPMKLVCGHISRDAL NKMFGSKLKCPCPYCPMEQSPGDAKQIFF
507	1857	A	3936	439	18	SHPFSPAPGICPDAPPPLPRPSKGLGHPGTAGA PGSGARCHPPSTCSPSWASPG*GAKASPALPR SHGVTLCKAQAHLCRGEDSKDASGSTSQA WEPG*GAWGMPCRCQPGALGSCFCPPGTTVQ RPAKQORDKRNRLGR
508	1858	A	3944	120	412	WCPAGTLDFFGPQEMVLLIEIVMNQLNHRNL IQLYAAIETPHEIVLFMEYECPK*W*GLGGGT TRHGASRGVCAHSIEGGELFERIVDEDYHLT EV
509	1859	A	3949	31	392	LTKTPSPREKGRGVLSVLLMMI*KCRVIFVKIP MVFFLQNFRCRILNVAIWTD*PNTL*KEQRG ITPDSKS*YKATKIKTMWYCHKNRYID/ERN RIEIPENPCIDCKIIFRKLSTMTQ
510	1860	A	3954	1013	885	FSETRACCPRLHSGRIEHAHCSLNIPGSSDPPT SASSVAATTG
511	1861	A	3956	1	1054	PPAWAPRSPLIWAPTSGRHPCRAALPWSTSSV RWQPEKQPPPAHGRPADSLSTAAGAELS AEGAGKSRGSGEQDWVNRPKTVRDTLLALH QHGHSGPFESKFKEPALTAVARTARRKPS PEPEGEVGPCKITTERPSRGCPHPQRGSRP*L LHFLCLRHHPPLPHLIPTGPHRLKRPRMP/SP MAALILVADNAGGSHASKDANQVHSTTRRN SNSPPSPSSMNQRLGPREVGGQAGNTGGL EPVHPASLPDSSLATSAPLCTLCHERLEDTH FVQCPSVPCHKFCFPCSRQSIKQQGASGEVYC PSGEKCPVGSNVPWAFMQGEIATILAGDVK VKKERDS
512	1862	A	3957	1086	3	QDRARLDCSSATSACNLRLPGS*DSPASASR VAGTTDTHHTWLILGSSVQTGFHDVGGQAG LELLTSGDPPISASESAGIMGMSHCVWP*SWG LSHHMAPPQDGGGRARGTPGPEQSFWNLS H*PRCQVPS*LMTQL/FWGRHQYNFTMKRGK LRHREACSLPLPGEPEGLQPSI*SQNPCSSPL FHHGL*AWLWCPPELLQGGARRH*RSPPS/FK CPATLSLTAWSQTKRLRSQFLLPWL*RAL*H PPCHWPSRRSLGDPLPRSQG*RDGT*ASTFC SYF*DTESHLVAQAGVQWRDLGSLQPPCPRL KIRFSRLSPSSYTHRYVPSHLAESCISSDRIP PSRPDRSRNSNSLSR
513	1863	A	3961	3038	476	VALTTSMCCNKQVTVIDKIKSASIADRCALH VGDHLSIDGTSMEYCTLAETQFLANTTDQ VKLEILPHHQTRLALKGPDHVKIQRSDRQLT WDSWASNHSSLHTNHHYNTYHPDCHRVPAL TFPKAPPPNSPPALVSSSFPTSMSAYSLSSLN MGTLPRLYSTSPRGTMRRRLKKDKFKSSL

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						SLASSTVGLAGQVVHTTETEVVLTADPYTGF GIQLQGSVFATETLSSPPLISYIEADSPAERC VLQIGDRVMAINGIPTEDSTFEEASQLLRDSSI TSKVTLIEIFDVAESVIPSSGTFHVKLPKKH VELGITSSPSSRKPGDPLVISDIKKGSAHRT GTLELGDKLLAIDNIRLDNCSMEDAVQILQQC EDLVKLKIRKDEDNSDEQESSGAIYTVELKR YGGPLGWTISGTEEPFDL*USSLTKGGLAERT GAIHIGDRILAINSSSLKKGKPLSEAIHLQMA ETVTLKIKKQTDASASSPKKFPISSHLSLGD VEEDSSPAQKPGKLSDMYP SHGCPVS DSAVD SWDGS AIDT SYGTEGTSFQASGYNFNTYD WRSPKQRGSVSPVTKPRSQTYPDVGLSYED WDRSTASGFAAGAAADSAETEQUEENFWSQALE DLETGQSGILRELEATMSGSTMSLNHEAPT PRSPAGSDRPSFQERSSSSRPHYSQTTTSNLT PS DVGKRSVTLRKMKEIKEIMSPTPVELHKVT LYKDSMEDFQFSVADGELLEKGVYVKNIRPA GPGDLGGLKPYDRLLQVNHVTRDFDCCLV VPLIAESGNKLDLVISRNPLASQKSIDQQLPG D*SEQNSAFFQQPSHGGNLETREPTNTL
514	1864	A	3967	833	800	LEKQGVSGMATKRLARQLGLIRRKSIAPANG NLGRSKSKQLFDYLVDFESTCWNDGKHHH SQEIEFPAVLLNTSTGQIDSEFQAYVQPEHPI LSEFCMELTGKQAQVDEGVPLKICLSQFCK WIHKIQKQKNIFATGISEPS/DF*SKIMCICYL VR*RSITY*SKHKSKGC
515	1865	A	3969	492	182	CRFWGISTHCDTCDPLSPQTTEG**EGDLWSL DLLGPEFLARKPLFKTKTYQSTF*SISKNE/FTC PNFIEEGTDLIF*QVKHNPCHRLTPBEGTVQL NRADS
516	1866	A	3977	2	1357	KMLC/QKESNYIRLKRAKMDKSMFVKIKTLGI GAFGEVCLARKVDTKALYATKTLRKDDVLL RNQVAHVKAERDILAEADNEWVVRLYYSFQ DKDNLVYFMDYIPGGDMMSLLIRMGIFPESL ARFYIAELTCAVESVHKMGFIHRDIKPDNILD RDGHIKLTDFGLCTGFRWTHDSKYQSGDHP RQDSMDFSNEWGDPSSCRCGDRKPLERRAA RQHQRCLAHSLVGTFPNYIAPEVLLRTGYTQL CDWWSVGVLFEMLVGQPPFLAQTPLETQM KVINWQTSIHPPQAKLSPEASDLIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PESRS AFKQFP*NHTTPTDTSNFDPAVDPDKLWSDDN EENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYIYNSQGEQQSDEDD QNTGSEIKNRDLVYV
517	1867	A	3980	1358	1022	FFFKKFTQSLGFLFSFSLFSCFFHHFVLCY VFLDRVPLCHPGWSAVVQSQVT/VNLPFSWD *RCRPPH/LANLCNFCRD/SFTTLPRVLNTWA QAIFQPQPKVLGLQV
518	1868	A	3986	974	666	SPEMESHPTQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGVRHVPCLANSVFSVEMQGLH VGQAGLELLTSGDLPALASQSAGITGSHRAR PENGFEFIF
519	1869	A	3994	751	126	NQGLRHVGLCRTCLVNQMFASSILGKSHHHS LISINQGHNALWKAAGPLPLKAGYCSQSPC DSLKYGSWDEKDLTVQRDTHKRSVLRWIS ORGKLA VEME EGHCLLVLPLGTECLGKPIV HLFSSEMGENRPMVGARHVYSNAALLSFTP

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						LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI AHVAFADLLLIITLPSYVIFC
520	1870	A	3999	882	698	QSFRLSLLSSWDYRHM*PRLANF*TVFCRDR/ SLALLPRLVSNVWPQAILPPRPVKVLGLQT
521	1871	A	4011	1346	1178	FFF*ETVSCSAS*AGVRSHDNSSLQPPSPGSSN PPTSASHVAGATGTHHAWLLSV
522	1872	A	4015	2	377	QGIALLTRMGESVKHVTGGYKLRTRPLEFAA IGDYLDTFALKLGTIDRIAQRUIKEEIEYLVELR EYGPVYSTWSALEGELAEPLGVSAICIGNCST AL*ELIDDMTEDFLVLRVILYSDSMK
523	1873	A	4018	341	19	ERVHNIQQAQRSPHFNARRSS/PRFNIVELP KVKEVCKTSKS/GQVIYKGVISIRLRANFLAEP L*NRREWDEAIKVLKEKQFLSKMVYPANLSF GNEGDI TSFPAK
524	1874	A	4020	1067	743	FFLRWSL/DSVAQAGVKWCNGLSLQAPPPGF TPFSCSLSPSSWDYRHPPLAN*LTNFLCF** RQGFTVLARMVLIS*PHDLPASASQSAGITGL SHCSWPTSSILS
525	1875	A	4021	781	351	QFRVIFFLRRSHSVAQAGMQWHDHSLLOPL PPRLKQ/F/SHLSPPSIWDYRRVPCLVNFISFF VETGSCQCLQLLGSSNPPASASQAGIASH QGQPE*SFDIRFACVIAALRETFQCLCSASRVN NKIINRPTHVPESSF
526	1876	A	4024	80	341	TPSSTSRGTTEEQSSKMAWQRREEKEHLNVR RSSAEDGWKADKP/VDG*TPGEDHLPTSPFQ LHHSSSEQLHHSVKSPPSLSFRLM
527	1877	A	4026	593	230	DFYLYPERKKRGQMMTAVSLTTRPQESVAFE DVAVYFTTKEWAIMGPAERALYRDVMLEN YGGCGPL*CHPTSKPALVFSLEQKESCFSPA TGSSLSRNDWRAGWIGYLELRRYTYLS
528	1878	A	4028	1160	242	GTSELLCIQRWNWGPAPPPRGLALAPTLQLL VEMGSAKSVPTPARPPPHNKLARVADPRS PSAGILRTPIQVESSPQGLPAGEQLEGLKHAQ DSDPRSFTLGIARTPMKTSSGDPSPVLVKLSE VFETEDSKSNLPPPEVLPPPEAPLSSELDLPLGT QLSVEBQMPPWNQTEFPKQVFSKEEARQPT ETPVASQSSDKPSRDPETPRSSGSMRNRWKP NSSKVL\GKSPLHPSQDDNSPGTLTLRQGKA AFKPLSENVSELK\EGAILGTGRLLKTEGRA WEQQQD\HDKENQHFLVES
529	1879	A	4039	2	366	KDMVLIMEMQSMITMKCPQYL*E*RKIPDITK CW*GCGSTGILFC/WS*PL*KTI*QPR*FKQI*T ILTIYSIM*EHTFHNA GV*LSDIYPRFMKGYV HTEICT*MFIAVLFFVVKTWKQF
530	1880	A	4057	358	3	LLEVNGNTIVTVFTKAQNKKNKGRSILFKQL RKYGSRIINLLKSKHDKNICTENYKT*MKEIEA /DTDKWKDILCSWIRRIHMKDILCSWIGRTHV VKISILPKVNYRFYLSIKIIMAI
531	1881	A	4061	50	278	TQGTTEEYKISSCEWVQASFSTPLITLHDFKIY HKATVIKMWVYWHRQ*KFSKN/RIESSEIEPH IYDQFIFDKGEKIQEKNSFFNM/MCWKNWIF T*KR
532	1882	A	4069	19	368	NDLLENFKFWE*FKE*LENINGTVTEKETGGV YKELSSPKYSGTRQFYGGTISNFPGKIIMVY KLFQNT/TEGRHPISLYEFRITLITPNKDNLYL QIWMFVSLMNIVILKCP
533	1883	A	4076	1	355	PIRKFTKVAG*KSNTPK*LAFLHINNEQFENKI/ ITNI/PIILASKRIKYSIGSLTKEMKDLYTETLLR KIKEDTNKWKDI/SCFVWGR/LNIVKMPK/VIC

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534	1884	A	4088	3	1931	IFNAIPKMPMMCMKIEKNSS IIDSSTRRMESERSPLYRQLIDLGYLSSSIWNC GAPGQDTKAQSMLEQSEKLRHLSTFSHQVL QTRLVDAAKALNLVHCHCLDIPTNQAFDMQR DLQITPKRLEYTRKKENELYESLMNLANRKQE EMKDMIVETLNTMKEELDDATNMEFKDVI VPENGEPVGTREIKCCIRQIQELIISRLNQAVA NKLISVDYLRSEFVGTLERCLQSLEKSQDVS VHITSNYLKQILNAAHYHVEVTFHSGSSVTRM LWEQIKQIIQRITWVSPPAITLWKRKVAQEA ESLSASKLAKSICSQFRTRLNSSHEAFAASLRQ LEAGHSGRLEKTEDLWLRVRKDHAPRLARLS LESRLQDVLHHRKPKLGQELGRGQYGVVYL CDNWGGHFPKALKSVVPPDEKHWNDLAEF HYMRSLPKHERLYDLHGSVIDYNYGGGSSIA VLLIMERLHRDI.YTGLKAGI.TLETQLQIAI.DV VEGIRFLHSQGLVHRDIKLNVLDDKQNRKI TDLGFCCKPEAMMSGIVGPIHMAPELFTGK YDNSVDVYAFGILFWYICSGSVKLEAFERCA SKDHLWNNVRRGARPERLPVFDEECWQLME ACWDGDPLKRPLGIVQPMQLQIMNRLCKS NSEQPNRGLDDST
535	1885	A	4090	2	417	ALMPHEANYEEIFLKTDKDMDGFESGLEVRE IFLKT/RLPSTLLAHIWALCDSKDCGKLSKD HFALAFHLITVQKLIKGDPLVLTPKISPSNR ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK HNRKRIWLRA
536	1886	A	4102	569	829	DHOK*KNIPCSWIGRINTVKMSILPKATYRFS AIPIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK EQNLEESHYLDKF*YYRAV
537	1887	A	4104	54	281	SIDCEHLIRRMVLDPKRLTIAQIKEHKWML IEVPVQRFPVLPQEENEPSIGEFNEQVLRML HSLGIDQOKTIE
538	1888	A	4109	141	314	IRHPLKIRSVVSHLKCFYKFILTFFFAGCSQPL VPRENTAWMNAIGLITLALPVS
539	1889	A	4111	268	1	ASRPWGHSTY*FNQQEVDTLKRPIASSEI*MM I*KFATVKKSPGPYRFTAEPSTHFKEDLVPIW PLFPKIYREGTLPHSFYEASITL
540	1890	A	4142	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE AALGDFLGLHRRTOQPAVDRLLSDASAQWR VRGHGGVRESGRAPQPGRRRRGRPRKRPR GRWRREGCGAGRGVCVAAWSQRSIAGNN DYRLFHKMSNSHPLRPFTAVGEIDHVHILSEH IGALLIGEYGDVTFVVEKKRFPFAHRVILAAR CQYFRALLYGGMRESQPEAEIPLQDTTAEFT MLLKYYTGRATLTDEKEEVLLDFLSLAHKY GFPELEDSTSEYLCILNIQNVCMITFDVASLY SLPKLTCMCCMFMDRNAQEVLSSEGFLSLSK TALLNIVLRDSFAAPEKDIFLALLNWCKHNSK ENHAEMQAVRLPLMSLTELNNVVRPSGLLSP DAILDAIKVRSESRDMDLNYRGMLPEENIAT MKYGAQVVKGELKSALLDGDTONYDLHDG FSRHPIDDDCKSGIEIKLGQPSIINHVRILLWDR DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS WQKLYFPARVCYRIRIVGTHNTVNKIFHIVAF ECMFTNKTFTLEKGLIVPMENVATIADCASVI EGVSRSRNALLNGDTKNYDWDSGYTCHQLG SGAIVVQLAQPYMIGSTRVLLWDCDDRSY
541	1891	A	4146	282	778	GTLGYFNGARGQPQDNFFAHQVSHHPISAC

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						HAESENFAFWQDMKWKNKFWGKSLEIVPVG TVNVSLPRFGDHFENKVTSCIHNVLSGQRW IEHYGEVLIRNTQDSSCHKITFCCKAKYWSSN VHEVQGA VLSRSGRVLHRLFGK WHEGLYRG PTPGGQCIWKP
542	1892	A	4147	44	433	SVDAYVCNDIVFSYRTTITILEGA*LTHRYVA QDPKQGGQLRSLHLTCDSAPAGSQGTWSTSCR INHILFRGGAQITFLATFDDSPKAVLGDRLLLT ANVSSENNTPTRTSKITTFQLELSVKDAVYTVV SSH
543	1893	A	4153	678	11	TISYPQCLTQMYFLISFANVDTFLPIMALDH YVAICSAQ*CSITP/ELCQGLPVA*AGSSLIS PVHTVIMSLAFCSSAQISHFYRDAYLLMKIA CSHT*NOHVFLGAVVFLAPCALILVSYRIA AAILRIPSPTRRRKACSSHLSLVTLFYGT LGICI*PPDSFSAQDALATIMYTVVTMLNPFY SLMNKEVQEAVRRLFSRGSSSHSSWCW
544	1894	A	4158	3	538	LLYAQAGVQ*NLSSLPQPAAGLKQSSHPSLP SSWDYRSTPHANFFVEMEFHHVAQAGLEL LGSGDLPTSTSHAGITGVSHHAPPLISSEGS LLGHLLCLPMVFPLLCVFLISSSLAGEEAA LRVQKLWPAVVLSHLPVCWFHCSGIWSEVIE LKVGREGHVLPWQAHVVEF
545	1895	A	4160	1	412	HPGLGLVPSEIFSPQDKKAADGSILAPARGE DLEAGLKGSFMDGRLQASVSFRIQRVGSAM QDTASAMPCLPYPTSHCFMAGGKSRSGW EELSGEPAPGWQVLAGYTTQARYLRDASE ANVGQPLRPVDP
546	1896	A	4174	1252	1190	FFQVFILFLIFKTEFHSCCPGAVQWHDLSL QPPPPRFKGFSCSLPSSWDYRHAPAHANFV FLVETGFLHV/GQASLELPTSGDTPASASQSA GITGVSHHA*PRASGRRCW
547	1897	A	4176	3029	1	AGPDGLAAPASCQAGRGQTRVPGAFSWLAP GSHHASEGLAPGVPPAGGVSAQELTAPPQEG WGLGAPPAAPRPESDEKRAAGSDAVRSFSGA RDSLQORRLGGTRGAGPAKGQAQRTMGPAS GFHSFPPRPHQEPSPRSSCWHLWHCPWPQ PSRLPRLTPAQLLQGGVLAAPPGP*HVPGL AQSPWPLPSGPRSP*DPLHQGALVPLPQGGSP HTAPHCLPSVLSPAIQQLPTAST/SSRSPAS TMAPIPSALAVWEPAGSSPOLSSAPADSSVLP ALPKVLPFWTQKPLLGCLCQSPPLSPDPQ/ RCPPACSPAAASSFSFESQPCSPASKASPAPA ALIVGPHHPP*SOQPQSQSVHHPGPGGPQPL AASSLFWMFCQPPPPHPQFLWHRPLPVTOKA LASPLCFRPAAGSLRQTPLPPQHPRPGLSAP/ PPPASGTSDDSDSRSPSASAARVWPPAISPPPP AARHRPHPEYFLSPCFSCGFRLLGRPRRQ ALQTPRAWDLPPGSSPAPLCSGPPL*APFPLP PFPRVA*LGSGHPPSAQVPLW*RCV*GHPI RPVGH*SGPPHSPPL*APPQAWPLEPPSRQC LQPLHLRAAQPLDPCCSLSPGPPLVPALPS WPGRP*SPSPASSQPPYHAGLPGPQSSPLPGL PQLPSLRSGSQQLFFQCPGPGAVWGKGSQ PLSPHPPPP/ARTQTFPVASRLSPGTAPYSVCL TPSRASSLPEVVLAASSLPKIPQSSGSLGPTSP MP*CFHRPSPPL/LSSFPFALRPQAPQFPLHP P*PPAPSPGCPLPPLAQHQPSPPSPHARSTLT PPLWPSLALLP*PLPPPPVPFSFASLLCSLPAH

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						GTPASPGGLGRSCLGKPTLPWISFWPPSGRLA PGTWQPW/PVSPAPLSCLSAWDPWELPSPQPQ VCSTAELPTSCLLSSPGPPAFQPPRFGCL*GPP GPPGLPPLQSSLSFPPPPPPVQPPAPPALQWG LHLPGGRTK
548	1898	A	4180	2369	844	RIHREEDFQFILKGIARLLSNPLLOTYLPNSTK KIQFHQELLVLFWKLCDFNKVQPRGALQGD GEQLPQ*PGGRDSVRLRGVQSCPSLELSPLG PSPHP*KLFFVLKSSDVLIDILVPLFFLNDAR ADQSRVGLMHIGVFILLLSGECNFGVRLNKP YSIRVPMIPVFTGTHADLLIVVFHKITSGHQ RLQPLFDCLLTIVNVSPYLKSLSMVTANKLL HLEAFSTTWLFSAQNHHLVFFLLEVFNNI IQYQFDGNSNLVYAIRKRSIFHQLANLPTDPP TIHKALQRRRRTPPELSTRTSGQGGAPPWRAPA PLPLQSQAPSRPVWLLQALTS*PRSPRCOR MAPCGPWNLSPSRAWMAARLRGSPARHGG SSGDRP/HSSASGQWSFTPEWVLSWKSILPLQ TIMRLQVLVPQVEKICIDKGLTDESEILRFLQ HGTLVGLLPVPHILIRKYQANSGTAMWFRT YMWGVYILRNVDPPVWYDIDVKLFQIRV
549	1899	A	4191	858	321	LPWQRLGVLLSRGKMAVGTWLESRTAQKT ALLQDGRRKVHYLFPDGKEMAEYDEKTSE LLVRKWRVKSALGAMGQWQLEVGDPAPLG AGNLGPelikESNANPIMRKDTKMSFQWRIR NLPPYKDVYSVSDQKERCIVRTTNKKYYK KFSIPDLDRHQLPLDALLSFAITPTAP
550	1900	A	4192	1	1980	IRHTGSDIAGVCGWLLSGPCGVGLDLDLSRL GASAMRRSEVLAEEIVCLQKALNHLREIWE LIGIPEDQRLQRTFVVKKHIELDMMAEEE SLKERLIKSSVCKELNTLCSELHVEPQEEG ETTLQLEKDLRTQVELMRKQKKERKQELKL LQEQDQELCAELCMPHYDIDSASVPSLEELNQ FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSENIALTL QKLLRQLEMQKSQNEAVCEGLRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRKALQLE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNNYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEELKARIELWEQHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQKNNKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRPPSGSK PVAASTCSGKKTPTTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS
551	1901	A	4194	3	1008	AWHEGLVSSPAIGAYLSASYGDSLVLVATV VALLDICFILVAVPESLPEKMRPVSWGAIQSW KQADPFASLKKVGKDSTVLLVCITVCLSYLPE AGIQYSSFFLYLRQVIGFGTVKIAAFIAMVGI LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML QLAWYGFGSQAWMMWAAGTVAAMSSITFP AJSALVSRNAESDQGVQAGIITGIRGLCNGL GPALYGFIFYMFHVELTELGPKLNSNNVPLQ GAVIPGPPFLFGACTVLSFLVALFIPEYSKAS GVQKHSNSSSGSLTNTPERGSDIEDIEPLLQDS SIWELSSFEPPGNQCTEL

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552	1902	A	4197	2	14302	ARPPAPGSRQKQKAAPGAAAAAELRGAR EPAPARRRGTMADGGEGEDEIQFLRTDDEVV LQCTATIHKEQKQLCLAAEGFGNRLCFLEST NSKNVPPDLSICTFVLEQSLSVRALQEMLAN VEKSEGQVDVEKWKFMKTAQGGGHRILL YGHAILLRHSYSGMYLCLSTSRSTDKLAFD VGLQEDTTGEACWWTHPASKQRSEGEKVR VGDDLLVSVSSERYLHLSYNGSLHVDAAF QQTLWSVAPISGSEAAQGYLIGGDVLRLLH GHMDECLTVPSGEHGEQRRTVHYEGGAVS VHARSLWRLETLRVAWSGSHIRWGQPFRLR HVTGKYLSLMEDKNLLMDKEKADVKSTA FFRSSKEKLDVGRKEVDGMDGTSEIKYGD VCYIQHVDITGLWLTYSQVDVKSVMGSIQR KAIMHHEGHMDDGISLSRSQHEESRTARVIR TVFLFNRFRGLDALSKKAKASTVDLPESVSL SLQDLIGYFHPDEHLEHEDKQNRRLALKNR QNLFQEEGMNINLVECIDRLHVYSSAAHFAD VAGREAGESWKSILNSLYELLAALIRGNRKN CAQFSGSLDWLSRLERLEASSGILEVLHCVL VESPEALNIIKEGHIKSIISLLDKHGRNHKVL VLCSLCVCHGVAVRSNQHLICDNLPPORDLL LQTRLVNHVSSMRPNIFLGVSEGSQYKKWY YELMVDHTEPFVTAETHLRVGWASTEGYSF YPGGGEWGGNGVGDDLFYGFGLHLWSG CIARTVSSPNQHLLRTDDVISCCDLAPSISF RINGQPVQGMFENFNIDGLFFPVVSFSAGIKV RFLGGRHGEFKFLPPPGYAPCYEAVLPKEKL KVEHSREYKQERTYTRDLLGPTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENIHELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLLTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIHQWY GIQQDVKNRRNPRLVPYPLDDRTKSKNKDS LREAVRLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWFYFETVTA GDMRVGWSRPGCQPDQELGSDERAFADGF KAQRWHQNEHYGRSWQAGDVVGCMDVM NEHTMMFTLNGEILLDDSGSELAFKDFDVG GFIPVCSLQVAVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFSGQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLP DRVDKDKKATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFFGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVLGDEKGKVHE SIKRSNCYMCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLF AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHPEEN RSVDIELTEQEELLKFHYHTLRYSACALG NHRVAHALCSHVDEPQLLYAIENKYMPLLR AGYYDLLIDHLSYATARLMNNNEYTPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISSNECYQSPFEFLDILKSKITQMLTB AVKEGSLHARDPVGGTTEFLFVPLIKLFYTLII

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						MGIFHNEDLKHLQLIEPSVFKEAATPEEESDT LEKELSVDDAKLQAGEEAAKGGKRPKEGLL QMKLPEPVKLQMCLLQLYLCDCQVRHRIEAI VAFSDDFVAKLQDNQRFYNEVMQALNMSA ALTARKTKEFRSPPEQINMLNFKDDKSECP CPEEIRDQLDFHEDLMTHCGIELDEDGSLDG NSDLTIRGRLLSLVEKVITYLKKKQAEKPVES DSKKSSITLQQLISETMVRWAQESVIEDPELVR AMFVLLHRQYDGGGLVRALPKTYTINGVSV EDTINLLASLGQIRSLLSVRMGKEEEKLMIRG LGDIMNNKVFYQHPNLMRALGMHETVMEV MVNVLGGGESKEITFPKMVANCCRFLCYFCR ISRQNKAMFDHLSYLLENSVGLASPAMRG STPLDVAAASVMDNNELALALREPDLEKVV YLAGCGLQSCQMLVSKGYPDIGWNPVEGER YLDFLRFAVFCNGESVEENANVVVRLIRPE CFGPALRGEGGNGLAAMEEAIAEDPSRD GPSPNSGSSKLTDEEEEDDTHMGNAIMTFY SALIDLLGRCAPEMHLIHAGKGEAIRSILRS LIPLGDLVGVISIAFQMPTIAKDGNNVEPDMS AGFCPDHKAAMVFLDRVYGIEVDFFLLHLL EVGFLPDLRAAASLDTAALSATDMALALNRY LCTAVLPLLTRCAPLFAGTEHHSALDLSLHT VYRLSKGCSLTKAQRDSIEVCLLSICGQLRPS MMQHLRLRLVFDVPLLNEHAKMPLKLLTNH YERCWKYYCLPGGWGNFGAASEEELHLSRK LFWGIFDALSQKKEQELFKLALPCLSAVAG ALPPDYMESNYVSMMEKQSSMDSEGNFNPQ PVDTSNITPEKLEYFINKYAEHSHDKWSMDK LANGWYGEIYSDSSKVQPLMKPYKLLSEKE KEIYRWPIKESLKTMLARTMKTERIREGDSM ALYNRTRRISQTSQVSVDAAHGYSRAIDMS NVTLSRDLHAMAEMMAENYHNIWAKKKKM ELESKGGGNHPLLVPYDTLTAKAKADREKA QDILKFLQINGYAVSRGFKDLELDTPSIEKRFA YSFLQQLIRYVDEAHQYILEFDGGSRGKGEHF PYEQEIKFFAKVVLPLIDQYFKNHLRYLSAA SRPLCSGGHASNKEKEMVTSFLCKLGVLRH RISLFGNDATSIVNCLHILGQTLDAITVMKTG LESVKSALRAFLDNAEDLEKTMENLKQGF THTRNQPKGVTQIINYTTVALLPMLSSLFHI GQHQFGEDLILEDVQVSCYRILTSYALGTSK SIYVERQRSALGECLAFAFAPFALETHLD KHNTYSIYNTKSSRERAALSPTNVEDVCPNIP SLEKLMEEIVELAESGIRYQMPHYMEVILPM LCSYMSRWWEHGPENNPRAEMCCTALNSE HMNTLLGNLKIYNNLGIDEGAWMKRLAVF SQPIINKVPQLLKTFLPLMEKLKKKAATVV SEEDHLKAEARGDMSEAELLILDEFTTLARDL YAFYPLLRFDVYNRAKWLKEPNPEAEELFR MVAEVFTYWSKSHNFKREEQNFVVQNEINN MSFLITDTKSKMSKAAVSDQERKKMKRKG RYSMQTSLIVAALKRLLPIGLNICAPGDQELIA LAKNRFSLKDTEDVVRDIIRSNIHQKLED AIRWQMALYKDLPNRTDDTSDEKTVRVL DIANVLFHLEQKSKRVGRRHYCLVEHPQSK KAVWHKLLSKQRKRAVACFRMAPLYNLPR HRAVNLFLQGYEKSWEITEEHYFEDKLIEDLA KPGAEPPEDEGTRVDPLHQLILLFSRTALT EKCKLEEDFLYMAADIMAKSCHDEEDDDG

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						<p>EEEVKSFEKEMEKQKLLYQQAHLDRGAA EMVLQTSISKGETGPMVAATLKLGLAHLNGG NSTVQQKMLDYLKEKKDVGFFQSLAGLMQS CSVLDLNAFERQNKAEGLGMVTEEGSGEKV LQDDEFTCDLFRFLQLLCEGHNSDFQNYLRT QTGNNTTVNIISTVDYLLRVQESISDFYWYY SGKDVIDEQGQRNFSKAIQVAKQVFNTLTYI QGPTGNQQSLAHSRLWDAVVGFLHVFHMH QMKLSQDSSQIELLKEMLMDLQKDMVMVLLS MLEGNVVGNTIGKQMVMDLVESSNNVEMIL KFFDMFLKLKDLTSSDTFKEYDPDGKGVISK RDFHKAMESHKHYTQSETEFLLSCAETDENE TLDYEEFVKRFHEPAKDIGNVAVLLTNLSEH MPNDTRLQTFLELAESVLNYFQFPLGRIEMG SAKRIERYFEISESSRTQWEKPVKESKRQFI FDVVNEGGEKEKMEFLVNFCEDTIFEMQLAA QISESDLNERSANKEESEKERPEEQGPRMAFF SLTVRSALFALRYNLTLMRMLSLKSLKKQM KKVKKMTVKDMVTAFFSSYWISFMTLLHFV ASVFRGFFRIICSLLLGGSLVEGAKKIKVAELL ANMPDPTQDEVRGDGEGERKPLEALPSED LTDLKELTEESDLSDFGLDLKREGGQYKLIP HNPNAGLSDLMSNPVPMPEVQEKQEQKAK EEEEKEEETKSEFEKAEGEDGEKEEKAKED KGKQKLRLHTRHYGEPEVPESAFWKILAY QQKLLNYFARNFYNMRLALFVAFADNFILL FYKYSTSSVVEGKELPTRSSSENKVTSLDSS SHRIIAVHYVLEESSGYMEPTVRILPILHTVISF FCIIGYYCLKVPLVIFKREKEVARKLEFDGLYI TEQPSDDIKQWDRLVINTQSFNNYWDKF VKRKVMDKYGEFYGRDRISELLGMDKAALD FSDAREKKKPKKDDSSLSAVLNSIDVKYQMW KLG VVFTDNSFLYLA WYMT</p>
553	1903	A	4199	31	767	<p>LPELNGRGAGLRRAPSERGGGAERTQQVAA LPLSHGHSHGGGRCRAER/VGAARGSAAC AYGLYLRLDKGRLQCLNESREGSGRGVFKPW ERADWRSKFVESDADEELFNIPFTGHVKLK GIIMGEDDDSHPSEMRLYKNIPQMSFDDTER EPDQTFSLNRDLTGELEYATKISRFSNVYHLSI HISKNFADTTKVFIYIGLRGEWTELRRHEVTI CNYEASANPADHRVHQVTPQTHFIS</p>
554	1904	A	4200	1	961	<p>GIPCTEMGNFDNANVTGEIEFAHYCFKTHSL EICIKACKNLAYGEEKKKCNFYVKTYLLPD RSSQGRKRTGVQRNTVDPFQETLKYQVAPA QLVTRQLQVSVWHLGTLARRVFLGEVIPLAT WDFEDSTTQSFWRHPLRAKADKYEDSVPPQS NGELTVRAKLVLPSRTRKLQEAQEGTDQPSL HGQLCLVVLGAKNLPVRPDGTLNSFVKGCLT LPDQQLRLKSPVLRKQACQWKHSFVFSGV TPAQLRQSSLELTVWDQALFGMNDRLGGT RLGSKGDTAVGGDACSQSKLQWQKVLSSPN LWTDMTLVH</p>
555	1905	A	4211	331	2419	<p>KENKARNLRMNQSRSDGGSEETLPQDH NHHENERRWQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQRLDGVKE QLASQPDRLDGTNYRDSVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTVRAVSRNTP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANRQQRSTSPVARKRTRTSQTSYVFN GSSSNIPRTRLASRGQNPAGSFSTLGRLRNGI</p>

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						GGAAGIPRANASRTNFSSTHNQSGGSELRORE GQRFGAAHVWENGARSNVTVRNTNQRLEPI RLRSTNSRSRSPIQRQSGTVYHNSQRESRPV QQTTRRSVRRRGRTRVFLEQDRERERRGTAY TPFSNSRLVSRITVEEGEESSRSSTA VRRHPTIT LDLQVRIRPGENRDRDSIANRTRSRVGLAE NTVTIESNSGGFRRTISRLESGIRTYVSTITVP LRRISENELVEPSSVALRSILRQIMTGFGELSSL MEADSESELQRNGQHL PDMHSELSNLGTDN NRSQHREGSSQDRQAQGDSTEMHGENETTOP HTRNSDSRGGRLRNPNNL VETGTLPLRLAH FFLLNESDDDDRIRGLTKEQIDNLSTRHYEHN SIDSELGKICSVICSDYVTGNKLRQLPCMHEF HHICIDRWLSENCTCPICRQPVLGSIANNHG
556	1906	A	4212	3	462	LQRQRQHPAAAPAVPVRCTFCFTDIVMPKR KSPENTEGKDGSKVTKQEPTRRSARLSAKPA PPKPEPKPRKTS AKKEPGAKISRGAKGKKEEK QEAGKEGTAPSENGETKAEIHSRSTVNVST SRGTPPSTLSVKGGQIETVRVKGTEN
557	1907	A	4213	774	507	ARRFSCLTQTSWGHRRHGPPRPAANFVFLVET GFLHIGQAGHKLPTSGDPPASASQARITGMS HRTWFLASFLIDSCKNFVYKIMYTL
558	1908	A	4225	3	1253	TYRHAEREHPETSSATKVSVDYRHKRPKLLD GDQDFSDGRTQKYCKEEDRKYSFQKGPLNRE LDCFNTRGRGRETQDQGVKEPFKPSKKDSIAC TYSNKNDVLRSSNDKWKEKKKKEGDCRKE SNSSSNQLDKSQKLPDVKPSPINLRKKS LTVK VDVKKTVDTFRVASSYSTERQMSHDLVAVG RKSENFHFVFEHL DSTQNTENKPTGEFAQEIIT IHHQVKANYFPSPGITLHERFSKMAIDHKADV NEIPLNSDPEIHRIDMSLAELQSKQAVIYESE QTLIKIIDPNLDRHDIERRRERLQNEDEHIFHI ASAAERDDQNSSFSKNYTTQRKDIITHKPFV EGNHRNTRVRPFKSNFRGGRCQPNYKSGLVQ KSLYIQAQYQRLRFTGPRGFTHKFRERLMRK KKVP
559	1909	A	4235	1	323	KFSIPFFLRWSFTLVPRLEGNDMISVHCNLGL LGLSHSPASASQVGGITGTQHTGLIFGLIET EFHHVGOAGLELLTSGDPPALAFQSAGITGVS HHAWLQVLNS
560	1910	A	4246	2	1569	TLSSLERVLMDIVTPVPQEEVKTIVRKCLEQ AALVNYSRLSEYAKIEGKKREMYELPVFCLA SQVMDLTIONQKDAENVGRLITPAKKLEDTIR LAELVIEVLQNEEHHAFAFWWS DLMVEH AETFLSLFAVMDMAALEVQFPDWD SFLFQ LLWDFLRTGLLICGNGKVFHKLQDLFAPLVV R/YMWDLDGSSPLAQSIHRGLLSRESWEPVNN GSGTSEDLFWKLDALQT FIRDHLHWFEEFQK HLEQRLKLMASDMIESCVKRTUIAFEVKLQK TSSIQQIFRVPQFNMAPCFNMGLMAKGSIQ KLVCSEMEMGQEFKMWYHYSKIDELIETV KEMITLLVAKFVTILEGVLA KLSRYDEGTLFS SFLSFTVKAASKYVDVPKPGMDVADAYVTF VRHSQDVL RDKVNEEMYIERLFDQWYNSSM NVICTWLTD RMDLQLHIYQLKTLRMVKKTY RDFRLQGVLDSTLNSKTYETIRNRLTVEEATA SVSEGGGLQGISMKDSDEEDEEDD
561	1911	A	4257	1300	654	SELVQFLLIKDQKKPIKRADILKHVIGDYKDI FPDLFKRAAERLQYVFGYKLVLEPEKSNITYL

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						INTLEPVEEDAEMRGDQGTPTTGLLMIVLGLI FMKGNTIKETEAWDFLLALGVYPTKKHLIFG DPKKLITDFVRQRYLEYRRIPHTDPVDYEFQ WGPRTNLETSMKVLFVAKVHNQDPKDW PAQYCEALADEENRARPQSPGAPSS
562	1912	A	4260	1	1498	MVTWLYRFLPTSNMAAKLRSLPPDLRLQF WLHARLQKCFLSRGCSSYAGAKASPLPGK MAMGLMCGRRELLRLQSGRRVHVSAGPSQ WLGKPLTTRLFFAAPCCCRPHYLFLAASGPR SLTSAISFAEVQVQAPPVVAATPSPTAVPEV ASGETADVQTAEEQSFALGLGSYTPVGLI QNLLEFMHVDLGLPWGAIAACTVFARCLIF PLIVTGQREAAARIHNHLEIQKFSRREAKLA GDHIEYYKASSEMALYQKKHGIKLYKPLILPV TQAPIFISFFIALREMANLPVPSLQTGGLWWF ODLTVSDPIYLPLAVTATMWAVLELGAETG VQSSDLQWMRNVIRMMPLITLPTMHFPTAV FMYWLSSNLSLVQVSCLRIPAVRTVLKIPQR VVHDLDKLPPREGFLESFKKGWKNAMTRQ LREREQMRNQLELAARGPLRQTFTHNPLLQ PGKDNPPNIPSSSSSSSKPKSKYPWHDTLG
563	1913	A	4265	623	116	MGGLAPTQLEPTREYQNTQLSVSYLLPEQN THGTRRTLSSQPSNNLPLPLSSSATMPSMQCK HRSPNGGLFRQSPVK/TPPIMSFQPVPGGV PRGSGNPPHGTSLTAPPALLPHPTHTPTQSF LIQENNTNHTSHHTHTYTETLSFFLYICVNN DRMEWGKSVF
564	1914	A	4270	3	368	ILKRKLSSLNSEVSTIQNTRMLAFKATAQLFIL GCTWCLGLLQVGPAAQVMAYLFTIINSLQGF FIFLVYCLLSQVQKQYQKWFEIVKSKSES ETYTLSSKMGPDSKPSGDDVFPRTSE
565	1915	A	4288	83	406	RNSRPLWCSPPASQPRQAPVSQSCCPLPSSSS PPSALLAPTQPRALGTLRLYECSPELGTTMLP PAWLLMLCQAPRPQDPDRLTQPEKSLQEAP GQTGASRTPRT
566	1916	A	4298	1041	229	LNSSQKLACLIGVEGGHSLDSSLSVLRSFYVL GVRYLTLTFTCTPWAESSTKFRHHMYTNVS GLTSFGEKVVEELNRLGMMIDLSYASDTLIRR VLEVSQAPVIFSHSAARAVCDNLLNVDDILQ LLKKNGGIVMVTLSMGVLQCNLLANVSTVA DHFDHRAVIGSEFIGIGNYDGTGRFPQGLAE DVSTYPLIEELLRSWSBEELQGVLRGNLLR VFRQVEKVREESRAQSPVEAEFPYQLSTSCH FHLGASEWTPRLIWR
567	1917	A	4299	1	1106	GATPLGSVGGRTGKMDAATLTIDTLRFAEFB DFPFTSEPVWILGRKYISIFTEKDEFI.SDVASRL WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ MIFAQALVCRHLGRDWRWTQRKRQPDYSYFS VLNAFIDRKDSYYSIHQIAQMVGEGKSIGQ WYGPNTVAQVLKLAFTDWSLAVHIAAMD NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRSPWRPLVLLPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHY FIGYVGEELIYLDPHITTQPAVEPTDGCIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSAQAF GAECCLGMTRKTFGLRFFFSMLG
568	1918	A	4300	2012	1843	SRKFLTITPVLVYFLTSFYTKYDQIHVFLNTVS LMSVLIPKLPQLHGVIRIFGINKY
569	1919	A	4302	186	531	WTFCLFL/WWVPESARWLLTQGHVKEAHRY

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						LLHCARLNGRPVCEDSFSQEVVRVNVCSMHI CVWVGVCVKCLPPRAHHIWQEKPLGFHRT VTESKLEAEGKTEKAREKERKKKS
570	1920	A	4308	3	869	RSGQGVYGLIGRRRFQQMDVLEGLNLLTIS GKRNLKRVYVLSWLRNKLHNDPEVEKKQG WTTVGDMEGCGHYRVVKYERIKFLVIALKSS VEVYAWAPKPYHKFMAFKSFADLPHRPLL DLTVEEGQRLKVYGSAGFHAVDSDGNSY DIYIPVHIQSQITPHAIIFLNTDGMEMLLCYE DEGVYVNTYGRUKDVVLQWGEEMPTSVAYIC SNQIMGWGEKAIEIRSVETGHLDGVFMHKRA QRLKFLCERNDKVFFASVRSGSSQVYFMTL NRNCIMNW
571	1921	A	4309	9	524	ASREMDVTKVCGEMRYQLNKTNMEKDEAE KEHREFRAKTNRDLEIKDQIEKLRIELDESK QHLEQEQKAALAREECI.RITELLGESEHQL HLTRQEKDSIQQFSKEAKAQAQQAQQREQE LTQKIQQMEAQHDKTENEQYLLTTSQNTFLT KLKEECCTLAKKLEQISQ
572	1922	A	4318	1	1119	GATPLGSGVGRGTGKMDAATLTDTLRFAEFE DFPETSEPVWILGRKYSIFTEKDEILSDVASRL WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ MIFAQALVCRHLGRDWRWTQRKRQPDYSFS VLNAFIDRKDSYYSIHQIAQMGVGEKSGSQ WYGPNTVAQVLKKLAVFDTWSSLAHVHAMD NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRPSWRPLVLLIPLRLGLAT DINEAYVETLKHCFHGWQFPQ/VVHREGK PNSAHYFIGYVGEELIYLDPHTTQPAVEPTDG CFIPDESFCQHPPCRMSIAELDPSIAVVRGGH LSTQAFGAECCLGMTRKTFGFLRFFFSMLG
573	1923	A	4333	363	1066	GQVPVGLASKPFQILYGHITNEVLSVGISTELD MAVSGSRDGTVIHITIQKGQYMRILRPPCESS LFLTIPNLAIWEGHIVVYSSTEEKTTLKVERM HYICFSINGKYLGSQILKEQVSDICIGEHIVTG SIQGFLSIRDHLNLNINPLAMRLPIHCVCVT KEYSHILVGLDGLIVVGKPAEVKPSISN FISHAVGDYFGSPSQLEKSPGINKLAKAFD FSKGSK
574	1924	A	4346	359	1234	MDTLEEVWANGSTALPPPLAPNISVPHRCLL LLYEDIGTSRVRYWDLILLIPNVLFILFLWK LPSARAKIRITSSPITFYILVFVVALVGIARA VVSMTVSTSNAA TVADKILWEITRFFLLAJEL SVIILGLAFGHLESKSSIKRVLAITTVLSLAYSV TQGTLEILYPDAHLSAEDFNITGHGGRQFWL VSSCFFFLVYSLVILPKTPLKERISLPSRRSFY VYAGILALLNLLQGLGSVLLCFDIEGLCCVD ATTFLYFSFAPLIYVAFLRGFFQSEPKILF
575	1925	A	4360	2038	1512	GCWWRHPWLASQRDCLDCRIQLAEKFKAV SKSPRPMNPIRVKEVYRLEEMKIFVRLEM KIIGSSGTPKLSYTGRRDRHFVPMGLYTVRT VNEPWTMGFSKSKKKFFYNKTKDSTFDLP ADSIAPFHICYGRLFWEWGDGIRVHDSQKP QDQDKLSKEDVLSFIQMHRA
576	1926	A	4365	69	500	QVEGRQGREVKRTAWRISPVWRPARCRRRST PQP/PE/PGAQQERHRQGEAPMQALDPRAEP GPQAQSHAACQPEPEPRVLLDPTAARGGVQ GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCAS EPLPLGGIRPTPGLEPKGRDLM

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577	1927	A	4366	785	502	SAPPKKKNGVLFSPRLKSSGAIWVHSTPTLW ASSNSRASTPKVAGITGARPHARJIFVFLIEMG FHNVCQAGL/DTLTLVICFPQPPKLLGLQM
578	1928	A	4367	1	221	FFFLLKKSRCVTQAGVQGFISLHPPPGFKRF SRLSLLSSWDYRHP/HAANFCIFSRDGVSPYW SGWSRTPDLR
579	1929	A	4383	1	224	FETESHVVTQAGMQWHNLGSLQPMPPGLKR FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP CWPGWSSTPDLK
580	1930	A	4397	410	94	SRLKPYSTNVTAKKLPATNIPNLDCTAKLYQ VFKKGNHILHELFFQNKEEGAPPNS/FYEASFT LRPKSDRDIAKEESYSTISLLSTDTKILMSKYK QLKSSDL
581	1931	A	4414	670	3	VLVHRQCGGILRLRKEAVSVLDSADIEVTD RLPHATIVDHRPQHRWLETCPAPPQLIQGKA RSAPKPSQASGHFVELVRGYAGFGLTLGGG RDVAGDTPLAVRGLLDGPAQRCGRLEVGD LVLHINGESTQGLT\HAQAVERRAGGPQLHL VIRRPLETHPGKPRGVGEPRKGVVPSWPDSP DPGGPEVTGSRSSSTSLVQHPPSRTTLKKTRG SPE
582	1932	A	4424	194	449	VLVIRKKRLEKLRHQLMPMYNFDPTTEEQDE LEQELLEHRDAASVQAATSVMQAMQKTTL PSIQGFLQRPRLVFTDVANAIHV
583	1933	A	4435	1	166	APGPPVPFPGSPPEQMPCPASMPP/DPPPGS PPEQMPCPVSAPP/GPPPGSPPEQMPCPVS SAPPALLQDTSV
584	1934	A	4439	1	628	SATPQQPSAPQHGGTLNQPVPFGMDESMYSQ APPQQLPSAQPPQPSNPPHGAHTLNSGPQPGT APATQHSQAGPATGQAYGPHTYTEPAKPKK GQQLWNRMKPAPGTVEVSSSTSRSDPI.I.I.PPR ALAPTQRASTVVLAPSPT/SEKVNHSQSSAR GNLSGKPDWP/LGHERVCGALLHRL*VGGG QGPHGKAAQGGGAAGAAAGRLGLYH
585	1935	A	4463	10	144	HKPVTNSRDTQEVPLEKAKQVLKIIATFKHTT SIFDDFAHYEKRO
586	1936	A	4464	1309	103	LNAESYVSFTTKLDIPTAAKYEYGVPLQTSDS FLRFPSSLTSSLCTDNNPAFVLNQAVKCTRK INLEQCEEIEALSMFYSSPEILRVPSRKKVPI TVQSIQISLNKTLTRREDTDVLQFTLVNAGH FSLCVNVVLEVKYSITYTDAGEVTKADLSFV LGTVSSVVVPLQKQFEIHLQENTQPVPLSGN PGYVVGLPLAAGFQPHKSGSIQTNNRYGQLT ILHSTTEQDCLALEGVRTPLVFGYTMQSGCK LRLTGALPCQLVAQKVSKLLWGQGFDPDYVA PFGNSQGP/ADMLDWVPIHFTQSFNRKDSQ LPGALVIEVKWTKYGSLLNPQAKIVNVTANLI SSSFPEANSNERTILISTAVTFVDVSAPAEAG FRAPPATNARLPFNFFFPFV
587	1937	A	4471	614	387	LLGRASAC/LQLQSSW/D/HRPMLPYLANFVF CKDR/SFTWLPRLVLNSWLQVILLPWFPPTGCD NKHEPPCPATKRRHSGSI
588	1938	A	4480	1720	1458	HDLGSLQPPPGFKRFSCLSLPSSWDYRLMPP CPANFCIII/DFLVETGFHHVGQASHELLTSGD PPTSASQAGITGMSYHTWFGES
589	1939	A	4487	922	332	APVTTSPRVGPW/RTALALRSLYRARPSLRC PPVELPWAPRRGHRLSPADDELYQORTISLLQ REAAQAMYIDSYNSRGMINGNRLGPCALL PHSVVQWNVVGSHQDITEDSFSLFWLLEPRIEI

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						VVVGTDGDRTERLQSQVLQAMRQRGLAVEVQ DTPNACATFNFLCHEGRVTGAALIPPPGGTSL TSLGQAAQ
590	1940	A	4492	1	472	FFFETESRSVAQAGVQWRDLGSLQAPPPGFT PFCLSLPSSWDYRPPPLRPANFFVFLVETGFP RFSRDGLDLLT/S/GDPPTSASQSAGITGVSHR ARPKRIGEPKRKCGNAVVPSTSLGDHRTVS VPHQGGLPGPIRVAPSSAGQREASQGPGR
591	1941	A	4495	1444	1116	LAARFTLAKTWNQLKRPTMDSIKKTRVIYIT MEYYADTERNEIMSFAAGTWVELEAILSKLM LKDNNVEDTTPQGA VPCTATAEGMKRLLFAL EPWDSSCFPHSSGV
592	1942	A	4496	2	919	RTRPLFSGRPTRPVCTMSDERRLPASVAVWL VCGGLSLLANAWGILSVGAKQKKWKPLEFL LCTLAATHMLNVAVPIATYSVVQLRRQRPDF EWNEGLCKVFVSTIFYTLTLATCFSVTSLSYHR MWMVCWPVNYRLSNAKKQAGHTVMGIWM GSFILSALPAVGWHDTSERFYTGCRFTVAEI GLGFGVCFLLLVGGSVAMGVICTAJALFQTL AVQVGRQADHRAFTVPTTVVEDAQGKRSSI DGSEPAKTSLQTTGLVTITVFIYDCMLGFPVL GPFSLADTHLSLPTYTWGDRDSSGGACVM
593	1943	A	4506	2	193	FFFEAESCSVPQAGVQRPDLGWLHAPPPGSC HFPASASQVAGTTTHARHHTQLIFAFLVENGL C
594	1944	A	4507	1327	647	KMAGGVRPLRGLRALCRVLLFLSQFCILSGG ESTEIPPYVMKCPNSGLCSRLPADCIDCTTNFS CTYGKPVTFDCAVKPSVTCVDQDFKSQKNFI NMTCRFQWQLPETDYECTNSTSCMTVSCPRQ RYPANCTVRADHVHCLGNRTFPKMLYCNWT GGYKWVYGLWLLRHHPRWGLGADRFYLG VAGTASGKLSFGGLGIWTLIDVLLIGVGYVG PADGSLYI
595	1945	A	4512	533	264	FFFKMESYSVARLECSGAISAPCNHLHLSNN SPASASRV/AGNIGARHHTQQIFVLLVQMRVH YVGQDGLDLL/NLMIHPPRSPKVLGLQA
596	1946	A	4513	3	1674	HASDHLYPNFLVNELILKQKRFEEKRFLD HSVSTNGHRWQIFQDWLGTQDQNDLANV NLMLELLVQKKQLEAESHAQQLMEFLK VARRNKREQLEQIQKELSVLEEDIKRV EEMS GLYSPVSEDSTVPQFEAPSPSHSSIIDSTEYSQP PGFSGSSQTKKQPWYNSTLASRRKRLTAHFE DLEQCYFSTRMSRISDDSRASQLDEFQECALS KFATRYNSVRPLAATLSYASDLYNGSQYKSLV FEFDRDCDYFAIAGVTKKIKVYEYDTVIQDA VDIHYPENEMTCNSKISCISWSSYHKNLLASS DYEGETVILWDGFTGQRSKVYQEHEKRCWSV DFNLMDPKLLASGSDDAKVKLWSTNLDNSV ASIEAKANVCCVKFSPSSRYHLAFGCADHCV HYIDLNTKQPMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKPYCLRSFKGHIN EKNFVIGLASNGDYIACGSENNSLYL YYKGLS KTLLTFKFDTVKSVLDDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANSQGTIKVLELV
597	1947	A	4518	536	824	RSLALSPGLECSGMISAHCNHLHLSGSDPPTS ASQVAEITSVRHHTWLIFCNLGMGFHHVGE QAGLELLTSWDPAILPSQAGIIGMSPHAWPP
598	1948	A	4524	1	384	FDTEFVNIGGDFDAAAGVFRICRLPGA YFFSF TLGKLPKRTLSVKLMKNRDEVQAMIYDDGSS

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						RRREMQSQSVMLALRRGDAVWLLSHDHDG YGAYSNHGKYITFSGLVYPDLAPAAPPGLG ASELL
599	1949	A	4526	366	776	MGQPAPYAEGPIQGGDAGELCKCDFLVFTSP NPEAVCEAGTPAMFQTAWRQMESCSIAQAG VQWRDPGSLHPPLGFKRFSCLSLPSSWDYK HAPPHANFCIFSRDQVSPCWPGWSRSLDLVI PPPWLPKVLGLQA
600	1950	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPGSS DPPASASRVAGTTGARHHTQLIFVFLVETGFH \MLARDGLKLLTSSDPPASASQSSWDYRREPP RLANFFVFLVETGSRVVAQAGVQWLFPGAIP LLISTGVLTCVSVDLGRFTFP
601	1951	A	4533	1460	403	HEVQESIHFLESEFSRGISDNYTLALITYALSS VGSPKAKEALNMLTWRAEQEGGMQFVWSSE SKLSDSWQPRSLDIEVAAAYALLSHFLQFQTSE GIPIMRWLSRQRNSLGGFASTQDTTVALKALS EFAALMNTERTNIQVTVTGPSSPSPVKFLIDT HNRLLLQTAELADGTANGSV/SISANGFGFAI CQLNVVYNVKAAGSSRRRSIQNQEAFLDV AVKENKDDLNHVDLNVCTSFSGPGRSGMAL MEVNLLSGFMVPSEAISLSETVKKVEYDHGK LNLVLDSVNETQFCVNIPAVRNFKVSNTOQA SVSIVDYYPERRQAVRSYNSEVKLSSCDLCS D VQRLPSL
602	1952	A	4540	1963	295	MRAPGRPALRPLPLPLLLLLSSPWGRAVPC VSGGLFKPANITFLSINMKNVLQWTPPEGLQG VKVTYTVQYFIYGQKKWLNKSECRNINRTYC DLSAETSDYEHQYYAKVKAIWGTCKSKWAE SGRFYPFLETQIGPPEVALTTDEKSISVVLTA PEKWKRNPELPSVMQIYNLKYNVSVLNT KSNRTWSQCVTNHTLVLTWLEPNTLYCVHV ESFVPGPPRAQPSEKQCARTLKQDSSEFKAK IIFWYVLPISITVFLFSVMGYSIYRYIHVGKEK HPANLILITYGNEFDKRFVPAEKIVNFINFL NISDDSKISHQDMSLLGKSSDVSSLNDPQPSG NLRPPQEEEEVKHLGYASHLMEIFCDSEENT EGTSFTQESLSRTIPPDKTVIEYEDVRTDI CAGPBEQELSLQEEVSTQGTLESQAALAVL GPQTLQYSYTPQLQDLPLAQEHTDSEGPPEE EPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCE PSEGDLGEEGLSRLYEAPADRPGENETY LMQFMEEWGLYVQMEN
603	1953	A	4543	3	600	YSAVEFVEQASGISDWWNPALRKRLSDSGL GMIAPIYYEDSLKDLSHSRVLQSPVSSDHAI LQAVIAGDLMKLIESYKNGGSLLIQGPDHCSL LHYAAETGNGEIVKYLDHGPSELLDMADSE TGETALHKAACQRNRAVCQLLDAGASLRK\ TDSKGKTPQERAQQAIGDPDLAA/YTIESRQN YKVIHEDLETA
604	1954	A	4548	3	938	QDNKVQNGSLHQKDTVHDNDFEPYLTGQAN QSNYSYPSMSDPYLSYYPSPGFPYSLNEAPW STAGDPPIPYLTYGQLSNGDHHFMHDAVFG QPGGLGNNTYQHRFNFFPENPAFSAWGTSGS QGQQTQSSAYGSSYTPPSSLGGTVVDGQPG FHSDTLKAPGMNSLEQGMVGLKIGDVSSA VKTGVSIVSSVALTGVLSGNGGTNVNMPVS KPTSWAALASKPAKPQPKMKTKSGPVMGGG LPPPIKHNMIDIGTWDNKGVPKAPVPQQAP

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						SPQAAPQPPQVAQPLPAQPPALAQPPYQSPQ QPPQ
605	1955	A	4553	2	2304	ILLEKRNCLLMOLEEATRLTSYLQSQLKSLC ASTLTVSSGSSRGLASSRGLASSRGLSSVS FTDIYGLPQYKFPDAEGSQLRFDLPFDLGR DAPFSEPPGPGSGFHKQRSLDTPQSLASLSSRS SLSSLSPSSPLDTPFLPASRDSPLAQLADSCE GPGLGALDRLRAHASAMGDEDLPGMAALQP HGVPDGDGEGPHERGPPASAPVGGTVTLRED SAKRLERRARRISACLSDSLSDSGVFEPLT KRNEAEEPA YGDTASNGDPQIHVGLLRDSG SECLLVHVLQKNPAGLAVKEDCKVHIRVYL PPLDSGIPNTYCSKALEFQVPLVFNEVFRIPV HSSALTLKSLQLYVCSVTPQLQEELGLIAQIN LADYDSLSEMQLRWHSVQVFTSLNHQGRGR LGVQERAPPGLTHTPSPSPA/STDAVTLLAR TTAQLQAVERELAEERAKLEYTEEEVLEMER KEEQAEAISERSWQADSVDSGCSNCTQTSPPY PEPCCMGIDSILGHFFAAQAGPYSPEKFQPSPL KVDKETNTEDLFLLEAAASL VKERPSSRRARGSP FVRSGITVRSQTFSPGARSQYVCRLYRSDSDS STLPRKSPFVRNTERLRLRYKQSCRSSLAEL MARTSLDLELDLQASRTRQRQLNEELCALRE LRQRLDAQLRGQTDLPWVLRDERLRGLLR EAERQTRQTKLDYRHEQAAEKMLKKASKEI YQLRGQSHKEPIQVQTFREKIAFFTRPRINPPL PADDV
606	1956	A	4555	3429	776	PGSGPGPAPFLAPVAAPVGGISFHLQIGLSREP VLLQDSSGDYSLAHVREMACSIVDQKFPEC GFYGM YDKILLFRHDPSTENILQLVKAASDIQ EGDLEIVLSASATFDFQIRPHALFVHSYRA PAFCDHCGEMLWGLVVRQGLKCEGCGLNYH KRCAFKIPNNCSGVRRRRLSNVSLTGVSITRT SSAELSTAPDEPLQKSPSEFIGREKRSNSQ SYIGRPIHLDKILMSKVVPHTFVIHSYTRPTV CQYCKLLKGLFRQGLQCKDCRFNCHKRCA PKVPNNCLGEVTINGDLLSPGAESDVVMEEG SDDNDSENRNGLMDDMEEAMVQDAEMAMA EQQNDSEMGQDPDPDHEDANRTISPSTSNIP LMRVVQSVKHTKRKSSTVMKEGWMVHYTS KDTLRKRHYWRLDSKCITLFQNDTGSRYYKE IPLSEILSLEPVKTSALIPNGANPHCFEITTANV VYYVGENVVPSSPSPNNSVLTSGVGADVAR MWEIAIQHALMPVIPKGSSVGTGTLNHRDISV SISVSNQCQIENVDISTVYQIFPDEVLGSGQFGI VYGGKHKRKTGRDVAIKIIDKLRFPTKQESQLR NEVAILQNLHHPGVVNLECMFETPERVFVVM EKLHGDMLEMLSSSEKGRLEPHITKFLITQILV ALRHLHFKNIVHCDLKPENVLLASADFPFQV KLCDFGFARIIGKSFRRSVVGTAYLAPEVL RNKGYNRSLDMWSVGVIYVSLSGTFFPNED EDIHDQIQNAAFMYPPNPWKEISHEAIDLNN LLQVKMRKRYSDKTLSPWLQDYQTWLDL RELECKIGERYITHESDDLWKEYAGEQGLQ YPHTLNPASHSDDTPEETEEMKALGERVSIL SRPWWLRASERPSPSAMAKRSRGPGRRCLL ALVLFCAWGTAVVAQKPGAGCPSRCLCFRT TVRCMHLLLEAVPAPQTSILDLRFNRRIE QPGAFRRLRLNLTLLNNNQIKRIPSGAFEDL ENLKYL YLYKNEIQSIDRQAFKGLASLEQLYL
607	1957	A	4563	1	4499	

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						<p>HFNQIETLDPDSFQHLPKLERLFLHNNRITHL VPGTFNHLES MKRLRLDSNTLHCDCEILWLA DLLKTYAESGNAQAAAJCEYPRIQGRSVATI TPEELNCERPRITSEPDADVTSGNTVYFTCR AEGNPKPEIWLNNNELSMKTD SRLNLLDD GTLMIQNTQETDQGIYQCMANKVAGEVKTQ EVTLYFGSPARPTFVIQPNTEVLVGESVTL ECSATGHPPPRISWTRGDRTPLPVDPVNIPTS GGLYIQNVVQGDSEYACSA TNNIDSVHATA FIIVQALPQFTVTPQDRVIEGQTVDFQCEAK GNPPPVIATWKGGSQLSVDRRLVLSSGTLRI SGVALHDQGGYECQAVNIIGSQKVVAHLTVQ PRVTPVFASIPSDTTVEVGANVQLPCSSQGEP EPAITWNKDGQVQVTESGKFHISPEGFLTINDV GPADAGRYECVARNTIGSASVSMVLSVNVVPD VSRNGDPFVATSIVEAIA TVDRAINSTRTHLF DSRPRSPNDLLALFRYPDPYTVEQARAGEIF ERTLQLIQEHVQHGLMVDLNGTSYHYNDLVS PQYLNLIANLSGCTAHR RVNNCSDMCFHQKY RTHDGTCCNNLQHPMWGASLTAFERLLKSVY ENGFNTPRGINPHRLYNGHALPMPRLVSTTLI GTETVTPDEQFTHMLMQWGF LDHDLSTV VALSQARFSDGQHCSNVCSNDPPCF SVMIPP DSRARS GARC MFVRSSPVC GSGMTSLLMNS VYPREQINQLTSYIDASNVYGSTEHEARSIRD LASHRGLLRQGIVQRSOKPLLPFATGPPTCEM RDENESPIPCFLAGDHRANEQLGLTSMHTLW FREHNRIATELLKLNPHWDGDTIYYETRKIVG AEIQHITYQHWLPKILGEVGMRTLGEYHGYD PGNAGIFNAFATAAFRFGHTLVNPLLLPGLD ENFQPIAQDHLPLHKAFSPFRIVNEGGIDPLL RGLFGVAGKMRVPSQLLNTELTERLFSMAHT VALDLAANIQRGRDHGIPPYHYR VVYCNLS AAHTFEDLKNEIKNPEIREKLRLYGSTLND LFPALVVEDLVPGSRLGPTLMCLLSTQFKRLR DGDRLWYENPGVFSQAQLTQIKQTSLARILCD NADNITRVQSDVFRVAEPHGYGSCDEIPRVD LRVWQDCCEDCRTRGQFNAFSYHFRGRSLE FSYQEDKPTKTRPRKIPSVGRQGEHLNSTS AFSTRSDASGTNDFQRVCSWEMQKTIIDLR TQKKLESRLSTTECV DAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPVNI PGACCPVCLQKRAEKP</p>
608	1958	A	4566	354	1135	<p>FSFLC/GVSGRLGLDSEEDYYTPQKVDVPKAL IIVAVQCGCDGTFLTTSQSGKVLACGLNEFNKL GLNQCMMSGIINHEAYHEVPYTTSTFLAKQLSF YKIRTIAPGKTHTAAIDERGRLLTFGCNKCGQ LGVGNYYKKRLGINLLGGPLGGKQVIRVSCGD EFTIAATDDNHIFAWGNGGNGRLAMTPTERP HGSDICTSWPRPIFGSLHHVDPDLSCRGWHTILI VEKVLNSKTIRSNSGLSIGTVFQSSSPGGGGE GGPDW</p>
609	1959	A	4567	1	412	<p>FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT PFSCLSLPSSWDYRPPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSH RARPRINLRNVYSFAVTYCLNYISLAMSSTL KLSFHVLSGS</p>
610	1960	A	4570	697	467	<p>ECRGVISAHCCTLCPLSSDSASAFRVARTT GTCDY AQLIF AFLVEMGFHHVGDGLHLL/N LVIRPPRPFKVLGLQA</p>

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611	1961	A	4571	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT WNPVNPESPRIPAPRLPKRMSGAPTAGAALM LCAATAVLLSAQGGPVQSKSPRFASWDEM VLAHGLLQLGQGCANTGAHPQSAERAGAR LSACGSACQGTGSTDPLAPESRVDPEVLHS LQTQLKAQNSRIQQLFHKVAQQQRHLEKQHL RIQHLQSQFGLLDHKLHDHEVAKPARRKRLP EMAQVPDPAHNVSRLHRLPRDCQELFQVGER QSGLEFIQPGSGPFLVNCKMTSDGGWTVIQR RHDGSVDFNRPWEAYKAGFGDPHGEFWLGL EKVHSITGDRNSRLAVQLRDWDGNAELLQFS VHLGGEDTAYSLQLTAPVAGQLGATTVPVPSG LSVPFSTWDQDHLRRDKNCAKSLSGGWWF GTCSHSNLNGQYFRSIPQQRQKLKKGIFWKT WRGRYYPLQATTMLIQPMAAEAAAS
612	1962	A	4575	162	3	PPFETESRSVAQAGVQWRDLSSLQPPPGASR GSPASASPVAGITGTRHHRTRG
613	1963	A	4584	687	321	PLAQRPRFLWVTVKTNHGWSSSTYPHFWS SNS/PASASQVAGIPNARHQARIIFVFLVEPRF HHVGRAGLGFL/NLAICLPQHPKVVLGLQACN LNKPHPAHKYISMIQFNVHFMCMCSVHIYI
614	1964	A	4589	727	299	PGSAQSAQRGRRRRARAGSATQITMYSFMG GGFLCAWVGITLLVAMATDHWMQYRLSGS FAHQGLWRYCLGNKCYLQTDLSIAYWNAIRA FMILSALCAISGIMGIMAF/GWVAVLMTFFA GIFYMCAVYRVECRRLSTPR
615	1965	A	4590	2	414	TILPEKIQAWAQKQCPQSGEEAVALVHLEK ETGRLRQQVSSPVHREKHSPLGAAWEVADFQ PEQVETQPRAVSREEPGSLHSGHQEQLNRKR ERRPLPKNARPSWPVPALADEWNTLHQEVTT TRLPAQSQEPVKD
616	1966	A	4592	773	488	DFALVAQAGVQWHNLGSPQPLPPGFKRFSC SLPSSWEYRCVPP/RLANFVFLVEMGFLHVQ AGLELPTSGDPPALASQSAGITGVTTVPSPG
617	1967	B	4595	84	478	XRHGLREPLLERRCAAASSFOHSSSLGRELPY DPVDTEGFEGGDMQERFLFPEYILDPEPQPT REKQLQELQQQQEEEEERQQRREERRQQL RARSREHPVVGHDPALPPSGVNCSCGGAEL HCQDAR*
618	1968	A	4596	2945	1188	ARSRNSARGVYGMCDTFLCFLEDLERNDG SAERPVMCSITLKKPLARRCFPAIHAYKGV MVGNETTYEDGHGSRKNITDLVEGAKKANG VLEARQLAMRIFEDYTVSWYWIIGLVIAMA MSLLSIILLHLLAGIMGWVMIIMEISELGYRIF HCYMEYSRLRGEAGSDVSLVDLGFQTFDFRV YLHLRQTWLAFMILSILEVILLIFLRKRILI AIALIKEASRAVGYVMCSLLYPLVTFFLLCLCI AYWASTAVFLSTSNEAVYKIFDDSPCFPTAKT CNPETFPSSNESRQCPNARCQFAFYGGESGYH RALLGLQIFNAFMFFWLANFVLALGQVTLA AFASYWALRKPDLLPAFFLFAFGALRYH TGSLAFGALILAIQIRVILEYLDQRLKAAEN KFAKCLMTCLKCCFWCLEKFIKFLNRNAYIM IAIYGTNFTSARNAFLLMRNIIRVAVLDKV TDFLLGKLLIVGSGVILAFFFTTHIRIVQDT APPLNYYWVPIITVTVGSYLAHGFSSVYGMC VDITFLCFLEDLERNDGSAERPVMCSITLKKL LNKTNKKAES
619	1969	A	4601	2	357	RTSVEPYLQEF/RKLSNNTKVVKTEYKATEY

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						GLAYGHFSYEFNSHRD VVVLDLQGWVTGNGK GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFN NQHVECEICHRSLSTRPSMEKPCKS
620	1970	A	4606	1	2415	MERLWGLFQRAQQLSPRSSQTVYQVRVEGPR KGHLEEEEDGEEGAETLAHFCMELRGPEP LGSRPQPNLIPWAAAGRAAPYL VLTALLIF TGAFLGQYVAFRGSCQACGDSVLVVSSEDVN YEPDLDFHQGRLYWSDLQAMFLQFLGEGRL EDTIRQTSLRERVAGSAGMAALTQDIRAALS RQKLDHVWTDTHYVGLQFPDPAHPNTLHWV DEAGKVGELPLEDPDVYCPYSAIGNVTGEL VYAHYGRPELQDLRARGVDPVGRLLLV RV GVISFAQKVINAQDFGAQGVLIYEPADFSQ DPPKPSLSSQAVYGHVHLGTGDPYTPGFPSF NQTQFPVASSGLPSIPAQPSADIASRLRLKL KGPVAPQEWQGSLLGSPYHLGPGPRRLRVVN NHRITPNNIFGCIERGSEPDHYVVGARDA WGPGAASAVGTAILLELVRTFSSMVSNRFR PRRSLLFISWDGGDFGSGVSTEWLEGYLSVL HLKAVVYVSLDNAVLGDDKFHAKTSPLTSL IESVLKQVDSPNHSQQLTYEQVFTNPSWD AEVIRPLPMDSSAYSFTAFVGVPAVEFSFME DDQAYPFLHTKEDTYENLHKVLQGRLPVA QAVAGLAGQLLRLSHDRLLPLDFGRYGDVV LRHIGNLNEFSGDLKARGTLQWVYSARGDY IRAAEKLREQIYSSEERDERLTRMYNVRIMRV EFYFLSQYVSPADSPFRHIFMGRGDHITGALL DHLRLRSNSSGTPGATSGTFQESRFRRL ALLTWDAACKGAANALSGDVWNIDNNF
621	1971	A	4610	793	334	ISRVDVFGSGIANVIAVAIFSIAPAFARLVRA NTLVLKQQTIFIESARSIGASDMTVLLRHILPGT GSSIVVFTTMRIGTSIISAASLSFLGLAQFPTP EWGAMLEARADMVIAFHVAVFPALAIFLT LAFNLLGDGLRDALDPKIKG
622	1972	A	4614	2	820	LVYVMIAIFCIASAMSLYNCLAALIHKIPYQG CTIACRGKNMEVRLIFLSGLCIAVAVVWAVF RNEDRWAWILQDILGIAFCLNLKTLKLPNFK SCVILLGLLLYDVFFVFTPFITKNGESIMVEL AAGPFGNNEKNDGNLVEATQQSPAPHEKLPV VIRVPKLIYFSVMSVCLMPVSILGFGDITVPGL LIAYCRRFDVQTGSSYTYVSVATVAYAGMIL TFVVLGALMKKGQFALLYLVPCTLITACQFV AWETVREMCKFWERVTS
623	1973	A	4619	17	691	TLVSVVEFVRRADLTREDLAPSSVDSGQAGF GCCESQLPNTMPSAFVSFFPVSIPTQT DWTEPWI.MGLATFHALCVLLTCLSSRSYRLQ IGHFLCLVILVYCAEYINEAAAMNWLPSKY QYFDSRGMFISIVFSAPLLVNAMITVVMWVW KTLNVMTDLKNAQERRKEKRRRKED*GAA AAWSLRPSRPPSAAPSAAVCAWASFQLTHG LKNRCFI
624	1974	A	4622	164	668	VSCYTALQSIMNQPEASANDPEPLCAVCGQAH SLEENHFYSYPEEVDDDLICHICLQALLDPLD TPCGHTYCTLCLTNFLVEKDFCPMDRKPLVL QHCKKSSILVNKLLNKLLVTCPPREHCTQVL QRCDLEHHFQTSQAWGTHL*SQLGRLRQED CLSPGVHHCSEV
625	1975	A	4625	474	473	CFLSPSPFLPPLLLSSSSSPFPLPPPTLLPSTLP PPLLIPSS*LSP

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626	1976	A	4629	249	3	KLKGNCEFCYHCNVCIFLMKK*GLFLC*IYFI LFFET*SHSFTRLCSGTISAHCSLQLQGSSNSP ASASQVAGIAGTHH
627	1977	A	4635	1	301	FFFFETKPPFAPQAGGQGPSRGSINPLPTGLK QFSGTLRSRSGNNGPRPPRVNFGILRGNVGP PGGAG*PRPPDLRGPPGLAPPQGGNNGDPP ARAYL
628	1978	A	4648	1357	782	KLFSQRLFGPHIQAINPSFLLSFFPS*LLAMR TVGNNAFILVFLVYRIVLLF*HV*PAYFQPSK NKTAKINCN*RPFLFLVCYLL*AELHIGIFIANF YDCIPNKLNEHLWPKLLQSLIFHVDGFLHK VFYICFTEFLFLVFL*LFIIKVSCH*CSITCVF SYKSAFVIFVVDNTRFFSFGF
629	1979	A	4660	18	999	HHELHTLELLQNPKEVLTRSEIQDVNYSLEAV KVKTVCQPLMKEMLRKFQVAVNLAEDTAH PKLVFSQEGRYVKNTASASSWPVFSSAWNYF AGWRNPQKTAVERFQHLSCVLGKNVFTSG KHYWEVESRDSLEAVGVCREDMGIDRS KMSPDVGIWAIYWSAAGYWPLIGFPGTPTQQ EPALHRVGVYLDRTGNVSFYSADVGVHLH TFSCSSVSRLRPFVWLSPLASLVIPPVTDK*G FSSPDQNSFPVQLRDTHPWALFCPSCLYFG WSIFWVSLTVFPGICPLCASQEAVPWEVGLA NGDGTGNFPRRFEIFL
630	1980	A	4669	2	358	FFFFFETESHVAQAGMQWRNLGSLPAPPPGF TPFFCLSLNMGWDYRPPPHLANFFVLLVETG FHDVQGDLDLTS*STPSASQSAEITGVSHC TRLKKIRFAKGHVEFFESHVE
631	1981	A	4674	953	614	TPIRGTDDEHEECTVQEYSAGKNTCLRPGAV AHTCNPCTLGGGRWIT*GSGVQDQPGPTWQ NPVFLERRPRALHSSPGLTTQRILWAQGLWV GAGSTGCSRGPREGVFRG
632	1982	A	4678	34	314	RSTHASMISPSFGFMGHLLRLEFEILPSTPNP *LPSYQGEAAGSSLISHLQTFSPDLKGVYCTFP ASGLAPVTHWTVSELSRSPVATATFC
633	1983	A	4696	1	1365	RTLGMGERRASQAPSSGLPAGGANGESPGG GAPFPSSGSSALLQAEVLDLDEDEDDLEVFS KDALMDMNSFSMPMPTSPLSMINQKFEDEP DLKDLFITVDEPESHVTIETFITRIITKTSRG EFDSSFEFVRRRYQDFLWLKGLKEEAHPTLII PPLPEKFIVKGMVERFNDDFIETRRKALHKFL NRIADHPTLTFNEDFKIFLTAQAWELSSHKKQ GPGLLSRMGQTVRAVASSMRGVKNRPEEFM EMNNFIELFSQKINLIDKISQRIYKEEREYFDE MKEYGPIHILWSASEEDLVDTLKDVASCIDRC CKATEKRMSGLSEALLPVVHEYVLYSEMLM GVMKRRDQIQAELEDSKVEVLYTKKADTDLL PEEIGKLEDKVECANNAKADWERWKQNM QNDIKLAFTDMAEENIHYEQCLATWESFLT SQTNLHLEEASEDKP
634	1984	A	4708	421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDQ WISKA VYKHREMCGLTSTGRKSHGLEKDRM FPHAIGGSCRAA*RRRKTLOFPCYH
635	1985	A	4709	42	341	YIKQPDAKERRRTVHWKETESEASEITIPPST PGVPQAPGHWEDYGRGDNFYLP*DPGGIVL WNIFNRMPIARKNITDGEHHEYLVPRLFHT SED
636	1986	A	4721	2	351	EKPDHFFPEGTSFIHEPRRN*GDLVHCLGGIS RSTTVTV*LMQKLNLSMNDAYYIVIMKMS

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						ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK MYFTIPSNHNAYQVDSVQST
637	1987	A	4726	664	253	NTGLTCSIQRKCGETQLYRREENRLILLQDH LKSESFQVLTLSRPLEFSGSLISAHCNLRPGSS DSSASSRAAGITGVHHHAWLIFFFLVETGFL HAG*AGLELLTSGDPPASASRSAGITGVSHHA RPRETRFL
638	1988	A	4734	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG TLERGHWNKMEFVLSVAGEIIGLGNVWRFP YLCYKNGGGGAFFIPYLVLFTCGIPVFLLETAL GQYTSQGGVTAWRKICPIFEGIGYASQMIVIL LNVYYIIVLAWALFYLFSSFTIDLPWGGCYHE WNTHEHCMEFQKTNGSLNGTSENATSPVIEFW
639	1989	A	4743	1040	699	QGLTLLPRMECSATITAHCSLELPGSIDLPTSA S*VARTTGTHHPWLILVLL*TWGSSYYVAQ AGLELLGSSNLPAAMVSQSAQIHGDHCAWA TSNHVLYTQELRRRKEG
640	1990	A	4771	527	2	GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN WIRRRPCLPSGCLKMNRIGPLQHSLLCCPGWS QTPGLKAILLRQPK*LGLQMESHSCPPAWSA MARSRLTATSASQVQAILLPQPGTTDSCSPS PDHEQQPLSWVLPPQKDMNPREQQVALGP QAAALPWA VWRNDCFPR
641	1991	A	4780	16	473	RPSSQCGGIFTGWKKGLAPELSELSSPPLPAR LQLAASPYFSPSWAECPPVPAGTHATWCLA RVWARMTPPGPAGIPSHPLPPPPERSVPISP FPARDSGSRQGHSTDRYKHTDAPRDAHRRVP QRDTDTGVHTGSGTHTHAHTPPEK
642	1992	A	4798	1	487	GYSFRCDIVDYSRPTALRMARTCWLYYFSK FIELLDITFFVLRRKNSQVTFHLVHFHTIMPW TWWFGVKFAAGGLGTFHALLNTAVHVVMY SYYGLSALGPAYQKYLWWKKYLTSLQLVQF VTVAIHISQFFFMEDCKYQFPVFACIMSYFSM FLLFLH
643	1993	A	4799	2	391	LMAFIEMHISGSLVYLKIKTKIYSYFSMLNLL QEIPLEILRISSPRDFTNISQGSNPHCFEITDT MVYFVGENNGDSSHPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQKGDHKS Q*ASVCTSPGQKGDHKSQ
644	1994	A	4800	488	101	AYPLFAVHPVHTECVAGVVGRAYLLCALFFL LSFLGYCKAFRESNKEGAHSSTFWVLLSIFLG AVAMLCKEQGITVLVRAATWLGPAFSVCPFP SYKDIWGWPCLCGVLHAYIPLLV
645	1995	A	4805	458	126	LLWTTVLCQTPARPQSTMHILGHILFLLLPV AAAQTTPGERSLPAFYPGTSGSCSGCGLSL PLLAGLVAADAVASLLIVGAVFLCARPRRSP AQEDGKYVINMPGRG
646	1996	A	4817	47	1033	LQGDWHL SFLSHFSRLHGGVPGRGLLEGNL LQQAQPHDMTSPFPGDRLLQVDGVILCGLT HKQAVQCLKGPGQVARLVLERRVPRSTQQC PSANDSMGDERTAVSLVTALPGRPSSCSVT DGPKF*SSN*KRIANGLGFSFVQMEKESCSHL KSDLVRIKRLFPQHFAEENGALAAGDILGRE WEGPRKASSSRCRGSWAMQLSVQAGPSFAS YYPAAVEVLHLLRGAPQEVTL LCRPPPGAL PELEQEWQTPELSADKEFTRATCTDSCTSPIL GSRGQLGGTVPPQMKGAWGLRPESQKAIR EGTMGAKTERDLGPVP
647	1997	A	4854	1044	335	PRVRGDWPLEKKKSNSNIHPIFSWCGSTD SKD

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						IVMPTYDLTDSVLETMGRVSLDMMSVQANT GPPWESKNSTAVWRGRDSRKRERLELVKLSRK HPELIDAAFTNFFFKHDENLYGPVVKHISFFD FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK QDSIYYEHFYNELQPWKHYIPVKSNDLLEK LKWAKDHDEEAKKJAKAGQEFARNNLMGD DIFCYFQTFRNMPYK
648	1998	A	4867	2030	837	AGMLPAVGSADEEDPAEEDCPPELVPMETTQ SEEEESGLGAKIPVTITGYLGAGKTLLNYI LTEQHSKRVAVILNEFGECSALEKSLAVSQG GELYEEWLELRNGCLCCSVKDNGLRAIENLM QKKGKFYDILLETGLADPGAVASMFVWDA ELGSDIYLDGIITVDISKYGLKHLAEKPDGLI NEATRQVALADAILINKTDLVPEEDVKKLRT TIRSNGLGQILETQSRVDSLNVLDLHAFDSL SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG NAKEEHLNMFQINLLWEKNVRNKNHNCMEV IRLGLVSKDKSQVIVQGVHLYDLEETPV SWKDDTERTNRLVLLGRNLDKDLKQLFIAT VTETEKQWTHFKEDQVCT
649	1999	A	4873	226	189	DGVSLPLPKLGVQWAQYWAHWQPLPGFKR FSCSLRSSWD*KCAPHPAFVFLVEMGFHRV GQAGLELRTSGDPPASASQSAGITGVSHLA*P TSMPLLPFQRLCVYI
650	2000	A	4874	2	437	FFFLRRSFAFVAQAGVQWCDLGSPPQLPPGF K*FSCSLSPSSWDYRHAPPCPS*FLYF**RQG FTMLARLVLS*PHDLTPSPQSASEIKGVSHR CPASFYFLKYYLEAKFCA*GECAPSAGVGA GYKRGHKSCLLINCVVQI
651	2001	A	4898	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATR PHMEPKASCPAAAPLMERKFHVLVGVTGSV AALKPLLVSKLLDIPGLEVAVVTTERAKHIFY SPQDIPVTLYSDADEWEMWKSRSDPVLHIDL RRWADLLLVAPLDANTLGKVASGICDNLTC VMRAWDRSKPLFCPAMNTAMWEHPITAQQ VDQLKAFGYVEIPCAKKLVCGDEGLGAMA EVGTIVDKVKEVLFQHSFGQS*PGISVMGV LYSEWVQAKSVKMDVGKIGGYPHLLNGGPA LSLPRGQACSRNLNWTGPGLSFFQPGAAAA
652	2002	A	4927	1	611	FRGRQTSRPARGFSPWRPFGTMQEPSSGECPA SP*LPCASNRLAFGGLIFPCAPLVYPAPFSPLL PAFSCAPRPAHHSRTHPSAPLVKPSRRAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWP LLGSAGSGLRGEA
653	2003	A	4965	2	283	FFFFI*DGVSFLCHPGWNAVARSWLTATSAR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHAILVLNS*QVICPPWPVKVLTLOA
654	2004	A	4968	3	437	RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGD IPAVGLGALGVIPVRVQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP PPCLTHLAAASCVVWCGRWKRDSEACQCD HSCSAVSQEDRCRSCSSCS
655	2005	A	4983	201	397	MNNNTTCIQPSMISSMALPIIYILLCIVGVFGN TLSQWIFLTKIGKKTSTHIYLSHLVTANLLVC
656	2006	A	4988	332	159	LVHKDMYREFEFAEQASNKHVTRCLTSLVI REVHIKTMR*HFLPIRLEKNKNKID
657	2007	B	5008	129	465	MAGMKTASGDYIDSSWELRVFVGEDPEAES

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						VTLRVTGESHIGGVLLKIVEQINRKQDWS DH AIWWEQKRQWLLQTHWTLDDKYGLADARLF FGPQHRPVILRLPNRRALRLX*
658	2008	A	5017	1	292	FFFFKETESHVTVQAGVQWHDLSLQPPPGF KRFSCLSLSSWDYRCAPHPANFVLVETGF HHVAQAGLKLLTL*SANLGLSTSLPIPLFILLS
659	2009	A	5018	17	338	RGHGKSLTGGTPGNWGDGLLVSEDSWHLIF T*NSLVSPVLGKWSFCLQGPGLSAVHTWFWL MAACWAVHVKTHMRPGLAVLPRLVLNSWS *AILLWPPKALGLQA
660	2010	A	5028	2	310	SRVDDFVGERRGGCDECLGHRGLRAVPLG HPGHLCLQPPGGPA*FLDYCRGCCPHVPVPGST AGSCPQKKTTPGPTVLCVCSFWIYQROEPH HRTGARWNH
661	2011	A	5050	752	431	RQSCSSTQAKVQWFHYGPLQSQPPGLKQSSQ LSLPNSRDHRHVPRLAIFSAETGSPYFAQAS LELLGSSHPPTSASQSARITGVSHRAWPLK*F NLNQYQTLTMN
662	2012	A	5054	48	103	ELNNGPFQMPLCNGGNLAVTGSWADRSPFH EAASQGRLLALRTLLSQGYNVNAVTLDHVTP LHEACLDHVAACARTLEAGANVNAITDGV TPLFNACSGSPSCAELLLEYGAQAQLESCLP SPTHEGASKGHHECLDILISWGIDVDQEIPIHSG TPLYVACMAQQFHCINWLIYAGAGVRKGGKY WDITPLPGAGHQSTQKLE*LFAMVEIWQ
663	2013	A	5066	951	580	VRNS*SFACASVYKHHYMDGQTPCLFVSSK ADLPEGVAVSGSPSAEFCRKHRLPAPVPFSCA GPAEPSTTIFTQLATMAAFPHLVHAELHPSSF WLRGLLGVVGA AVAAVLSFSLYRVLVKSQ
664	2014	A	5071	550	1	LSFIEVLSMEQVNTVVRVFFVVLGFSSRLRLQ QLLFVIFIJ.YLFTLTGTNAIITVLDRLHPT MYFFLAISCSEICYTFVIVPKMLVDLLSQKK TISFLGCAIQMFSFLFFGSSHSFLAAMGYDR YMAICNPLRYSVLMGHGVCMLMAAAWAC GFTVSLVTTSLVFHLPFHSSNQHE
665	2015	A	5074	496	692	QQYHNTGSAGHHAHCQVGHSPHVHYPSGCG PL*IQRGLPSFNSLEGHSLKDSGHEESVQLDSE HDVQRLSYCDTAVNDVLNTSVTSMGSGMPD HDQNEGFHCREECRLGHSRCWMPRNPMP RSKSPEHVRNIALSIEATAADVEAYDDCGPT KRTFATFGKDVSDHPAERPTLK GKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL PTKPSVSYEIVDPGITARRC
666	2016	A	5080	408	248	IMLLSTSS*VYFQSSTKDSHFFLDFDQKTGPPL VGPKAQLSGLQLQPCLYKRR
667	2017	A	5081	129	247	DLTNSHFFLDFDQKTGPPLGGPKAQFSSLQLQ PCVY*RR
668	2018	A	5086	852	233	NKSNDRWVQIKTAYKYFF*KNGDNYNWVF RALPTTFADIENTLYLLFRDASQFFYLGHV IFGDLEYVTVEGGIVLSRELMLKRLNRLLDNSE TCADQSVIWKLSSEDKQLAICLYAGVHAENA EDYEGRDVFNTKPIAQLIEEALSNPQQVVEG CCSDMAITFNGLTPOKMEVMMYGLYRLRAF GHYFNDTLVFLPPVGSND
669	2019	A	5101	1	329	PGRPTRPPLLTLAHVSPAPGSPCDSLAQPG ASGV*VQHDSHPPLLCSQCLSEPVPESHGPP RGCOHEAAPCPRGPGSDGLHHASACASLPP SPILPVLLPELGPL
670	2020	A	5102	3	547	DAWGNRCAVGAAPRLIHLHLCCTPADPSRKP

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						DEL*NMNGRVDYLVTEEEINLTRGPSGLGFNI VGGTDQQYVNSDSGYVVSRIKENGAAALDGR LQEGDKILSVNGQDLKNLLHQDAVDLFRNA GYAVSLRVQHLQVQNGPIGHRGEGDPGSGIPI FMVLVPVFALTMVAAWAFMR YRQQL
671	2021	A	5105	672	400	RDGREELCLQOEPTLPSRICSSAPLLYFLFICPF VLLLLLLISLLCLYWKARKLSTLRNTRKEKA LWVDLKEAGGVTTNRMED*EEDECN
672	2022	A	5148	72	314	IYFSYNIFLKITELLNDVERLKQALNGLSOLT YTSGNPTRKRSQSLDTLQHQVKSLEQQLAVS NQAHGALQEYVLAPCS
673	2023	A	5152	210	335	REILCSRIGRLNTV*MSLFPNLTCLRNAIPKIPA NHFEVET
674	2024	A	5153	3	2953	LTEDQPFIDILQKSLQEANITEQTLAEAYLDA SIGSSQQFAQQLHPSSSASFTQASNVSNYSG QTLQPIGVTHVPVGASFASNTVGVQHGFMQH VGISVPSQHLNSSQISGSGQIQIGSFGNHP MMITNNLDGSQLKKGSGQAPSNVSGGLLV HRQTPNGNSLFGNSSSPVAQPVTVPFNSTNF QTSLPVHNIIQRLAPNSNKVPINIQPKIQM GQONTYNVNNLGIQQHHVQQGISFASASSPQ GSVVGPHMSVNTVNQNTKPVTSQAVSSTG GSIVHSFPMGQPHAPQSQFLIPTSLSVSSNVH HVQTINGQLLTQPSQLISGQVASEHVMLNR NSSNMLRTNQPYTGPMNNQNTAVHLVSGQ TFAASGSPVIANHASPQLVGGQMPLOQASPT VLHLSPGQSSVSQGRPGFATMPSVTSMGSPSR FPAVSSASTAHPSLGSQVQSGSSGNSFTGDQL TQPNRTFVPVSVSHRLPVSSSKSTSTFNTPGT GTQQQFFCQAQKKCLNQTSPISAPKTTDGLR QAQIPGLLSTTLPGQDSGSKVISASLGTAPQ QEKVVGSSPGHPAVQVESHSGGQKRPAAKQ LTKGAFILQQLQRDQAHTVTPDKSHFRSLSD AVQRLLSYHYVCQGSMPTEEDLRKVDNEFETV ATQLLKRTQAMLNKYRCLLEDAMRINPPAE MVMIDRMFNFQEEASLSRDKRLALVDPEGFQ ADFCCSFKLDKAAHETQFGRSDQHGSKASSS LQPPAKAQGRDRAKTGVTEPMNHQDFHLVP NHIVVSAEGNISKKTECLGRALKFDKVLVQ YQSTSEEKASRREPLKASQCSPGEGHRKTSS RSDHGTESKLSILADSHLEMTCNNSFQDKSL RNSPKNEVLHTDIMKSGGEPQPDQLTKSLET TFKNILELKKAGRPQSDPTVSGSVELDFPNF SPMASQENCLEKFIPDHSEGVVETDSILEAAV NSILEC
675	2025	A	5154	599	1880	LKKMEPFSCDTFVALPPATVDNRHFGKNSDR LYDEVQEVVYFPAVVHDNLGERLKCTYIEID QVPETYAVVLSRPAWLWGAEMGANEHGVC GNEAVWGREEVCDEEALGMDLVRLGLERA DTAEKALNVVDLLEKYGGGNCTEGRMVF SYHNSFLIADRNEAWILETAGKYWAAEKVQE GVRNISNQLSITTKIAREHPDMRNYAKRKQW WDGKKEFDFAAAYSYLDATAKMMTSSGRYCE GYKLLNKHKGNTTFETMMEILRDKPSGINME GEFLTASMVFILPDSSLPCIHFFTGTPDPER SVFKPFIFVPHISQLLDTSSPTFELEDLVKKKS HFKPDRRHPLYQKHQQALEVNNNEEKAKI MLDNMRKLEKELFREMEILQNKHL DVEKIV NLPQCTKDEIQYQSNLSVKVSS

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676	2026	A	5155	2	306	FFFLRRSLALSPRDCGLQWRNLGSLQAPPPG FTPFSCSLSPSSWDYRRPPRPANFLYF**RRG FTLLARMVVIS*PHDPPASASQSAGITGVSHRA RPT
677	2027	A	5167	97	740	FFHSVDLLALEQSKTFYKPDWFDIVSEVKCC KEAVCVIDMSSFTFEITSTGDQALEVLQYLF SNDLDVPVGHIVHTGMLNEGGGYENDCSIAR LNKRSMFISPTDQVHCWAWLKKHMPKDS NLLLEDVTWKYTALNLIGPRAVDVLSLSYA PMTDPHFPSLFCKEMSVGYANGIRVMSMHT GEPGFMLYPIEYRWGFTMLSTLVSNS
678	2028	A	5183	1919	2018	PALCRLRDDMTVCVADFGLSKKIYSGDYRQ GRIAKMPVKWIAIESLADRVYTSKSDVWAFG VTMWELATRGMTYPYGVQNHMYDYLLHG HRLKQFEDCLDELCKI**SQSP
679	2029	A	5190	39	499	RESQVKHFMRKIDLCSSGSEVILATSSDE KHPPENIDGNPETFWTTGMFPQEFICHHK VRIERLVIQSYFVQTLKIEKSTSKEPVDFEQWI EKDLVHTEGQLQNEEIVAHGDSATYLRFIIVS AFDFHASFVSHVSAEGTVVSNLSS
680	2030	A	5204	541	92	EILAVLKLACGDISLALMVAATAVLTLAPL LLICLSYLFILSAILRVPSAAGRCKAFSTCSAH RTVVVVFYGTISFMYFKPKAKDPNVDKTVAL FYGVVTPSLNPIIYSLRNAEVKAAVLTLRGG LLSRKASHCYCCPLLSAGIG
681	2031	A	5207	10	247	VPDNGDVTKLPVCSTLVEETSLTVSEAMEQSI KNESPLPGTLAHTCNTSTLGGRRWIT*GREF DTSMANMVKPCLYRK
682	2032	A	5210	2	231	FFFETESYSITQAGVQVWPNLSSLKTLPPGFK*F SCLSLPSSWDYRCLPPCPANFCIFSRNGVLPC WPGWSRTPDLS
683	2033	A	5218	85	402	CPSVSGLIKSDLRHRHINIGITNVDVKAVSNIF MILLRSMYRINVKPYFT*LFPSRVNC*SVIG YARCYTFLIF*LFL*IPADSPTDQEPKTVMLSK QSESAI
684	2034	A	5220	1	194	NLMKEMQNLSNENHKTWEEYKDTK*IMSYF YG*ALNVIKMAVLPKLMYRFSATLVKIPQHL TDS
685	2035	A	5228	260	440	LHSQDGNSDPRKPQGEMLSAHAFVQTCGEED QKKTQVVPINFTELSKCS*S*KIMSGERE
686	2036	A	5239	79	508	GGEAAARAALKSSPRPHRVGRRERGVGGMMS AFSEAALEKKLSELSNSQSVQTLWLHHR KHSRPVTVWERELRKAKPNRKLTFYLAND VIQNSKRKGPEFTKDFAPVIVEAFKHVSSETD ESCKKHLGRVLSIWEERS
687	2037	A	5244	1	428	MAAVVAATALKGRGARNARVLRGILAGATA NKASHNRTRALQSHSSPEGKEEPEPLSPELEYI PRKRGNPKMAVGLAWAIGFPCGILLFILTKR EVDKDRVKQMKARQNMRLSNTGEYESQRFR ASSQSAPSPDVGSGVQT
688	2038	A	5249	1	1407	LQQTEDKSLNQGSSSEEVAGSSQKMGQPGP SGSDSLATALHRLSLRRQNYLSEKQFAEEW QRKIQVLADQKEGVSGCVTPTESLASLCTTQS EITDLSSASCLRGFMPEKLQVVKPLEGSQILY HWQQLAQPNLGTILDPRPGVITKGTQLPGD AIYHISDLEDEEEGITTQVQQPLEVEEKLSTS KPVGTGIFLPITSAGGPVTATANPGKCLST NSTFTFTTCRLHPSDITQVTPSSGFPSLSCGSS GSSSNTAVNSPALAYRLSIGESITNRRDSTTT

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						FSSTMSLAKLLQERGISAKVYHSPISENPLQPLPKSLAIPSTPPNSPSHSPCPSLPFEPRVHLSNFLASRPAETFLQEMYGLRPSRNPPDVGQLKMNLDRLKRLGIARVVKNPGAQENGRCQAEI GPQKPD SAVYLN SGSSLLGGLRRNQSLPVM GSFAAPVCTSSPKMGVLKED
689	2039	A	5254	2	2621	LSLFGSRALGRSGARAMAKAKKVGARRKAS GAPAGARGGPAKANSNPFVKNRQKFQILG RKTRHDVGLPGVSRARALRKRTQTLLKEYKE RDKSNVFRDKRFGEYNSNMSPEEKMMKRFA LEQQRHHEKKSIYNLNEDEELTHYGQSLADIE KHNDIVDSDSAEDRGTLSELTAHFGGGG GLLHKKTQGEGEREKKPSRKELIEELIAKSK QEKREKQAQREDALELTEKLDQDWKEIQTL SHKTPKSENDRDKKEKPKPDAYDMMVRELGF EMKAQPSNRMKTEALAKEEQEHLRKLEAB RLRLMLGKDEDENVKKPKHMSADDLNDGFV LDKDDRLLSYKDGKMNVEEDVQEEQSKEA SDPESNEEGDSSGGEDTESDSPSHLDLES NVESEEEENKPAKEQRQTPGKGLISGKERAG KATRDELPTTFAAPESYEELRSLLLGRSMEEQ LLVVERIQKCNHPSLAEGNKAKLEKLFGLLE YVGDLATDDPDLTVIDKLVVHLVHLCQMF ESASDAIKFVLRDAMHEEMEEMETKGRAALP GLDVLITLKITGLLFPTSDFWHPVTPALVCL SOLLTKCPILSLQDVVKGLFVCCFLFYVALS QRFIPELINFLGILYIATPNKASQGSTLVHPFR ALGKNSSELLVVSAREDVATWQSSLSLRWA SRLRAPSTEANHIRLSCLAVGLALLKRCVLM YGSLPSFHAIMGPLRALLTDHLADCSHPQELQ ELCQSTLTMESQKQCRPLTCEKSKPVPLKL FTPRLVKVLEFGRKQGSKEEQERKRLIHKHK REFKGAVREIRKDNQFLARMQLSEIMERDAE RKRKVKQLFNSLATQEGEWKALKRKKFKK
690	2040	A	5261	1	304	FFFFVFLVETGFHHVGGAGLELLTSGDPPTW ASQSAGITGVSHCSWPVTYVLTLLHAVRNVLFKRTFPLKSSSFLSYDKEIFPLIVLKFYLVTLT SFVK
691	2041	A	5270	3	158	NCHTTHCTANWVHLPGTPPGWKIDGFAAAL EVLSSFFFFLKFSYKPNIV
692	2042	A	5282	56	1268	GMEPVGCCGECRGSSVDPRSTFVLSNLAEEV ERVLTFLPAKALLRVACVCRVRECVRRVLR THRSVTWISAGLAEGHLEGHCLVRVVAEEL ENVRILPHTVLYMADSETFISLEECRGHKRAR KRTSMETALALEKLFKQCCQLGIVTPGIVVT PMGSGSNRPQIEIGESGFALLFPQIEGKIQPF HFIKDPKNLTLEHQLETVGLLDNPELRVVLV FGYNCCCKVGASNYLQQVSTFSDMNILAGG QVDNLSSLTSEKNPLDIDASGVVGLSFGSHRI QSATVLLNEDVSDEKTAEAAQRLKAANIPE HNTIGFMFACVGRGFQYYRAKGNVEADAFR KFFPSVPLFGFFNGEIGCDRIVTGNFILKCN EVKDDDLFHSYTTIMALIHLGSSK
693	2043	A	5301	362	507	EEIKERFGPLVITYWYGFQELDCNRERGILLK ACFTNTVTLCHSIA
694	2044	A	5310	1	204	RVLTAINHTLKENLRKFYKGGKDKPLDLRPK KTRAMRRRLNMHEENLTKKQHRKERLYPL RKYAACA
695	2045	A	5315	125	1596	ETRSTAVKSEVQVCISLLLEDRTMPKKAAP

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						TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP SSLFESLISPIKTETFFKEFWQKPLLQQRDDPA LATYYGSLFKLTDLKSLSRGMYYGRDENV CRCVNGKKKVLNKDGKAHFLQLRKDFDQKR ATTQFHQPQRFKDELWRIQEKLECYFGSLVGS NVYITPAGSQGLPPHYDDVEVFILQLEGEKH WRLYHPTVPLAREYSVEAEERJGRPVHEFML KPGDLLYFPRGTIHQADTPAGLAHSTHTVIST YQNNSWGDFLLDTISGLVFD TAKEDVELRTG IPRQLLLQVESTTVATRRLSGFLRTLADRLEG TKELLSSDMKKDFIMHRLFPYSAGDGAELSTP GGKLPRLDSVVRQFKDHI VLTVPDQDQSD ETQEKMVYIYHSLKNSRETHMMGNEEETFH GLRFPLSHLDALKQIWNSPAISVKDLKLTDE EKESLVLSLWTECLIQVV
696	2046	A	5318	1476	742	LMKXYLEAAELGEISDIHTKLLRLSSSGTET SLQDIDSRLSPGGSLADAWAHQEGTHPKDRN VEKLQVLLNCMTETIYYQFKDKAERRLAYN EEQIHKFDKQKLYYHATKAMTHFTDECVKK YEAFLNKSEE WIRKMLHLRKQLLSLTNQCFDI EEEVSKYQEYTNELQETLPQKMF TASSGIKHT MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE LAENNHILESGGSLTMDGGLRNVDCI
697	2047	A	5320	244	478	LDYNFFLFEMTFGLVVSQAGVQWHDLSQFP PPGFKQFSCSLSPSSWDYRHLPPHLANFSREG VSPSWPGWSRTPDFR
698	2048	A	5324	266	714	LPIRKSLSRSVRSGFPTSQSPITRNLDTAGSGC LAKTVTGSFLFRNVGLRGLVAGGII GALLGTP VGILLMAFQKYSGETVQERKQKDRKALHEL KLEEWKGRQLQVTEHLPEKIESSLQDEPENDA KKIEALLNLPNPSVIDKQDKD
699	2049	A	5334	699	277	RPHGHLVCISSAGLSGVNGLADYCAASKFAA FGFAESVFVETVQKQKGKITTIVCPFFIKTGM FEGCTTGCPSLPILEPKYAVEKIVEAILQEKM YL YMPKLLYFMMFLKSFPLKTLGLLIADYLG LHAMDG FADQKK
700	2050	A	5344	3	614	PTAEEMSSLTPESSPELAKRSWFGNFI SL DKEE QIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLS QTSFRAEYKASGGPSVFQKPVRFQVDISSSEG PEPSPRRDGSGGGGIYSVTFTLISGPSRRFKRV VETIQAQLLSTHDQPSVQALADEKNGAQTRP AGAPPRSLQPPGRPDPELSSSPRRGPPKDKK LLATNGTPL
701	2051	A	5346	3	1383	HASVLCRVMAASKTQGA VARMQEDRDGSC STVGGVGYGDSKDCILEPLSLPESPGGTTTLE GSPSVPCIFCEEHFPVAEQDKLLKHMIEHKIV IADVXLVADFQRYILYWRKRFTEQPTDFCSV IRINSTAFEEQENYFLLCDVLPEDRILREELQ KQRLREILEQQQERNDTNFHGVCMFCNEEF LGNRSVILNHMAREHAFNIGLPDNIVNCNEFL CTLQKKLDNLQCLYCEKTFRDKNLTKDHMR KKQHRKINPKNREYDRFYVINYELGKSWEE VQLEDDRELLDHQEDD WSDWEEHPASAVCL FCEKQAEETIEKLYVHMEDAHEFDLLKIKSELG LNFYQQVKLVNFIRRVHQCRCYGVCHVKFKS KADLRTHMEETKHTSLLPDRKTWDQLEY YFP TYENDTLLWTLSDSESLTAQE QENENVPIISE DTSKLYALKQSSILNQLLL
702	2052	A	5356	2502	1540	MAAATRGCRPWGSLGLGLVSA AAAAWD

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						LASLRCTLGAFCECDFRPDLPGLECDLAQHL AGQHLAKALVVKALKAFVRDPAPTKPLVLSL HQWGTGKSYVSSLLAHYLFQGGRLSPRVH HFSPVLHFPHPSHIERYKKDLKSWVQGNLTA CGRSLFLFDEMCKMPPGLMEVLRPFLGSSWV VYGTNYRKAIFIFISNTGGEQINQVALEAWRS RRDREILLQLEPVISRAVLDPNPHHGFSNSGI MEERLLDAVVPFLPLQRHHVRHCVLNELAQL GLEPRDEVVQAVLDSTTFFPEDEQLFSSNGCK TVASRIAFFL
703	2053	A	5380	278	657	LFLQKLRLMKTEEBARTHTIEIMFLRKEQKQL EERLEFWMEKYDKDTEMKQNELNALKATKA SDLAHLQDLAKMIREYEQVIIEDRIEKERSKK KVKQDLLELKSIVKLQAWWRGTMRREIGGF KM
704	2054	A	5381	1	1003	FRGRAVKMAAVVEVEVGGAAGERELDEV DMSDLSPEEQWRVEHARMHAKHRGHEAMH AEMVLILIALTVVAQLLLVQWKQRHPRSYN MVTLFQMWVVPPLYFTVKLHWWRFLVIWILF SAVTAFTFRATRKPLVQTTPRLVYKWFLLIY KISYATGIVGYMAVMFTLFGNLNLFKIKPEDA MDFGISLLFYGLYYGVLERDFAEMCADYMA STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV SEEGIENTYRLSCNHVFHEFCIRGWCIVGKK QTCPCYCKEVDLKRMFSPNWERPHVMYGGQL LDWLRYLVAWQPVIGVVQGNLYLGL
705	2055	A	5396	3	675	IYDRDPLQLATRAGQPLDINMAGEPKPYRKP GNKRPLSALYRLSKPEFLSVGGYVFDYDYY RDDDFYNRLFDYHGRVPPPPRAVIPLKRPRVA VTTTRRGKGVFSMKGGSRSTASGSTGSKLKS DELQTIKKELTQIKTKIDSVLGRLDKIEKQK AEAEAQKLLLEESLVLIQEECVSEIADHSTEEP AEGGPDADGEEMTDGIEEAFDEDDGGHELFLQ IK
706	2056	A	5410	2	98	GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI S
707	2057	A	5415	6	287	PFKLTSPFLSHAFSSGQERKVFIELNHIKKCNT VRGVFVLEEFGNITILLGLDSHGNSNLGAP EEGLGAGRKRTSVEKSGGAGVTRKKRDP
708	2058	A	5423	3	291	SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE
709	2059	A	5424	679	347	RIRHEEKRGSRGRRTSEEDTPKKKKKHKGG SEFTDILSVHPSDVLDMFVDPNEPTYCLCHQ VSYGEMIGCDNPDCEIWFHFACVDLTTKPK GKWFCPRCVQEKRRKK
710	2060	A	5442	1073	559	QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPTPSSSFRSSTPTGSEYDEEVDY EESDSDESWTTESAISSEALLSSMCMNGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPKCRCGKSYKTAQGLRHHTINFHPV SAEIRKMQQ
711	2061	A	5449	1	319	GDSLCPVQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPVSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD LYRDIPELQGF
712	2062	A	5499	91	749	RPTPOHGDFWMQPLTKDAGMSLSSVTLASAL QVRGEALSEEIWSLLFLAAEQLEDLRNDSS DYVVCPSALLSAAGSLSFQGRVSHIEAAPF

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						KAPELLQQQSEDEQPDASQMHVYSLGMTLY WSAGFHVPPHQPQLQCEPLHSILLTMCEDQPH RRCTLQSVLEACRVHEKEVSVYPAPAGLHIR RLVGLVLGTISEVSREPCFSSSSCWSCVAIKI
713	2063	A	5506	22	478	VEELILVSRLDPHLHTPMYFFLAHLSFLDLST TSSIPQLLYNLNGCDKTISYMGCAIQLFLGL GGVECLLLAVMAYDRCAICKPLHYMVMIN PRLCRGLVSVTWGCGVANSLAMSPVTLRLPR CGHHEVDHFLCEMPALIRMACISTV
714	2064	A	5514	25	220	AIRPYWCENNIGIGKLTADGKAFADPEVLR RLTSSVSCALDEAAAAALTRMAESTANAGQS DK
715	2065	A	5526	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAM GRTALFHHSOGSSGYESLRDSEATGSASSAP DSMESGAASPGARTSLKSPKKRATGLQRR RLIPAPLPDITLGRKPSLPQWVDLPPLAG SLKEPFEIKVYEIDDERLQRPPTPREAPTQ LACVSTRRLAERRQRLREVQAKHKHLCCE LAETQGRMLLEPGRWLEQFEVDPELEPESAE YLAALERATAALEQCVNLCKAHVMMVTCFD ISVAASAAIPGPQEV DV
716	2066	A	5529	458	790	SPGYGENKFTVTSXNIAVPLCEMNKIYSYSD SSSERTMDLVLEMCNTNSIHWCIGISGRQLG KLHPSSSLCLALTLSSVQGLQSIGLRLTDTF LKRTYEYDDIAQVCV
717	2067	A	5531	3	460	NSEDLLKYFNPESWQEDLDNMYLDTPRYRG RSYHDRKSKVDLDRLNDDAKRYSCTPRNYS VNIREELKLANVVFPRCLLVQRCGGNCGCG TVNWRSTCNSGKTVKKYHEVLQFEPGHIKR RGRAKTMALVDIQLDHIHERCDCICSSRPPR
718	2068	A	5586	311	88	AVLKNMAPMTALGLLDLHILNLI.FI.SAGEDF TSVSEIMMYILLVFLTLWLLIEMIYCYRKVS KAEAAQENA
719	2069	A	5598	1	330	KNCANEAVVQKILDRVLSRYDVRRLRPNFGSM LATNSTRGLNEDELMAGHEKDSSSESDSC PPSPGCSFTEGFSFDLLNPDYVPKVDKWSRFL FPLAFLFNIVAERC
720	2070	A	5628	798	148	LPPAQIPEAWLLANVVVLILVPLKDRLLDP LLLRCCLKPSALQKMGFMFGFTSVIVAGV LEMERLHYIHNETVSQQIGEVLYNAAPLSIW WQIPQYLLIGISEIFASIPGLEFAYSEAPRSMQG AIMGIFCLSGVGSLLGSSLVALLSLPGGWLH CPKDFGNINNCRMDLYFFLLAGIQAVTALLF VWIAGRYERASQGPASHRSRFRDRG
721	2071	A	5632	146	536	MSALIVRKLRSALTLFSELPTVLGANVNAA KLHETALHHAAKVKNVDLIEFMIEFGGNIYA RDNRGKKPSDYTWSSAPAKCFEYYEKTPLT LSQLCRVNLKATGVRGLEKIAKLNIPPLRID YLSYN
722	2072	A	5638	3	3806	CPSLDIRSEVAELRQLENCVVEGHLQILLMF TATGEDFRGLSFPRLTQVTDYLLFRVYGLES LRDLFPNLAVIRGTRFLGYALVIFEMPHLRD VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLOPAGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRCVPCP HGMACTARGECCHECLGGCSQPEDPRACV ACRHL YFQGACLWACPPGTYYQESWRCVTA ERCASLHSPVGRASTFGIHQGSCLAQCPSGFT RNSSSIFCHKCEGLCPKECKVGTKTIDSQAA

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						QDLVGCTHVEGSLILNRQGYNLEPOLQHSL GLVETITGFLKIKHSFALVSLGFFKNLKLIRGD AMVDGNYTLYVLDNQNLQQLGSWVAAGLTI PVGKIYFAFNPRCLLEHIYRLEEVTGTRGRQN KAEINPRINGDRAACQTRTLRFVSNVTEADRI LLRWERYEFLAARDLLSFIVYKESPFQNAE HVGPDACGTQSWNLLDVELPLSRTQEPGVTL ASLKPWTQYAVFVRAITLTTEEDSPHQGAQS PIVYLRITLPAAPTVPQDVISTSNSSSHLLVRW KPPTQRNGNLTYLVLWQRLAEDGDLYLND YCHRGRLRPTSNNDPRFDGEDGDPEAMESD CCPCQHPPGQVLPPLEAEASFQKKFENFLH NAITIPISPWKVTSSNKSPQRDSGRHRRAGPL RLGGNSSDFEIQEDKVPRAVL SGLRHFTFY RIDIHACNHAAHTVGCSAATFVFARTMPHRE ADGIPGKVAWEASSKNSVLLRWLEPPDPNGL ILKYEIKYRRLGEEATVLCVSRLRYAKFGGV HLALLPPGNYSARVRATSLAGNSWTDVAF YILGPEEEDAGGLHVLLTATPVGLTLLVLAA LGFFYGKKRNRITLYASVNPEYFSASDMYVPD EWEVPREQISIRELGQGSFGMVYEGGLARGE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVRLLGVSQGPVIMELMTR GDLKSHLRSLRPEAENNPGLPQALGEMIQM AGEIADGMAYLAANKFVHRDLAARNCMVSQ DFTVKIGDFGMDRVDYETDYRKGGKGLLP VRWMAPESLKDGIPTTHSDVWSFGVVLWEIV TLAEQPYQGLSNEQVLKFVMDGGVLEELEG PLQLQELMSRCWQPNPRLRPSFTHILDSIQEEL RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSP TPRDCSPQNGGPGH
723	2073	A	5672	1	216	LAWIDNILEKEKETDKKRKRKGAHEDCD EEPQFPFPPSVIKIPMESVQSDPQNGIHLAKR SSSWYSYL
724	2074	A	5704	4235	940	ARGRRSRPVWAASWGGGRPAARRRPRGLA ATMGFELDRFDGDVDFDLKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQEGSCPARCRGR LSAKELNHVLPKRLILKLDIKCAYATRGCGR VVKLQQLPEHLERCDFAPARCRHAGCGQVLL RRDVEAHMRDACDARPVGRQEGCGGLPLTH GEQRAGGHCCARALRAHNGALQARLGALHK ALKKEALRAGKREKSLVAQLAAQLELQMT ALRYQKKFTEYSARLDSLSRCVAAPPGGKGE ETKSLTLVLRDSSGLGFNIIGRPSVDNHDG SSSEGIFVSKIVDSGPAAKEGGLQIHDRIEVN GRDLSRATHDQAVEAFKTAKEPIVVQVLRRT PRTKMFPTPPESQLVDTGTQTDITFEHIMALT KMSSPSPVLDPYLLPEEHPSAHEYDYPNDYI GDIHQEMDREELEEEVDLYRMNSQDKLGLT VCYRTDDEDDIGIYISEIDFNSIAAKDGRIREG DRIIQNGIEVQNREEAVALLTSEENKNFSLLI ARAEQLDEGWMDDDRNDLDDLHMDMLE EQHHQAMQFTASVLQKKHDEDDGGTTDTAT ILSNQHEKDSGVGRITDESTRNDESSEQENNG DDATASSNPLAGQRKLTCSQDITLGSGLPFS NESFISADCTDADYLGIPVDECERFRELLEK CQVKSATPYGLYYPGSLDAGKSDPESVDKE LELLNEELRSIELECLSVRAHKMQQLKEQYR ESWMLHNSGFRNYNTSIDVRRHELSDITELPE KSDKDSSA YNTGESCRSTPLTLEISPDSNLR

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						AAEGISCPSSSEGAVGTTEAYGPASKNLLSITE DPEVGITPTYSPLKELDPNQPLESKERRASDG SRSPTPSQKLGSAYLPSYHHSPYKHAHIPAHA QHYQSYMQLIQKSAVEYAQSQMSLVSMCK DLSSPTPSEPRMEWKVKIRSDGTRYITKRPVR DRLLRERALKIREERSGMTTDDAVSEMCK GRYWSKEERKQHLVKAKEQRRRREFMMQSR LDCLKEQQAADDRKEMNILELSHKMMMKR NKKIFDNWMTIQELLTHGTSKSPDGRVYNSF LSVTTV
725	2075	A	5707	3	1770	QISTEVSEAPVANDKPKTLVVKVQKKAADLP DRDTWKGRFDLMSCVGYAIGLGNVWRFPY LCGKNGGGAFLIPYFLTLIFAGVPLFLLCCLG QYTSIGGLGVWKLAPMFKGVGLAAAVLSFW LNIYYIIVISWAIYLYNSFTTTLFPWKQCDNP WNTDRCSNYSMVNTTNMTSAVVEFWERN MHQMTDGLDKPGQIRWPLAITLAIAWILVYF CIWKGVGWGTGKVYFSATYPYIMLILFFRGV TLPGAKEGHLFYITPNFRKLSDEVWLDAAATQ IFFSYGLGLSLIALGSYNFSHNVYRDSIIVC CINSCSMFAGFVIFSVGFMAHVTKRSIADV AASGPGLAFLAYPEAVTQLPISPLWAILFFSM LLMLGIDSQFCTVEGFITALVDEYPRLLRNR ELFLAAVCIISYLIGLSNITQGGIYVFKLFDYYS ASGMSLLFLVFEFCVSISWYFVGNRFYDNIQE MVGSRPCIWWKLCWSFTPIIVAGVFIFSAVQ MTPLTMGNVYVFPKWGGVGVWLMALSSMVL IPGYMAYMFLTLKQSLKQRIQVMVQPSDIV RPENGPEQPQAGSSTSKEAYI
726	2076	A	5711	156	423	PRRDPGRTPELRGSAPRKTGANMPVRRGHVA PQNTFLGTIIRKFEGQNKFIANARVQNCALII YCNDGFCMTGFSRPDVMQKPCCTD
727	2077	A	5716	3	274	HASEYFFKLCSFQVFLSFPLATIVDVLVVIP LVKSPNVHYVYVLLVLGSLFYIPLIHFKIRL AWFEKMTCYLQLLFNICLPDVSEE
728	2078	A	5737	1899	649	IQASRASPYPRVKVDFALSCHEDLLAPISEPIE WKYHSPDEEISLGPACWLWDFLRRSQAGFL LPLSGGVDSAAACLIYSMCCQVCEAVRSGN EEVLADVRTIVNQISYTPQDPRDLGRLTTC YMASKNSSQETCTRARELAQQIGSHHISLND PAVKAVMGIFSLVTGKSPLFAAHGGSSREN ALQNVQARIRMVLAAYLFAQLSLWSRGVHGG LLVLGSANVDESLLGYLTKYDCSSADINFIGG ISKTDLRAFVQFCIQRFQLPALQSILLAPATAE LEPLADGQVSQTDDEDMGMTYAELSVYGKL RKVAKMGPYSMFCKLLGMWRHICTPRQVAD KVKRFFSKYSMNRHKMTTLTPAYHAENYSPE DNRFDLRPFLYNTSWPWQFRCIENQVLQLER AEPQSLDGVD
729	2079	A	5741	1	5976	PGCAARLSRARAPGPGAAGAGRKRLADPGPP PASRRLRAPGSRPRLAPCTRRAAQPAHARMA PRAAGGAPLSARAAAASPPFPQTPPCFVPLL LLLLGAARAGALEIQRFPSPPTNNFALDG AAGTVYLAAVNRLYQLSGANLSLEAAAVG PVPDSPLCHAPQLPQASCEHPRLTDNYNKL QLDPGQGLVVVCGSIYQGCQLRRRGNISAV AVRFPFAAPPAEPVTVFPSMLNVAANHFNAS TVGLVLPFAAGAGSRLLVGATYTYGSSFF PRNRSLEDHRENTPELAIRSLDTRGDLAKLFT

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						FDLNPSDDNLIKQGAKEQHKLGFVSAFLHP SDPPPGAQSYAYLALNSEARAGDKESQARSL LARICLPHGAGGDAKKLTESYIQLGLQCAGG AGRGDLYSRLVSVPFARERLFAVFERPQGSPA ARAAPAALCAFRFADVRAAIRAARTACFVEP APDVVAVLDSVVQGTGPACERKLNQLQPEQ LDCGAAHLQHPLSILQLKATPVFRAPGLTSV AVASVNNYTAVFLGTVNGRLLKINLNESMQ VVSRRVTVAYGEPVHHVMQFDPADSGYLY LMTSHQMARVKVAACNVHSTCGDCVGAAD AYCGWCALETRCTLQDCTNSSQQHFWTSA SEGPSRCPAMTVLPSEIDVRQEYPGMILQISGS LPSLSGMMACDYGNIRTVARVPGPAFGHQ IAYCNLLPRDQFPFPNPQDHTVEMSVRVN GRNIVKANFTTYDCSRTAQVYPHTACTSCLSA QWPCFWCSQQHSCVSNQSRCEASPNFTSPQD CPRILLSPLAPVPTGGSQNLVPLANTAFFQG AALECSFGLLEEFVAVWVNESVVRCDQVVLH TTRKSQVFPLSLQLKGRPARFLDSPEPMTVM VYNCAMGSPDCSQCLGREDLGHLCMWSDGC RLRGPLQPMAGTCPEIRAIEPLSGPLDGGT LLTIRGRNLGRRLSDVAHGVWIGGVACEPLP DRYTVSEEIVCVTGPAPGPLSGVVTVNASKE GKSRDRFSYVPLVHSLEPTMGPKAGGTRITI HGNDLHVGSSELQVLVNDTDPCTELMRITDTSI ACTMPEGALPAPVPVCFVRERRGCVHGNLTF WYMQNPVITAISPRRSPVSGGRITTVAGERFH MVQNVSMVAVHHIGREPTLCKVLNSTLITCPSF GALSNASAPVDFINGRAYADEVAVAEELLDD PEEAQRGSRFRDYLFPNQFSTAKREKWKH HPGEPLTLVIHVSTKGAGKEQDSLGLQSHEY RVKJGQVSCDIQIVSDRIHCSVNESLGAAVGQ LPITIQVGNFNQITATLQGGSETAIVSVICSV LLLSVVALFVFCTKSRAERYWQKTLQME EMESQIREIRKGFALQTDMDTLTKELNRSQ GIPFLEYKHVTRTFFPKCSLYEERYVLPSTQ LNSQSSQAQETHPLLGEWKIPESCRPNMEE GISLFSSLLDNKHFLIVFVHALEQQKDFAVRD RCSLASLLTIALHGKLEYTYSIMKELLVDLID ASAAKNPKMLMRRTESVVEKMLTNWMSICM YSCLRETVEPFLLLCALQKQINKGSIDAITG KARYTLNEEWLLRENIEAKPRNLNVSFQCG MDSLSVRAMDTDTLTQVKEKILEAFCKNVFPY SQWPRAEDVDLEWFASTQSYILRDLDTSV VEDGRKKLNTLAHYKIPEGASLAMSLLDKKD NTLGRVKDLDTKEYFHLVLPDELAEPKSH RQSHRKKVLPFIYLRLLSTKGTQKFLDDL KAILSIREDKPLAVKYFFDFLEEQAEKRGSD PDTLHIWKTNSLPLRFVWNILKNPQFVFDIDK TDHIDACLSVIAQAFIDACSIDLQLGKDSPTN KLLYAKEIPEYRKIVQRYKQIQDMTPLESEQE MNAHLAEESRKYQNEFNTNVAMAEIYKYAK RYRPQIMAALEANPTARRTQLQHKFEQVVAL MEDNTIYECYSEA
730	2080	A	5744	3	292	QPSPLFHSLETQLLRTAQLPEQVSWPWGQ VANGKGNQRNMGSPQPSLLAFERNLELQIMG LGYSLLMGKLRPRVAKDTRLVHRDSTPSPLT LKD
731	2081	A	5747	1	382	FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC FRVDEVNWTIWNINVGIINEDPGNCEGVKRT

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						LSFSLRSSRVSGRHWKFNALVPLLREASARD RQSAQPPEVYLRQFSGSLKPEDA EVFKSPAAS GEK
732	2082	A	5753	198	3	AQAESSTVASPEATAGPLCTRIPNVPPPIPRP PGKLAQQLPCSPVRFTSARIPPASRPQTKS
733	2083	A	5754	2	2223	AAGPPGLEAEGRAPEASAGPGPGGDAAEITPGL PPAHSGTLMMAFRDVTQIANQNISVSSSTAL SVANCLGAQTVQAPAEPAAGKAEQGETSGR EAPEAPAVGREDASAEASAGASGAADG ATAPKTEEEEEETAEVGRGAEEAGDLEQ LNRTSTSTKSASGSEASASASKDALQAMILS LPRYHCENPASCKSPTLSTDLRKRLYRIGLN LFNINPDKGIOFLISRGFIPDTPIGVAHFLQK GLSRQMIGEFLGNSKKQFNRDVLDVVDDEM DFSSMELDEALRKFAHVRVQGEAQKVERLIE AFSQRVCMCNPEVVQGFHNPDTIFLAFAILL NTDMYSPNIKPDCKMMLED FIRNLRGVDDG ADIPREL VVGIERIQKELKSNEDHVTYVTK VEKSIVGMKT VLSVPHRRLVCCSRLFEVTDV NKLQKQAAHQREVF LFNLDLVLKLC PKKKK SSTYTFCKSVGLGMQFQLFENEYYSHGILV TPLSGSEKKQVLHFCALGSDMQKFVEDLKE SIAEVTLEQIRIEWELEKQOGTKLSFKPCGA QGD PQSKQGSPTAKREAAALRERPAESTVEVSI HNRLQTSQHNSGLGAERGAPVPPDLQSPPR QQT PPLPPPPPTPPGTLVQCQIVKIVLDKPC LARMEPLLSQALSCYTSSSDSCGSTPLGGPG SPVKVTHQPLPPPPPYNHPHQFCPPGSLH GHRYS SGRSLV
734	2084	A	5788	8	362	SSVMGDLVGQGLEEQIVARDENSWLIDGGTP IDDVMRVL DIDEFPQSGNYETIGGFMMFLR KIPKRTDSVKFAGYKFEVVDIDNYRIDQLLV RIDS KATALSPKLPDAKDKEESVA
735	2085	A	5827	1	1257	MVFSAVLTAFHTGTSNTTFVVYENTYMNITL PPPFQHPDLSPLLRYSFETMAPTGLSSLTVNST AVPTTPAAFKSLNPLQITLSA MIFILFVSFLG NLVVCLMVYQKAAMRSAINILLASLAFADM LLAVLNMPFALVTILTTRWIFGKFFCRVSAMF FWLFVIEGVAILLISDRFLITVQRQDKLNPR AKVLIASWATSFCVAFPLAVGNFDLQIPSRA PQCVFGYTTNPGYQAYVILISLISFFIFLVILY SFMGILNLRHNLRIHSYPEGICLSQASKLGL MQLQRP FQMSIDMGFKTRAFTTILFAVIVC WAPFTTYSLVATFSKHFYQHNFESTWLL WLCYLK SALNPLIYYWRIKKFHDACLDMMMP KSFKFLPQLPGHTKRRIRPSAVYVCGEHR TVV
736	2086	A	5870	3	268	FTRSD ELARHYRTHTGEKRFSCPLCPKQFSRS DHLTKHARRHPTYPDMIEYRGRRTFRIDPP LTSEVESSAGSGGPAPSFTTCL
737	2087	A	5871	2	521	LTWPQLFLETPELLHMSRPAEDGPSPGALVR RSSSLGYISKAEEYFLKSRSDLMFEKQSERH GLARRLTARRFPASSEQAQQLFNELKPAV DGANFIVNHMRDQNNYNEEKDSWNRVART VDRLCLFVVTPVMVVGTAWIFLQGVYNQPPP QPFPGDPYSYNVQDKRFI
738	2088	A	5881	1	1160	LVVTATAILAFNEYTRMSTSELISELFNDCG LLDSSKLC DYENRNTSKGGELPDRPAGVGV YSAMWQLALTLILKIVITITFGMKIPSGLFIPS MAVGAIAGRLLGVGMEQLAYYHQEWTVFNS

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						WCSQGADCITPGLYAMVGAACLGGVTRMT VSI.VVIMFELTGGLEYTVPLMAAAMTSKWVA DALGREGHYDAHRLNGYPFLEAKEEFAHKTL AMDVMKPRRNDPLLTVLTQDSMTVEDVETII SETTYSGFPPVVVSRESQRLVGFVLRRLDLSIE NARKKQDGVVSTSIYFTEHSPPLPPYTPPILK LRNILDSPFTVTDLTPMEIVVDIFRKLGLRQC LVTHNGRLLGIITKKDVLKHIAQMANQDPDSI LFN
739	2089	A	5892	2	916	TLQLAASVPFFAISLISWWLPESARWLINGKP DQALQELRKVARINGHKEAKNLIEVLMSSV KEEVASAKEPRSVLDLFCVPVLRWRSCAMLV VNFSLISYYGLVFDLQSLGRDIFLLQALFGA VDFLGRATTALLSFLGRRTIQAGSQAMAGL AILANMLVPQDLQTLRVVFAVLGKGCFGISL TCLTYKAELEFPTPVRMTADGILHTVGRGA MMOPLILMSRQALPLPLLYGVISIASSVLV FFLPETQGLPLPDTIQDLESQKSTAAQGNRQE AFTVESTSLLEIVALHGAL
740	2090	A	5900	2	426	RPIKTLGIGHFHFSVDGVHFLTQREVQNLWKE NLILDTAKKHGYEVVDFTITMGRYKEFLQG KCGCHFHEVVKSKLSKEYNFIMKRSRNMH GRYFSNQSKLQOGTVTNFRSPYHVRGPINQV CSEILLSRMCANKRTM
741	2091	A	5910	3	412	RMPESTLLIICENGYLEAPLPTIKQEEDDHDV VSYEIKDMCIKCFHFSSVSKILRLIEIEKRER QRELKEKIREERNKLAEMGEDGEKEFEQEE EEEEEEEEEEPLPEIFIPSTPSPILCGFYSEPG KFWV
742	2092	A	5936	1	482	MGCRLCCVVFCLLQAGPLDTAVSQTPKYL TQMGNDSIKCEQNLGHDTMYWYKQDSKK FLKIMFSYNNKELINETVPMRFPSPKSPDKAHL NLHINSLELGDSAVYFCASSQDTALQSHCIPV HKPPGSARKLQGSVCTCTQGSSLSHSLMASDG VPVC
743	2093	A	5938	1	1566	MNSFFGTPAASWCLLESVDVSSAPDKEAGRER RALSQQRGGAWSGSLEWSRQSGDRRRL GLSRQTAKSSWSRSDRTCCCRRAWWILVPA ADRARRERFIMNEKWDINSSENWHPIWNVN DTKHLYSDINITYVNYLHQPQVAIFISYF LIFFLCMMGNTVVCFTVMRNKHMHTVTNLF LNLAISDLLVGIFCMPITLLDNIIAGWPFNTM CKISGLVQGISVAASVFTLVAIAVDRFQCVVY PFKPKLTKTAFVIMIIWVLAIMSPSAVMLH VQEEKYYRVRLNSQNKTSPPVWCREDWPNQ EMRKITYTTLFANIYLAFLSLIVIMYGRIGISLF RAAVPHTGRKNQEQWHVVSRRKKQKIKMLLI VALLFILSWLPLWTLMLSDYADLSPNELQII NIYTYFFAHWLAFGNSSVNPIIYGFFNENFRRG FQEAFLQLCQKRAKPMAYALKAKSHVLIN TSNQLVQESTFQNPHEGETLLYRKSAEKPQEQ LVMEELKETTNSSEI
744	2094	A	5966	149	327	SHVCVSHYAGSSGCPAGAGAGAVAGISAVA LYDYQGGRLGVARGAWMEAPDIRQGDGM
745	2095	A	5970	413	856	GAPHTDWAWAPTMSGSGRGRQGTGLASS PLSLPLLAGVTGILATELFDOMARPAACMV CGALMWIMLILVGLGFFIMEALSHFLYVPFL GVCVCGAIVTGLFPETKGTQFQISKELHRL NPPRAQGPTWRSLEVIQSTEL

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746	2096	A	5971	3	1343	AQTARRIGLELDTEGHRLFVAFSGCTVYLPLS RCARHGACQORSCLASQDPYCGWHSSRGCVDI RGSGGTDVDQAGNQESMEHGDCQDQATGSQ SGPGDSAYGVRRDLPPASASRSVPIPLLASV AAAFALGASVSGLLVSCACRRARRRRGKDIE TPGLPRPLSLRLARLHGGGPEPPPPSKDGDA VQTPQLYTTFLPPPEGVPPELACLPTPESTPE LPVKHLRAAGDPWEWNQNRNNAKEGPGRSR GGHAAGGPAPRVLVRPPPGCPGQAVEVTTL EELLRYLHGPPPRKGAEPAPLTSRALPPEP APALLGGPSRPHECASPLRLDVPPEGRCA PARPALSAPAPRLGVGGRRLPFSGHRAPPAL LTRVPSGGPSRYSGGPGKHLLYLGRPEGYRG RALKRVDVEKPQLSLKPFLVGPSSRQAVPNG GRFNF
747	2097	A	5998	2	754	DHASLPCSWNHRFDVETRHVFIGDHSGQVTI LKLEQENCILVTTFRGHTGGVTALCWDVPVQ RVLFSGSSDHSVMWDIGGRKGTAEIQGHN DRVQALSQAQHTRLISCGGDDGGVWVNM VERQETPEWLDSDSCQKCDQPPFWNFKQMW DSKKIGLRQHCRKCGKAVCGKCSSKRSSPL MGFEFEVRVCDSCHEAITDEERAPTATFHDSK HNIVHVHFDATRGWLLTSGTDKVIKLWDMT PVVS
748	2098	A	6001	2	747	AMVFGGVVPYVPQYRDIRRTQADGFSTYV CLVLLVANILRLFWFGRRFESPLLWQSAMIL TMLMLKLCTEVRVANELNARRRSFTAADS KDEEVKVAPRRSFLDFDPHHFWQWSSFSYV QCVLAFTGVAGYITYLSIDSALFVETLGFLAV LTEAMLGVPQLYRNHRHQSTEGMSIKMVL WTSGDFAKTAAYFLKGAFLQFSVCGLLQVLV DLAILGQAYAFARHPQKPAPHAVHPTGTAL
749	2099	A	6002	2	447	GRPDRSELVRMHILEETFAEPLSQATQMKLK RARLADDLNEKIAQRPGMELVEKNILPVDSS VKEAIGVGKEDYPHTQGDFFDEDSDSLSP DQPASQESQGSAAASPSEPVSSESPVTNTPT AQFASVSPTVPEFLKTPPTAD
750	2100	A	6004	2	427	LLTQAMLVLPHPQWFTPGPRLQAQGPCQEG WRWELRLRNYVPEDEDLNKRVRPOAKPDAY QEKVKEQLEAAKPEPVIEVDLAKLAPRKPD WDLKRDVAKKLEKLLKRTQRAIAELIRERLK GQEDSLDSAVDAATEHKTC
751	2101	A	6007	33	1280	TDQAKVDNQEKLVRSAEDVSTVPTQPDNPF SHPDKLKRMSKSVPAFLQDESDDRETDTASE SSYQLSRHKSSPSSLTNLSSSGMTSLSSVSGS VMSVYSGDFGNI.EVKGNIQFAIEYVESLKE HVFVAQCKDLAAADVKKQSDPYVKAYLLP DKGKMGKKKTLVVKKTLNPVYNEILRYKIEK QILKTQKLNLSIWHRDTFKRNSFLGEVELDLE TWDWDNKQNKQLRWYPLKRKTAAPVALEAE NRGEMKLALQYVPEPVPGKKLPTTGEVHIWV KECLDLPLRGSHLNSFVKCTLPDTSRKSRSQ KTRAVGKTTNPIFNHTMVYDGFREPDLMEAC VELTVWDHYKLTNQFLGGLRIGFTGKSYGT EVDWMDSTSEEVALWEKMNVPNTWIEATL PLRMLLIKISK
752	2102	A	6028	108	1283	KEIFSPFELISVKPLCLLLGVTCSSQMAFEELL SQVGLGRFQMLHLVFIPLSLMLLIPHILLNF AAAIPIGHRCWVHMLDNNTGSGNETGILSEDA

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						LLRISIPLDNSLRPEKCRRFVHPQWQLHLNG THSTSEADTEPCVDGWVYDQSYFPSTIVTKW DLVCDYQSLKSVVQFLLLTGMLVGGIIGGHV SDRFGRFRILRWGLLQLAITDTCAAFAPTFPV YCVLRFLAGFSSMIISNNSLPITEWIRPNSKAL VVILSSGALNIGQILGGLAYVFRDWQTLHV ASVPPFFVFLLSRWLVESARWLITNKLDEGL KALRKVARTNGIKNAEETLNIEVVRSTMQEE LDAAQTKTTVWDLFRNPSMRKRICILVFLRK KNLKEKA
753	2103	A	6043	1	1470	DSFESILRLIFEIHSSEKGDIVVFLACEQDIEK VCETVYQGSNLPDLGELVVVPLYPKEKCSL FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN SVRFVIDVGVERKVVNPRIRANSLVMQPIQ SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTP LKPAEMQEANLTSVMVLFMKRIDIALGLHCDP MNRPAPESLMQALEDLDYLAALDNDGNLSE FGIMSEFPLDPQLSKSILASCEFDCEVLTIA AMVTAPNCFSHVPHGAEEAALTCWKTLHPE GDHFTLISIKAYQDTTLNSSSEYCEKWCERD YFLNCSALRMADVIRAEELLEIKRIELPYAEP FGSKENTLNKIKALLSGYFMQIARDVDGSGN YLMMLTHKQVAQLHPLSGYSITKKMPEWVLF HKFSISENNYIRITSEISPELFMQLVPQYYFSNL PPSESKDILQQVVDHLSPVSTMNKEQQMCET CPETEQRCTLQ
754	2104	A	6055	2	394	YYALHHWPFDDLLCQTTGAIFQMNMYGSCIF LMLINVDRYAAIVHPLRLRHLRRPRVARLLC LGWVALILVFAVPAARVHRPSRCRYRDLVLR LCFESFSDDELWKGRLLPLVLLAEALGFLPLA AVVYSS
755	2105	A	6059	3	1795	LGLGSGTLLSVSEYKKKYREHVLQLHARVKE RNARSVKITKRPTKLLIAPESAAPPEALGPAEE PEPGRARRSDTHFNRLFRDEEGRRPLTVVL QGPAGIGKTMAAKKILYDWAAGKLYQGQVD FAFFMPCGELLERPGTRSLADLILDQCPDRGA PVPQMLAQPQRLFILDGADLPALGGPEAAP CTDPFEAASGARVLGGLLSKALLPTALLVTT RAAAPGRQLQGRLCSPQCAEVRGFSKDKKKK YFYKFFRDERRAERAYRFVKENETLFCFCFV PFVCWIVCTVLRQQLGRDLRSRTSKTTTSVY LLFITSVLSSAPVADGPRLQGDRLNLCRLARE GVLGRRAQFAEKELEQLELRGSKVQTLFLSK KELPGVLETEVYQFIDQSFQEFALAALSYLLE DGGVPRTAAGGVGTLLRGDAQPHSHLVLT RFLFGLLSAERMRIERHFHFCMVSEVKQEA LRWVQGGQGGCPGVAPEVTEGAKGLEDTEB PEEEEEGEENYPLELLYCLYETQEDAFVRQA LCRFPELALQVRFCRMDVAVLSYCVRCPPA GQALRLISCLVAAQEKKKKSLGKRLQASLO GG
756	2106	A	6060	12	436	SGRPTRPAKPTGQGMGRFMLTLVCQGSIMMS ARDLIMNLTQLPGLFHHLRFLEELRLSGNH LSHIPGQAFSGLYSLKILMLHNNQLGGIPAQA LWELPSQLSLRLDANLISLVPERSFEGLSLRLH LWLDNLTALTEPS
757	2107	A	6063	54	419	ITPLGLGAADMCAPFWLLLLLLQEGSQRRRL WRWCGSEEVVAVLQESISLPLEIPPDEEVENII WSSHKSLATVVPKKEGHPATMVTNPHYQG

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						QILTMLRLSLQQPSASWPRDCSSSCSW
758	2108	A	6066	125	438	IGISCPATIFVPMFSHSLIGEEYQLPYNNMV PSDPSYEDMREVVCVKRLRPVSNRWNSDEC LRAVLKLMSECAWHNPASRLTALRIKKTLAK MVESQDVKI
759	2109	A	6072	3	650	PGRFRPAAL EERAMEKLEKVPFQNRGKGT LSSIIPNNSDTRKATETTSLSKPEYVNPDFRW SKDPSSKSGNLLSETSEVGWTSNPEELDPIRLA LLGKSGLSQVGSATSHPVSCQEPIDEDQRISP KDKSTAGREFSGQVSHQTTSENQCTPIPSSTV HSSVADMQNMPPAAVHALLTQPSLSAAPFAQ RYLGLTLPSTGSTLPQCHAGNATVW
760	2110	A	6077	3	730	PLRLTLMEEVLLGLKDREGYTSFVND CISSG LRGCMLELPLRGRQLQLEACGMRRKSLTRK VICKSDAPTGDVLLDEALKHVKETQPPETVQ NWIELLSGETWNPLKLHYQLRNVRERLAKNL VEKGVLTTTEKQNFLLFDMTHPLTNNNIKQR LIKKVQEA VLDKWVNDPHRMDRRLALILYL AHASDVLEN AFAFLLEQYDLATKRVRQLLD LDPEVECLKANTNEVLWAVVAFTK
761	2111	A	6078	833	390	IVSFHLSGFKKFRVPFSLSVHGLQVDEYHSV HQKLSADMADHSNLRSLVGAEDARLMRD MKTMKSR YMELYDLNRDLLNGYKIRWNNH TELLGNLKAVNQAIQRAGRLRVGPKNQVIT ACRDAIRSNNTLTKIMRVGTASS
762	2112	A	6079	2	2686	KKAITCGEKEKQDLIKSLAMLKDOFRTRDRGS HSDLWSSSSLESSSFLPKQYLDVSSQTDISG SFGINSNNQLAEKVRLRLRYEAKRRRIANLKI QLAKLDSEAWPGVLDSEDRLLINEKEELLK EMRFISPRKWTQGEVEQLEMARKRLEKDLQ AARDTQSKALTERKLNSKRNLVRELEEAT RQVATLHSQLKSLSSMQSLSSGSPGSLTSSR GSLVASSLDSSTSASFTDLYDPFEQLDSELQ SKVEFLLLEGATGFRPSGCITTIHEDEVAKTQ KAEGGGRLQALRSLSGTPKSMTSLSPRSSLS PSPPCFPLMADPLLAGDAFLNSLEFEDPELSA TLCELSLGN SAQERYRLEEPGTEGKQLGQAV NTAQGCGLKVACVSAAVSDES VAGDSGVYE ASVQRLGASEAAAFDSDESEAVGATRIQIALK YDEKNKQFAILLIQLSNLSALLQQDQKVNIR VAVLPCSESTTCLFRTRPLDASDILVFNEVFW VMSYPALHQKTLRVDVCTTDRSHLEEC LGG AQISLA EVCRS GERSTRWYNLLSYKYLKKQS RELKPVGVMAPASGPASTDAVSALLEQTAVE LEKRQEGRSSTQTLED SWRYEETSENEAVAE EEEEEEVEEEEGEEDVFTEKASPDMDGYPAK VDKETNTETPAPSPTVVRPKDRRVGTPSQGPF LRGSTIIRSKTFSPGPQSQYVCRLNRSDSDSST LSKKPPFVRNSLERRSVRMKRSPPPQPSYK SLRSERLIRTS LDLELDLQATRTWHSQLTQEIS VLKELKEQLEQAKSHGKELPQWLREDEFR LLLRMLEKRM DRAEHMGELQTDKMMRAAA KDVHRLRGQSCKEPPEVQSFREKMAFFTRPR MNIPALSADDV
763	2113	A	6082	3	1558	PHPIRFSKLCVSFNNQ EYNQFCVIEEASKANE VLENLTQGKMCLVPGKTRKLLFKFVAKTED VGKKIEITSVDLALGNETGR CVVLNWQGGGG DAASSQEALQAARSFKRRPKLPDNEVHWGSII IQASTMIISRVPNISVHLLHEPPALTNEMYCLV

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						VTVQSHEKTQIRDVKLTAGLKPQGDANLTQK THVTLHGTELCDSEYPALLTDIPVGDLLHPGEQ LEKMLYVRCGTVGSRMFLVYVSYLNTTVEE KEIVCKCHKDETVTETVFPFDVAVKFFVSTKF EHLERVYADIPFLMTDILLSASFWALTIVSSE LHLAPSMITVDQLESQVDNVILQTGESASECF CLQCPSLGNIEGGVATGHYISWKRTSAMENI PIITTVITLPHVIVENIPLHVNADLPFSGRVRES LPVKYHLQNKTDLVQDVEISVEPSDAFMFSG LKQIRLRILPGTEQEMLYNFYPLMAGYQQLPS LNINLLRFPNFTNQLRRFIPTSFVKPQGRLM DDTSIAAA
764	2114	A	6093	1	1422	AAADLANSNAGAAVGRKAGPRSPSPAPAP PPPAPAPPTLGNNHQESPGWRCCRPTLRERN ALMFNNELMADVHFVVGPPGATRTVPAHKY VLAVGSSVFYAMFYGDIAEVKSEIHIPDVEPA AFLILLKMYMSDEIDLEADTVLATLYAAKKYI VPALAKACVNFLETSLEAKNACVLLSQSRLF EPELTQRCWEVIDAQAEMALRSEGFCEIDR QTLHIVTREALNTKEAVVFEAVLNWAEAE KROGLPIITPRNKRHVLGRALYLVRITMTLEE FANGAAQSDILTLEETHSIFLWYTATNKPRLD FPLTKRKGAPQRCRHFQSSAYRSNQWRYRG RCDISQFAVDRRVFIAGLGLYGSSSGKAEYSV KIELKRLGVVLAQNLTKFMSDGSSTNFPVWF EHPVQVEQDTFYTASAVLDGSELSYFGQEGM TEVQCGKVAFFQFCSSDSTNGTGVQGGQIPE LIFYA
765	2115	A	6099	1	1150	SGFTHYAIYDFIVKGSCFCNVHADQCIPVHGF RPVKAPGTFHVMVHGKCMCKHNTAGSHQCH CAPLYNDRPWEEADGKTGAPNECRTCCKNG HADTCHFDVNVWEASGNRSGGVCDQCQHN TEGQYQCRCKPGFYRDLRRPFSAPDACKPCS CHPVGSAVLPAANSVTFCDFPNSGDCPCKPGVA GRRCDRCMVGYWGFQDYGCRPCDCAGSCD PITGDCISSHTDIDWYHEVPDFRPHNKSEPP WEWEDAQGFSAHLLHSGKCECKEQLGNAKA FCGMKYSYVLKIKLSAHDKGTHVEVNVKIK KVLKSTKLKIFRGKRTLYPESWTDRCCTCPIL NPGLEYLVAGHEDRTGKLVNMSFVQHWK PSLGRKVMIDILKRECK
766	2116	A	6103	2	384	MTAAATATVLKEGVLEKRSGLLQLWKRKR CVLTERGLQLFEAKGTGGRPKELSFARIKAVE CVESTGRHIYFTLVTEOGGEIDFRCPLEDPGW NAQITLGLVKFKNQAIQTVRARQSLGTGT VS
767	2117	A	6106	1	542	SGSSHASDGSGFQELRICSEDQTLIAGMCSLP MARYYIIKYADQKALYTRDGQLLVGDPVAD NCCAEEKICTLPNRGLDRTKVPIFLGIQGGSRC LACVETEEGPSLQLEDVNIIEELYKGGEEATRF TFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQ PVQLTKESEPSARTKFYFEQSW
768	2118	A	6109	3	292	FILQAVLQLSSQEARYKAFGTCVSHIGAILAF YTPSVISSVMHRVARCAAPHVHILLANFYLLF PPMVNPIIYGVKTKQIRDSLGSIEKGCYNRE
769	2119	A	6110	1	711	RHEPSCSNGVASTKSKQNHSKYPAPSSSSSSS SSSSSSPSSVNYSESNSTDTKSQHHSTSNQ ETSDSEMEMEAEHYPNGVLGSMSTRIVNGAY KHEDLQTDDESSMDRHPRRQLCGGNQAATE

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						RILFGRELQALSEQLGREYGKNLAHTEMLQD AFSLLAYS DPWSCPVGQQLDP IQREP VCAAL NSAILESQNL PKQPPLMLALGQASECLRLMA RAGLGSCSFARVDDYLH
770	2120	A	6125	2	570	YFGLNLHVQH LGNNVFLQLT LGAVILLANC VAPWALKYMNRRASQMLLMFLAICLLAIF VPQEMQMLREVLA TLGLGASALANTLAFAH GNEVIPTIRARAMGINATFANIA GALAPLMM ILSVYSPPLPWIIYGVFFPISGFAFLLLPETR NK PLFDTIQDEKNERKDPREP KQEDPRVEVTQF
771	2121	A	6126	909	353	RSFVLDTASAI CNYN AHYKNHPKYWCRGYF RDYCNIAFSFNSTNHVALRDTGNQLIVTMS C LTKEDIGWYWC GIORDFARDDMDFTLIVT DDKGT LANDFWSGKDL SGNKTRCKAPKV V RKADRSRTSILICILITGLGIISVISHLTRRRS QRNRRVGN TLKPF SRVLTPKEMAPTEQM
772	2122	A	6148	7	810	FVLGILALSH TISPFMKNKFFASFPNRQYQLLF TQSGGENKEEII NYEFDTKDLVCLGLSSIVGV WYLLRKH WIANNLFG LAFSLNGVELLHLNN VSTGCILLGGLFIYDVFWVFGTNVMVTVAKS FEAPIKL VFPQDLLEKGLEANNFAM LGLGDV VIPGFIALLLRFDISLKNHTHTYFYTSAAYIF GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLV ALAKGEVTEMFSY ESNPKDPAAVTESKEGT EASASKGLEKKEK
773	2123	A	6161	3	1088	CQPMLVTRKNHPKLLLRRTESVAEKMLTNW FTFLLYKFLKESAGEPLFMYCAIKHQMEKG PIDAITGEARYSLSEDKLIRHLIDYKTLTLNCV NPENENAPEVPVKGLDCDTGTQAKEKLLDA AYKGV PYSQRPKAADMDLEWRQGRMARIL QDEDVTTKIDNDWKRLNTLAHYQVTDGSSV ALVPKQTSAYNISNSSTFTKSLRYESMLRTA SSPDSLRSRTPMITPDLESGTKLWHLVKNHHDH LDQREGDRGSKMVSEIYLRLLATKGTLQKF VDDL FETIFSTAHRG SALPLAIK YMFDFLDEQ ADKHQIHDADVRHTWKSNCPLRFWVNVIK NPQFVFDIHKNSITDA CLSVV
774	2124	A	6163	860	125	KTAVKKRNLNPVFNETLRYSVPQAE LQGRVL SLSVWHRESLGRNIFLGEVEVPLDTWDWGSE PTWLP LQPRVFPSPDDLPSRGLLALSLKYVPA GSEGAGLPPSGELHFWVKEARDLLPLRAGSL DTYVQCFVLPDDSRASRQRTRVRRSLSPVF NHTMVYDGF PADLRQACAE LSLWDHGALA NRQLGOTRLSLGTGSSYGLQVPWMDSTPEEK QLWQALLEQPCEWVDGLPLRTNLAPRT
775	2125	A	6191	2	392	ARGIGSLGRDHSGSGGGTGMA GAWVRKAAD YVRSKDFRDYLMSTHFWGPVANWGLPIAAIT DMKKKSPEIISRMTFAL*CYSLTFVRFAHYVQ PWNWMLMGCHTAVDFDQLISSMPCISHGMT ASASAL
776	2126	A	6217	1	827	FRGYWGVREAFIDASWSGGLGPGKPGMKIT RQKHAKKHLGFFRNNGVREPYQLLDGTFC QAALRGRIQLREQLPRYLMGETQLCTTRCVL KELET LGKDLYGAKLIAQKCQVRNCPHF KNA VSGSECLSMVEEGNPHHYFVATQDQNL SVK VKKKPGVPLMFIIQNTIMVLDPSPKTI AFVKA VESGRLSQCMRKKVSNISKRN RV**KTLNRG RRKKRKKISGPNPLSCLKKKKKAPDTQSSASE KKRKRKRIRNRNRPKVLSEKQNAEGE

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777	2127	A	6236	1038	1402	YYQISSLPISIVNGIFLWLLICIFLAXQGGSR* FQPFGRPRGGGHLRSGVLGQPGQHGETP/SFF YNSKISPALWGPVPVPSALGGEAGKSL*PRRQ RFQGGIAPLPSRVRGRAKLFLKKK
778	2128	A	6237	422	913	ASFFHHHRGAFLLLAIPGS*GQDQSLIHWNS AVSNADLLDLKW*LDHLEEKMPLEVKVVP PQVLSEPN*RSGGCFSAPSFEVPPWTGEVKP/ SPQRDGGALGQGPLGIPSDSILALLKKQT*RA LLNWPLGSLRRSSCFGQGDQDLKPRSGLC NSFRYRR
779	2129	A	6249	420	36	ARAPSPSFSVRDVELSDPARERGERMPVAVGP YGQSQPSCFDRVKMGFVMGCAVGMAGAL FGTFSCLSSILVSSSG/SGMRGRELMGGIGKTM MQSGGTGTFMAJMGIRC*PWLFTTSVPSH QSOFMY
780	2130	A	6263	415	1380	RIMRMCDRGIQMLITTVGAFAAFSLMTIAGV TDYWLYSRGVCRTKTSNDNETSRKNEEVM HSGLWRTCCLEGAFRGVCKKIDHFPEDADYE QDTAEYLLRAVRASSVFPILSVTLFFGGLCV AASEFHRSRHNVLSAGIFFVSAGLSNIIGIIVYI SANAGRTPGQRIDSKKSYSGWSF/YTSGAFS FIIGR/IC*GVGLPWHIYIEKHQQLRAKSHSEF LKKSTFARLPPYRYRFRRRSSSRSTEPSRDLS PISKGFHTIPSTDISMFTLSRDPSKITMGTLLNS DRDHAFLQFHNSTPKEFKESLHNNPANRRTT PV
781	2131	A	6274	832	318	RIIKYKDLKQTLAIKTA YPRCKCLVEMDQIFH LQVKQKQLACLCTWQARDPCPPSTKVVL/L VGPGMGCMVALFQDSIAWSNKSMPSSLSAIS QSPCQVQAPEGSSPHLPTLSFTCLSWQGGD LEFLGDLKGCSELKNFQELITQSALVHPKADV WWYCGRPLLGLTLPNS
782	2132	A	6281	1324	393	WISLPSSLLCRKNGSSAEDDRRIGEPSAEEAEG EREDWGIGSA*SVGAVSKVPSARF*RTYPSIE DEEEVTHQKSSSDSNSEHRKKKTSRSRNK KKRKNKSSKRKHRYSDSDSNSESDTNSDSD DDKKRVKAKKKKKKKKHKTKKKKNKTKK ESSDSSCKDSEEDLSEATWMBQPNVADTMDL IGPEAPIHTSQDEKPLKYGHALLPGEAAMA EYVKAGKRIPRRGEIGLTSEEIGSFECGYVM SGSRHRRMEAVRLRKENQIYSADEKRALASF NQEERRKRESKILASFREMVHKKTKGKDDK
783	2133	A	6305	201	1032	WDDYPQALRRREAAGLHFLQPPGRVRGQ LRGITGPAWYCHSPSHLLSAFCHLPTPSRCP AMARPPVPGSVVVPNWHS/RRGQGVPLHS AQEPAGVWAA*AASAAAALSIDTASYKIFV SGKSGVGKTALVAKLAGLEVPVHHETTGIQ TTVVFWPAKLQASSRVVMFRFEFWDGESA LKKFDHMLLACMENTDAFLFLPSFTDRASFE DLPQQLARIAGEAPGVVRMVIGSKFDQYMHHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG
784	2134	A	6308	86	96	GSSPDASLITMKNQDKNGAAKQSNPKSSP GQPEAGPEGAQERPSQAAPAVEAEGPSSQA PRKPEGAQARTAQSGALRDVSEELSRQLEDIL STYCVDNNOGGPGEDGAQGEPAEPEDAESR TYVARNGEPEPTPVVNGEKEPSKGDNPTEER QSDEVGDRDHRRPQEKKAKGLGKETLLM QTLNLTSTPEEKLAALCKKYAELLEHRNSQ KOMKLLQKKQSQLVQEKDHLRGEHSKAVLA

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						RSKLES LCRELQRHNRSLKEEGVQRAREEEE KRKEVTSHFQVTLNDIQLQMEQHNERNSKLR QENMELAERLKKLIEQYELREEHIDKVFHKH DLQQQLVDAKLQQAQEMLKEAERHQREKD FLLKEAVESQRMCELMKQEQETHLKQQLALY TEKFEFQNTLSKSSEVFTTFKQEMEKMTKKI KKLEKETTMYSRWRSSNKALLEMAEEKTV RDKELEGLQVKIQRLEKLCRALQT/GAQ*PVR GQRWGSHTSAVRIFS
785	2135	A	6319	1493	889	SPQGPLLRVSPVSAAGASSVTPGGAQPGVTTT PPSLVAVAPAGSAAGPAAGWQ*HAGCR/WT KLPSWGMRFPMKIFFSEYRSISTRISHDAL* EKCTQPAKPLSMIR/TGSSVSPG/PLVKWNNWT RREFRNSGTRVVSSCCGMSCMYSFLGHCSV/S QDLPLVHVDVGWQPPLGPTVGLRPLPLHD TTPCOKLVVDDLDWA
786	2136	A	6320	551	135	RWLPVAECDSSCVGCTGEGPGNCKECISGYA REHGQCADVDECSLAECTCVRKNENCVNTP GSYVCVCPDGFEET/RRCLCAAGRG*SHRRRK PDTAALPRRPVMCRTPYPLNYSEGCPEVENV ALRMPSPAVDSGGERLPAL
787	2137	A	6330	1693	227	DYVLTAEHLHRQSPGVSGFLSVFNLNMAIMG SGILGLAYVMANTGVFGFSFLLLTVALLASYS VHLLLSMCIQATYLG*TNFYFMVLPAAH*LTCL PLIEFLQSL*NSL*AVTSYEDLGLFAGLPGKL VVAGTHIQNIGAMSSYLLIKTELPAAIAEFLT GDYSRYWYLDGQTLIIICVGI VFLALLPKIG FLGYTSSLSFFFMMFFALVVIKKWSIPCPLTL NYVEKGFGQISNVTDCKPKLFHFSKESAYALP TMAFSFLCHTSILPIYCELOSPSKKRMQNVTN TAIALSFLIYFISALFGYLTIFYD/GTTKAORGE VTCHRIKDKVESELLKG***IP*SHDVVVMITV KLCILFAVLLATVPLIHFPARKAVTMMFFSNFP FSWIRHFLITLALNIIIVLLAIYVPDIRNVFGVV GASTSTCLIFPGLFYLKLSREDFLSWKLGV GCFC/LLSFKTSILRNSLSVYIIPASRKSIYFKI
788	2138	A	6351	1	6622	PRSLCPSLWAEAAVLADGGLRRRRRLRGTM SASFVPNGASLEDCHCNLFCLADLTGKWKK YVWQGPTSAPILPVTEEDPILSSFSRCLKADV LG/VWRRDQRPERRREL*IFWGGEDPVLTLF TMTYQKKKMECGRMDFFPMNAVLCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFIFLHGDSNVCTSVEINQHQPVY LLSEEHITLAQQSNSFFQVILCPFGNLGTLTGQ AFKMSDSATKKLIGEWKQFYPISSCLKEMSE EKQEDMDWEDDSLAAVEVLVAGVRMITYPAC FVLVPQSDIPTSPVSGTHCSSSCLGVHQVPAS TRDPAMSSVTLTPPTSPEEVQTVDPQSVQKW VKFSSVSDGFNSDSTSHHGGKIPRKLANHV DRVWQECNMNRAQNKRYASASSGGLCEEAT AAKVASWDFEATQRTNCSCLRHKNLKSRL AGQQGQAPSLGQQQQLPKHKTNEKQEKSEK PQKRPLTPFHHRVSVSDDVGMADASASQRL VISAPDSQVRFNSNIRVNDVAKVTPQMHGTE MANSPQPPPLSPHPCDVDEGVTKTPSTQS QHIFYQMPTDPLVPSKPMEDRIDLSQSFPQ YQEA VEPTVYVGTA VNLEEDANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFQGQESV TSVTELMVQCKPLKVSDELVQQYQIKNQCL SAIASDAEQEPKIDPYAFVEGDEEFLFPDKKD

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						<p>RQNSEREAGKKHKVEDGTSSVTLSHEEDA MSLFSPSIKQDAPRPTSHARPSTSLIYDSDL VSYTDLNLFNSDEDELTPGSKRSANGSDDK ASCESKTGNLDPLSCISTADLHKMYPTPPL EQHIMGFSPMNMNNKEYGSMDDTTPGGTVLE GNSSSIGAQFKIEVDEGFCSPPKSEIKDFSYY KPENCQILVGCSMFAPLKTLPQYLPLIKLPEE CIYRQSWTVGKLELLSSGSPMPFIKEGDSNM DQYGTAYTPQTHTSCGMPPSSAPPSNSGAGI LPSPSTPRFPTPTPTPTPTPTPGAGGPASAGS VKYENDLYSPASTPSTCRPLNSVEPATVPSIP EAHSLYVNLILSESVMNLFKDCNSDSCCICVC NMNIKGADVGVYIPDPTQEAQYRCTCGFSAV MNRKFGNNSGLFFFEDELDIIGRNTDCGKEAE KRFEALRATSAEHVNGGLKESEKLSDDLILL QDQCTNLFSPFGAADQDPFFKSGVISNWVRV EERDCCNDCYLALEHGRQFMDNMSSGKVD ALVKSSCLHPWKRNDVSMQCSQDILRMLLS LQPVLDQAIQKKRTVRPWGVQGPLTWQQFH KMAGRGSYGTDESPEPLPIPTFLLGYDYDYL LSPFALPYWERLMEPYGSQORDIAYVVLCP NEALLNGAKSFFRDLTAIYESCRLGQHRFVS LLTDGMRVGSTASKKLSEKLVAEWFSAAD GNNEAFSKLKYAQVCYDLGPYLASPLDS SLLSQPNLVAFTSQSLITPPQMTNTGNANTPS ATLASAASSTMTVTSGVAISTSVATANSILTT ASTSSSSSNLNSGVSSNKLSPFPFGSMNSNA AGSMSTQANTVQSGQLGGQOTSALQTAGISG ESSSLPTQPHPDVSESTMDRDKVGIPDGDSDH AVTYPPAIVVYIDFFTYENTDESTNSSSVWTL GLLRCLFEMVQTLPPHIKSTVSQIIPCQYLLQ PVKHEDREIYPQHLKSLAFSAFTQCRRLPTS TNVKTLTGFGPGLAMETALRSPDRPECIRLYA PPFILAPVKDKQTELGETFGEAQKYNVLFV GYCLSHDQRWLASCTDLYGELLETCINIDVP NRARRKKSSARKFGLQKLWEWCLGLVQMSS LPWRVVIGRLGRIGHGELKDWCLLSRRNLQ SLSKRLKDMCRMCGISAADSPSILSACL VAM EPQGSFVMPDSVSTGSVFGSTTLNMQTSQ NTPQDTSCTHILVFPTSASVQVASATYTENL DLAFNPNNDGADGMGIFDLDLTDGDDLDPDII NLPASPTGSPVHSPGSHYPHGGDAGKGQSTD RLLSTEPHEEVFNILQQPLALGYFVSTAKAGP LPDWFWSACPQAQYQCPLFLKASLHLHVP QSDLLHSHKSHPLDSNQTSDVLRVLEQYN ALSWLTCDPATQDRRCLPIHFVVLNQLYNI MNML</p>
789	2139	A	6359	1	2002	<p>TGTLTEDGLDVMGVVPLKGQAFPLVPEPRR LPVGPLLRALATCHALSRLQDTPVGDPMDLK MVESTGWVLEEEPAADSAFGTQVLAVMRPP LWEPQLQAMEEPPVPSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSELLGLLVMRNLKP QITPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLLIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFFKLLPKVLVQGTVFARMAP EQKTELVCLEQLQYQVCGMCGDGDANDCGAL KAADVGISLSQAEASVVSPFTSSMASIECVPM</p>

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						VIREGRCSLDTSFSVFKYMAL YSLTQFISVLIL YTINTNLGDLQFLAIDL VITTTVAVLMSRTGP ALVLGRVPPGALLSVPLSSLLQMVLTG VOLGGYFLTLAQPFVPLNRTVAAPDNLPNY ENTVVFSLSSFQYLILAAA VSKGAPFRRLTN NVPFLLASAL*SSVLVVLVLSPLHGLALR NITDTGFKLLLVGLVTLNFVGGHLAGERARF VPPRLPAPPPAQAGSKKRFKQLERELAEQPW PPLPAGPLR
790	2140	A	6380	76	1059	SSAGSARKLQVMALAARLWRLPFRRGAAP GSRLPAGTSGSRGHCPCFRFGFEVMGNPGT FKRGLLSALS YLGFETYQVISQAAVHATA KVEEILEQADYLYESGETEKL YQLLTQYKESE DAELLWRLARASRDVAQLSRTSEEEKLLVY EALYAKRA/L/EKNESSFASHKWYAICLSDV GDYEGIKAKIANAYIIEHFKAIELNPKDATS IHLMGWICYTFAEMPWYQRRJA*NACLQLPF *FPPYEKALGYFHRAEQVDPNFYSKNLLLG KTYLKLHNKKLA AFWLMKAKDYPAHTEED KQIQTEAAQLLTSFSEKN
791	2141	A	6434	3	1460	IALLIVDGLAWDDQGGALLHISPSKLIL*QDS SGMS/YVMVRCITITRAFFKSLCHICQYSIGPQ *VTCFGQDACE*KSTAN*GG*RE**PQVLFF AFLSNPAVKFGRMSKKQRDSLYAEVQKHQQ RLQEORQQQSGEAEALARVYSSSISNGLSNLN NETSGTYANGSVIDLPKSEGYYNVVSGQSP DQSGLDMTGIGKQIKQEPYDLTSVPLFTYASS FNMGQLAPGITMTEIDRIAQNIKSHLETQY TMEELHQLAWQHTTYEEIKAYQSKSREALW QQCAIQITHAIQYVVEFAKRITGMELCQNDQ ILLKSGCLEVVLVRMCRAFNPNNTVLFEG KYGGMQMFKALGSDDLNEAFDAKNLCSL QLTEEEIALFSSAVLISPDRAWLIEPRKVQLQ EKIYFALQHVQKNHLDDETLAKLIAKIPTITA VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF NPDCAACK
792	2142	A	6440	92	781	SRGTFRCFCRDFFPCFSNMRLFLWNAVLTFLV TSLIGALIFEPEVKIEVLQKPFICHRKTKGGDL MLVHYEGYLEKDGSLFHSTHKHNNQGPIWFT LGILEALKGWGPGA*K/DMCVGEKRKLIPPA LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH ESFQEMDLNDDWKLKDEVKAYLKKBEFEKH GAVVNESHHDALVEDIFDKEDEKDGFI SAR EFTYKHDEL
793	2143	A	6446	3201	152	PRLKRLVITEEDGGARPEALGKIAPRTPAELG ARADQELVTALMCDLRRPAAGGMMDLAYV CEWEKWSKSTHCPVPLACAWSCRNLIAFTM DLRSDDQDLTRMIHLDTEHPWDLHSIPSEHH EAITCLEWDQSGFGFLFSRWPTGQKICWS MGVSTLAINSWESSVGLSVEGGPHLWALS WLHNGVKLALHVEKSGASSFGEKFSRVKFS PSLTLFGGNAMEGWIAVTVSGLVTVSLLQP SGQVLATSTESLCRLRARVALADIAFTGGGNI VVATADGSSAIPVQFYKVCVSVVSEKCRIDT DILPSLFMRCTTDLNRKDKFPAITHLKFLARD MSEQVLLCASSQTSSIVECWSLRKEGLPVNNI FQQISPVVGDQOPTILKWRILSATNDLDRVSA VALPKLPISLTNTDLKVASDTQFYPLGLAL AFHDGSVHIVHRLSLQTMVFFYSSAAPRPVD EPAMKRPRTAGPAVHLKAMQLSWTSLALVG

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						IDSHGKLSVALRLSPSMGHPLEVGLALRHLLFL LEYCMVTGYDWWDLHVVQPSMVQSLVEKL HEBYTRQTAALQQVLSTRILAMKASLCKLSP CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT PDKSPGDRLTEICTKITDVIDKVMNLKTEEF VLDMNTLQALQQLQWVGDFVLYLLASLPN QPCPTSEPCPTSEPSPTSEPSPTSEPS*SLCAG SLLRPGHSFLRDGTSGLMRELMMVIRIWGLL KPSCLPVYTATSDTQDSMSLLFRLLTKLWICC RDEGPASEPDEALVDECCLPSQLLPSLDWL PASDGLVSRLOPKQPLRLQFGRAPTLPGSAAT LQLDGLARAPGQPKIDHLRRLHLGACPTTEC KACTRCGCVTMLKSPNRTTAVKQWEQWIK NC/LVRWALVAGAPQLPLSPAAPQLLSYPSA APEPGCKSHRSPWTLGAVNLSPCRAVEG RGPDACVTSRASEEAPAFVQLGPQSTHSPRT PRSLDHLHPEDRF
794	2144	A	6490	418	585	NGDKADLENESCRAQVLMFVVPALWEAEGG GSIEPRDLRLQ*AVITPLTPAWVTQ
795	2145	A	6499	395	1027	KLLWLPPHSEQKRSPLYHPQGPSGTTSPAFS SHSPPPSLQAPISAAFLRTHGHISASGLRMP FPH/H*NAFLLVFPQORSQTS/PSHYLCREVEF DHHHHLCLSLLESSPLFHHRVLCVCPKQNVN STRAQIFCLFVHIVGCRICINTFPLHLHLWL HFLQIFLCKKNKSVKLGKTVVGRGCQSAAGS DTRVRAAVGAPGLPVEPLV
796	2146	A	6503	68	936	HSALLTHSSFCVFTLCQDFFTYSSMSEEVTYA DLQFQNSSEMEKPEIGKFGKAPPAPSHVWR PAALFLTLLCLLLIGLGVLASMFHVTLKJEM KKMNKLQNISEELQRNISLQMSNMNINIKIR NLSTTLQTIATKLRELYSKEQEHKCKPCPRR WIWHKDSYFLSDDVQTVQESKMACAAQN ASLLKINNKNALFEIKSQSRSYDYWLGLSPEE DS/YSWYESG*YNQPSAWVIRNAPDLNNMY CGYINRLVYQYYHCTYKQRMICEKMANPVQ LGSTYFREA
797	2147	A	6507	1	881	PGSTHASARSQVPRSAGEAAPHSSRRPPGLLPH APRAASAQLEERMMDPHPGMTLQEGDCRGS QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ ESALAKLLLTCCSALRPRATQARGSSRLVAS WVMQIVLGILSAVLGGFFYIRDYTLVTSGA AIWTGAVAVLAGAAAFYKRGGTYWALLR TLLALAAFSTAIAALKLWNEDFRYGYSYNS ACRISSSSDWNTAPTQSPEEVRLHLCTSFMD DMLKALFRTLQAMLLGVWILLASLTPLWL /SL/RGECSPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSSRRPPGLLPHAP RAASAQLEERMMDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLVASW VMQIVLGILSAVLGGFFYIRDYTLVTSGAAI WTGAVAVLAGAAAFYKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYNSAC RISSSSDWNTAPTQSPEEVRLHLCTSFMDM LKALFRTLQAMLLGVWILLASLTPLWLYC WRMFPTKGVSP
798	2148	A	6528	912	2287	VPNYLPSVSSAIGGEVPQRYVWRFICGLHSAP RFLVAFAYWNHYLSCTSPCSCYRPLCRLNFG LNVVENLALLVLTYSSESDF/TWVPG*GRSG

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						EVFPEGTGLPLPHSDLPTSWCGHSLQCGSQSS FPPAIHENAFIVFIASSLGHMLLTCLWRLTKK HTVSQEDGLSLAGAPRQPRRSRTSVLRIRV MVRWELSSNGNPGRGVGLGLGLGNKLRVV GQNLGL*HCVWVWVETGE*KRWRLQMGIE* GVASRRQ*VRNSVRLVCHNSSAPPMYMGFF SPTVFGGGVGG*LHVTFILHPPEVEAAGIPLL GPSLPQRQGREHIVVLAAPACAPFHDR*WEP REIRPSP*ELGLRGEPTLSYPASCRVIRQPI*D RKSYSWKQRLFIINFISFFSALAVYFRHNMYC EAGVYTIFAILEYTVVLTNMAFHMTAWWDF GNKELLITSQPEEKRF
799	2149	A	6529	1	874	FFFQRIINFIEHSGSVSLLALACDLGWCEDWS CCLVQGGGDLVDVVQTNHGEDEAGGDTDSV DEARCKESQQAQENLRDLCLCSFAKDKIL QNEGSEFEHEETRTKQAALDGEPLGGGQLTA VHLHPSKEQQQGGGERQRGARTHWRGW EKRRRVRLRPPSGKLRADQPVRLGGPTPS/T ELPGLQPHAPTHTA/PATPTYSPADTPNPV RWKCPPLVEPRTRQLCRERTRKACPPKRPPL GLPGDFTGPVTHHAPPVSPTGASGQERRAEP GAVSYAHASATK
800	2150	A	6544	2	662	SAQRWAAVACRWGCRLLALLLVPGPGGAS EITFELPDNAKQCIFYEDIAQGTCTLEFQVITG GHYDVDCRLEDPDGKVLKEMKKQYDSFTF TASKNGTYKFCFSNEFSTFTHTKVYDFQVG ETHLCFLVR/DRVSALTQMESACVSIHEALKS VIDYQTHFRLREAQGRSRAEDLNTRVAYWSV GEALLLVVSIGQVFLKSFSDKRTTTRVGS
801	2151	A	6556	1	1319	TPCMECIKGEGLREPQNLSCSQREPQTEGSM DGWRRMPRWGLLLLLWGSCITFGLPTDTTTF KRIFLKRMPISRESLKERGVDMARLGPEWSQP MKRLTLGNTTSSVILTNYMDTQYYGEIGITP PQTFKVVFDTGSSNVVWPSSKCSRLYTACVY HKLFDASDSSSYKHNGTELTLRYSTGTVSGFL SQDIITVGGITVTQMFGEVTEMPALPFMLAEF DGVVGMGFIEQAIGRVPTIFDNIISQGVLKED VFSFYNRDSENSQSLGGQIVLGGSDPQHYE GNFHYINLIKTVWQIQMKGVSVGSSTLLCE DGCLALVDTGASYISGSTSSIEKLMEALGAKE KRLFDYVVKCNEGPTLPPTFLFLGGKDTPLT SADYLFQESYSSKKLSTLAHAMYIPPTGPTL VALGATFURKFYTEFDRGNPHGFALAR
802	2152	A	6567	13	6147	MCLGRMGASSPRSPFVGPAPGLFFCCGGSL LAVVLLALPVAWGQCNAPEWLPFARPTNL TDEFEPGTYLNYECRPGYSGRPFSIHLKNS VWTGAKDRCKRKRSCRNPPDPVNGMVHVIK IQFGSQIKYSCTKG YRLIGSSSATCIISGDTVIW DNETPICDRIPCGLPPTITNGDFISTNRENFHY GSVVTYRCNPGSGGRKVFLVGEPSIYCTSDND DQVGWISGPAPQCIIPNKCTFPNVENGILVSD NRSLSLNEVVEFRQCPGFVMKGPRRVKCOA LNKWEPELPSCSRVCQPPDVLHAERTQDCK DNFSPGQEVFYSCEPGYDLRGAASMRCTPQG DWSPAAPTCEVKSCDDFMGQLLNGRVLPV NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESLWNSSVPVCEQIFCSPFPVINGRHTGKP LEVFFFGKAVNYTCDPHPDRTGSFDLIGESTIR CTSDPQGNVWSSPAPRCGILGHCAQAPDHL FAKLKTQTNASDFPIGTSKLYECREPEYYGRPF

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						SITCLDNLVWSSPKDVCKRKSCKTPDPVNG MVHVITDIQVGSRLNYSCCTTGHRLIGHSSAECI LSGNAAHWSTKPPICQRI PCGLPPTIANGDFIS TNRENFHYGSVVTYRCNPGSGGRKV FELVGE PSYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV ENGILVSDNRSLSLNEVVEFRCPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLHA ERTQRDKDNFSPGQEVFYSCPEGYDLRGAAS MRCTPQGDWSPAAPTCEVKSCDDFMGQLLN GRVLFVNLQLGAKVDFVCDGFLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPVPNG RHTGKPLEVFPFGKAVNYTCDFHPDRGTSFD LIGESTIRCTSDPQNGVWSSPAPRCGILGHC QAPDHFLFAKLKTQTNASDFPIGTSKLYECP EYYGRPFSITCLDNLVWSSPKDVCKRKSCKTP PDPVNGMVHVITDIQVGSRLNYSCCTTGHRLI HSSAECILSGNTAHWSTKPPICQRI PCGLPPTI ANGDFISTNRENFHYGSVVTYRCNLGSRGRK VFELVGEPSYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLSLNEVVEFRCP GFVMKGP RRVKCQALNKWEPELPSCSRVCQ PPEILHGEHTPSHQDNFSPGQEVFYSCPEGY DLRGAASLHCTPQGDWSPAAPCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDGFL KGSSVSHCVLVGMRS LWNSSVPVCEHIFCPN PPAILNGRHTGTSPGDIPYGKEISYTCDFHPDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFFASPTIPINDFEFFVGTS LNYECRPGYFGKMFISCLNLVWSSVEDNC RRKSCGPPPEPFGMVHINTDTQFGSTVNYSC NEGFRIGSPSTTCLVSGNNVTWDDKAPICEII SCEPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSYCTSKDDQVGVWSS PPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPAAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDFHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLGTFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RILQTNEENSRVLP
803	2153	A	6574	2	3233	HGRSARLAAPAEAMPGRPPAGSRLRLLLL LLLPPLLLLRLGSHAGNLTVAVVPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAADV LKWE HNPAVFLGPGCVYAAPVGRFTHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRRLGWERQALMLYAYRPGDEEHCF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVYICSSPDAFRTLM LLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGDVDSARQAFQAAKIITYKDPDNPEYL EFLKQLKHLAYEQNFMTMEDGLVNITPASFH

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						DGLLLYIQAVTETLAHGGTVTDGENTQRMW NRSFQGVGTGYLKDSSGDRDTDFSLWMDPE NGAFRVVLNNGTSQELVAVSGRKLNWPLG YPPDPKCGFDNEDPACNQDHLSTLEVLALV GSLSLGILIVSFFIYRKMQLKELASELWRVR WEDVEPSSLERHLRSAGSRLTSLGRGSNYGSL LTTEGQFQVFAKTAYYKGNLVAVKRVNRKR IELTRKVL FELKHM RDVQNEHLTRFVGACTD PPNICILTEYCPRGSLQDILENESITLDWMFYY SLTNDIVKGMFLHNGAICSHGNLKSNCVV DGRFVLKITDYGLESFRDLDEQGHVTYAKK LWTAPELLRMASPPVRGSAQGDVYSFGHILQE IALRSGVFHVEGLDLSPEHIEVTRGEQPPFR PSLALQSHLEELGLLMQRCAEDPQERPPFQ QIRLTLRKFNRENSSNLDNLLSRMEQYANNL EELVEERTQAYLEEKRAEALLYQILPHSVAE QLKRGETVQAEAFDSVTITYPSDIVGFTALSAE STPMQVVTLLNDLYTCFDAVIDNFDVYK VET IGDAYMVVSGLPVRNRLHACEVARMALAL LDAVRSFRIRHRPQELRLRIGIHTGPVCAGV VGLKMPRYCLFGDTVNTASRMESNGEALAKI HLSSETKAVLAEFGGFELELRGDVEMKGGK KVRTYWLLGERGSSTRG
804	2154	A	6585	2	3837	DAPGRPPVRLPTMELEDGVVYQEEPPGGSGAV MSERVSLAGSTYREFERLIVRYDEEVVKELIP LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQYEREKALRKHAEEKFIEFEDSQEQKK DLQTRVESLESQTRQLELKAKNYADQISILEE REAEKKEYNALHQRHTEMIMHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFFLP AGDGLLTPDAQKGGETPGSEQWKQELSQR SHTSLKDELSDVSGGSKATTTPASTANSVVA TPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVTGSAENEEKSEVQAIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSLIGDVDEGADLLGMGREVENLI LENTQLETKNALNIVKNDLIAKVDELTCCK DVLQGELEAVKQAKLKLEEKNRLEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFRTRVE MARVLMERNQYKERLMELQEA VRWTE MIR ASRENPA MQEKKRSSIWQFFSRLFSSSNNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPPVYLRLPDEKDTSMKLWCA VGYNLSGGKTRDGGSVVGASVFKDVA GLD TEGSKQRSASQSSLDKLDQELKEQKELKNQ EELSSLVWICTSTHSATKVLIDAVQPGNILD FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMSTNSAETDSLGGITVVG SAEGVTGAATSPSTNGASPMVKPPEMEAE SEVDENVPTAEEVATEEGNAGSAEDTVADIS QTGVVYTHEVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SLSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVYQPKAMKIEKSFDAHPRKESQYRQ LAWVGDGVVVSIRLDSTLRLYHAHTYQHLQ DVDIEPYVSKMLGTGKLGFSFVRITALMVSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NRLWVGTVNGVHISPLTETVILHQGRLLGLR ANKTSGVPGNRPGSVIRVYGDENSDKVTPTGT FIPYCSMAHAQLCFHGHHRDAVKFFVAVPGQV ISFQSSSSGTDLTGDKGRGHLHRSLVVRRP
805	2155	A	6605	469	2602	FGRLLWGTAFKSWKMKAPIPHILLIYATFTQ SLKVVTKRGSADGCTDWSIDIKKYQVLVGEF VRIKCALFYGYRTNYSLAQSAQSLMWYKS SGPGDFEPIAFDGSRMKEEDSIWFRPTLLQ DSGLYACVIRNSTYCMKVSISLTVGENDTGL CYNKMKYFEKAELSKSKEISCRDIEDFLPT REPEILWYKECRTKTWRPSIVFKRDTILLIREV REDDIGNYTCELKYGGFVVRRTTETLTVTAPL TDKPPKLLYPMESKLTQETQLGDSANLTCRA FFGYSGDVSPLIYWMKGEKFIEDLDENRVWE SDIKILKEHLEGEVSISLIVDSVEEGDLGNYS CYVENGNGRRHASVLLHKRELMYTVELAGG LGAILLLLVCLVTIYKYKIEIMLFYRNHFGA EELDGDNDKYDAYLSYTKVDPDQWNQETGE EERFALEILPDMLEKHYGYKLFPPDRDLIPTGT YIEDVARCVDQSKRLIIVMTPTNYVVRGWSIF ELETRLRNMLVTGEIKVILIECSELGIMNYQE VEALKHTIKLLTVIKWHGPKCNKLSKFWKR LQYEMPFKRIEPIHTEQALDVSEQGPFGELQT VSAISMAAATSTALATAHPDLRSTFHNTYHS QMRQKHYYRSYEYDVPTGTPLPLTSIGNQHT YCNIPTMLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW
806	2156	A	6614	3	1584	NSARGGVGVRGARAMATVQEKAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKRRHRLKRHNDCFVGEADVIFSHL IQNKYFGDVIDPRAKVVRVCQALMDYKVF AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSFHVNISSLSPQVINEVWQE ETIGRLLQLVDLPLDLSLLKQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSQSDQEDWLSA AIDCLEYLPDQMVEISRSFPEQPDRTDLVKE LLFDAIGRYYSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNRFEFRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVFLMDHQKDVFKIPGT LVHKIVSVKILMAIQNGRDPNRDAGYICYQRI DQRDYSNITEKTIDEELL YLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEHFGD
807	2157	A	6615	4198	2094	FGIVGTFALETDELSDRDPAPISLCDFGAMR PQILLLLALLITGLAAQHDKVPCKM/VKML CPDRVDKKVSCQVLGLLQVPSVLPDPTETLD LSGNQLRSILASPLGFYTLRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLS NVLMDIEDGAFEGPLRLTHLNLNRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASQPOAEFOLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTGFPQDSKGHAPSEGWSALPLSAPSGNAS GRPLSQLNLDLSYNEIELPDSFLEHLTSLCFL NLSRNCLRTFEARRLGLPLCLMLLDLSHNALE TLELGARALGSLRLLQLQGNALRDLPPYTF NLASLQRLNLQGNRVSPCGGPDEPGPSGCV AFSGITSLRSLSLVDNEIELLRAGAFLHTPLTE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LDLSSNPGLEVATGALGGLEASLEVALQGN GLMVLQVDLPFCFICKRLNLAENRSLHPAW TQAVSLEVLDLRNNSFSLPGSAMGGLETSLR RLYLQGNPLSCCGNGWLAAQLHQGRVDVDA TQDLICRFSSQEEVSLSHVRPEDCEKGGGLKNI NLIIIITFILVSAILLTTLAACCCVRRQKFNQQ YKA
808	2158	A	6619	153	1852	FKALSQYIYTNTHLEREAFAFEVAILLRMEEG ARHRNNTTEKKHPGGGESDASPEAGSGGGGV ALKKEIGLVSACGIIVGNIGSGIFVSPKGVLEN AGSVGLALIVWVTGFTTVVGALCYAELGVNI PKSGGDYFYVKDIFGGLAGFLRLWIAVLVTYP TNQAVIALTFSNYVLQPLFTCFPPESGLRLLA AICLLLTWVNCSSVRWATRVQDIFTAGKLL ALALIIMGIVQICKGEYFWLEPKNAFENFQEP DIGLVALAFLQGSFAYGGWNFLNYVTEELV DPYKNLVPAIFISIPLVTFVYVFANV/ALYVT AMSPQELLASNAVAVTFGEKLLGVMAWIM PISVALSTFGGVNGSLFTSSRLFFAGAREGHLP SVLAMIHVKRCTPIPALFTCISTLLMLVTSD MYTLINYPVGFNYLFYGVTVAGQIVLRWKKP DIPRIKINLLFPITYLLFWAFLLVFSLWSEPVV CGIGLAIMLTGVPVYFLGVYWQHKPKCFSDFI ELLTLVSQKMCVVVYFEVERGSGTEANED MEEQQQPMYQPTPTIKDKDVAGQPQ
809	2159	A	6621	1041	223	QDSRKMLPSTSVNSLVQNGVLSNRDAAARH TAGAKRYKYLRRLFRFRQMDFEFAAWQMLY LFTSPQRVYRNPHYRKQTKDQWARDPAFL VLLSIWL CVSTIGFGFVLDMGFFETIKLLWV VLIDCVGVGLLIATLMWFISNKYL VKRQSRD YDVEWGYAFDVHLNAFYPLLVLHFIQLFHN HVILTDITFIGYLVGNLWLVAVGYTYVTF GYSVGLLFFSALPFLKNTVILLYPAPLILLYG LSLALGWNFTHTLCSFYKYRVK
810	2160	A	6623	160	822	SPASGHCRLNGAAVAMFGCLVAGRLVQTA QQVAEDKFVFDLPDYESINHVVFMLGTTPFP EGMGGSVYFSYPDSNGMPVWQLLGFVTNGK PSAIFKISGLKSGEGSQHPFGAMNIVRTPSVAQ IGISVELLDMAQQTPVGNAAVSSVDSFTQFT QKMLDNFYNFASSFAVSQ/VPDDTQ/RPSEMF IPANVVLK WYENFQRRTSTEPSLLENITWIKIN F
811	2161	A	6627	18	3367	LEGSINTERAKYYLTITIMPHFTVTKVEDPEEG AAASISQEP SLADIKARIQDSDEPDLSQNSITG EHSQLDDGHKKARNAYLNNSNYEEGDEYF DKNLALFEEEMDTRPKVSSLLNRMANYNLT QGAKEHEEAENITEGKKKPTKTPQMGTFMG VYLPCLQNFVILFLRLTWVVGTAQVLQAF AIVLICCCCTMLTAJMSAIATNGVVPAGGSY FMISRALGPEFGGAVGLCFYLGTTFAAAMYIL GAIEIFLYIVPRAAIFHSDDALKESAAMLNN MRVYGTAFVLVLMVLVVFIVRVYVNFASLFL ACVIVSILAIYAGAIKSSFAPPHFVCM LGNRT LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNTVSIQIGIPGLASGIEN LWSNYLPKGEIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGLKD AQKSIPIGTILAILTTSFVYLSNVVLFACIEGV VL RDKFGDAVKGNLVVGTLSWPSFWVTVIGS FFSTCGAGLQSLTGAPRLQAIAKDNIPFLRV

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						FGHSKANGEPTWALLLTAAIAELGILIASLDL VAPILSMFFLMCYLFVNLACALQTLRLTPNW RPRFRYYHWALSFMGMSICLALMFISSWYYA IVAMVIAGMIYKYIEYQGAKEWGDGIRGLS LSAARFALLRLEOPPHTKNWRPQLVLLKL DEDLHVXHPRLITFASQLKAGKGLTIVGSVIV GNFLENYGEALAAEQTIKHLMEAEKVKGFCQ LVVAAKLREGISHLIQSCGLGGMKHNTVVM GWPNGWROSEDARA WKTFIGTVRVTTAAHL ALLVAKNISFFPSNVEQFSEGNIDVWVWHDG GMLMLLPFLKQHKVWRKCSIRFFTVQLE DNSIQMKKDLATFLYHLRIEAEVEVEMHDS DISAYTYERTLMMEQRSQMLRHMRLSKTER DREAQLVKDRNSMLRLTSIGSDEDEETETYQ EKVHMTWTKDKYMASRGQKAKSMEGFQDL LNMRPDQSNVRRMHTAVKLENTVVKNSHEA KLVLNMPGPFRNPEGDENYMEFLEVLTEGL ERVLLVRGGGSEVITYS
812	2162	A	6628	66	640	AVCTMSEMAELSEL YEESDQLQMDVMPGEG DLPQMEVSGSGRELRLPSRSGAQQLEEGP MEEEEEAPMAAPEGKRSLANGPNAGEQPGQ VAGADFESEDEGEFDDWEDDYDYPEEQLS GAGYRVSAALEEADKMFLRTREPALDGGFQ MHYEKTFFDQLAFIEELFSLMVNRLTEELG CDEIIDRE
813	2163	A	6630	708	1355	AKMGAYKYIQELWRKKQSDVMRFLLRVC WQYRQLSALHRAPRPTRPDKARRLG YKAKQ GYVYIYIGVFVAVIYRIRVRRGGRKRPVPG ATYGKPVHGVNQLKFARSLQSVAEERAGR HCGALRVLNSYVWGEDSTYKFFEVLIDPFHK AIRRNPDQTWITKPVHKKHREMRGLTSAGRKS RGLGKGHKFHHTIGGSRRAAWRRRNLTQLH RYR
814	2164	A	6635	201	1705	KGTEMNKSRLWQSRRRHGRSHQONPWFLRL DSEDRSDSRAAQAHDSDGHGDDSPSTSSGT AGTSSVPPELPGFYFDPEKKRYFRLLPGHNNCN PLTKESIRQKEMESKRLRLQEEDRRKKIARM GFNASSMLRKSQGLFNVNTNYCHLAHELRLS CMERKKVQIRSMPSALASDRFNILADTNS DRLFTVNDVTVGGSKYGINLQSLKTPTLKV MHENLYFTNRKVNSVCWASLNHLDSSHLLC LMGLAETPGCATLLPASLFVNSHPAGIDRPG MLCSFRIPGAWSCAWSLNIQANNCFTGLSR RVLLTNVVTGHRQSFQNSDVLAAQFALMA PLFNGCRSGEIFAIDLRCGNQKGWKATRLF HDSAVTSVRILQDEQYLMASDMAGKIKLWD LRTTKCVRYEGHVNEYAYLPLHVHEEEGIL VAVGQDCYTRIWSLHDARLLRTIPSPYPASKA DIPSVAFSSRLGSGRGAPGLLMAVGQDLYCY SYS
815	2165	A	6643	659	3282	NKNILEVPSARTTRIMGDHLDLLGVVLMAG PVFGIPSCSFDGRIAFYRNCNLTPVQVLNTE RLLLSFNYYRTVTASSFPFLEQLQLELGSQYT PLTIDKEAFRNLNLRILDGSSKIYFLHPDAF QGLFHLFELRLYFCGLSDAVLKDGYFRNLKA LTRLDSLKNQIRSLYLHPSFGKLSLSKIDFSS NQIFLVCEHELEPLQGKTLFFSLAANSLYSR VSVDWGKCMNPFRRNMVLEILDVSGNGWTV DITGNFNSAISKSAFSLILAHHIMGAGFGFHN IKDPDQNTFAGLARSSVRHLDLSHGFFVSLNS

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						RVFETLKDLKVLNLA YNKINKIADEAFYGLD NLQVLNLSYNLLGELYSSNFYGLPKVAYIDL QKNHIAIQDQTFKLEKLQTLDLRDNALTTIH FIPSIFDIPLSGNKLVTLPKINLTANLIHLENR LENLDILYFLLRVPHLQILINQNRFSSCSGDQ TPSENPSLEQLFLGENMLQLAWETELCWDVF EGLSHLQVLVYNHNYLNSLPPGVFSLTALR GLSLNSNRLTVLSHNDLPANLEILDISRNLQ APNPDVFSVLSVLDITHNKFICECELSTFINWL NHTNVTIAGPPADIYCVYPSLSGVSLFSLSTE GCDEEEVLKSLKFSLFVCTVTLTFLMTLTV TKFRGFCFICYKTAQRLVFKDHPQGTEDMY KYDAYLCFSSKDFTWVQNALLKHLDTQYSD QNRFNLCFEERDFVGENRPAIQDAIWNRSR KIVCLVSRHFLRDGWCLEAFSYAQGRCLSDL NSALIMVVVGSLSQYQLMKHQSIQGFVQKQQ YLRWPEDLDQVGVFHLKLSQQLKKEKEKK KDNNIPLQTVATIS
816	2166	A	6646	1	3811	RDRAGVRPAGKQHAAAAYFDVGGDRPWDS GNTQLPPRPVVKANAMFGAGDEDDTDFLSPS GGARLASLFLGDQAAAGHGEFFQYTAPKQP KKGQGTAAATGNQATPKTAPATMSTPTILVAT AVHAYRYTNGQYVKQKFGAAVLGNHTTR EYRILLYISQQPVTVARIHVNFELMVRPNY STFYDDQRQNW SIMFESEKAAVEFNKQVCIA KCNSTSSLDVLSQDLIVADGPAVEVGDLSLE VAYTGWLFQNHVLGQVFDSTANKDKLLRLK LGSQKVIKGWEDGMLGMKKGKRLILVPPA CAV GSEG VIGWTQATDSLVEFEVRRVKIA KDSGSDGHSVSSRDSAAPSPIGADNLSADPV VSPPTSIFFKSGEPALRTKSNLSSEQLAINTSPD AVKAKLISRMAMKMGQPMPLPILPPQLDSNDSEI EDVNTLQGGGQPVVTPSVQPSLQPAHPALPQ MTSQAPQPSVTGLQAPSAALMQVSSLD SHSA VSGNAQSFQPYAGMQAYAYPQASAVTSQLQ PVRPLYPAPLSQPPHFQSGDMSFLMTEAR QHNTIRMAVSKVADKMDHMLTKVEELQKH SAGNSMLIPSMVMTSMIMSNIRIQENER LKQEILEKSNRIEQNDKISELIERNQRYVEQS NLMMEKRNNSLQTATENTQARVLHAEQEKA KVTEELAAATAQVSHLQLKMTAHQKKETEL QMQLTESLKETDLLRGQLTKVQAKLSELQET SEQAQSKFKSEKQNRKQLELKVTSLEELTDL RVEKESLEKNLSERKKKSAQERSQAEEIDEI RKSQYQELDKLRQLLKKTRVSTDQAAAEQLS LVQAELQQTWEAKCEHLLASAKDEHLQYQ EVCAQRDAYQQLVQLQEKSVCFACLALQA QITALTQNEQHKELEKNKSQMSGVEAAAS DPSEKVKKIMNQVFQSLRREFELEESYNGRTI LGTIMNTIKMVTLLQNNQEQEKEESSSEEEE EKAEEPRRPSQEQSASASSGQPQAPLNRERP ESPMVPSEQVVEEAVPLPPQALTTSDGHRR KGDSEAEALSEIKDGSLLPELSCPSHRVLGPP TSIPPEPLGPVSMDSCEESLAASPMMAKVPDN PSGKVCVREVAPDGPLQESSTRLSLTSVPEE GDPLALGPESPGEPQPPQLKDDVTSSTGPHK ELSSTEAGSTVAGAALRPSHHSQRSSLSGDEE DELFGATLKALRPKAQFEEDDEDEVSMKGR PPPTPLFGDDDDDDDDWLG
817	2167	A	6649	63	1073	FFRSSDNGSPIRQYE/HSTPAHQGPVMSGLEG

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						KS/ARNSQLRIVLVGKTGAGKSATGNSILGRK VFHSGIAAKSITKKCEKRSSSWKETELVVVD TPGIFDTEVPNAETSKEIIRCILLTSPGPHALLL VVPLGRYTEEEHKA TEKILKMFGERARSMIL IFTRKDDLGDNLHDYLRAPEDIQDLMDIFG DRYCALNNKATGAEEQAQRAQLGLIQRVV RENKEGCYTNRMVQRAEEIEQKQTQAMQEL HRVELEREKARIREEYEEKIRKLEDKVEQEK KKQMEKKLAEQEAHYAVRQQRARTEVESKD GILELMTALQIASFILLRLFAED
818	2168	A	6660	357	1890	APSGSWTRVVLTLDPCLSRSPRSLDPGMP GISARGLSHEGRKQLAVNLTRVLALYRSILDA YIEFFITDNLWDTLPCSWQEAALDGLKPPQLA TMLLGMPGEGEVVRYRSVWPLTLLALKSTA CALAFTRMPGFQTPSEFLENPSQSSRLTAPFR KHVRPKQHEIRLOELVKKLSDFTLGLHPCG RRGLRPGVHLSRFMA LGLMLVKSIEGDQRL VERAQRLLQELLQALEKEEKNPQVVQTSR HSPHHVVRWVDPALCELLLPLENPCQGRA RLLLTGLHACGDL SVALLRHFSCCEPVVALA SVGCCYMKLSDPGGYPLSQWVAGLPGYELP YRLREGACHALEEY AERLQKAGPLRTHCY RAALETVIRRAPELRRPGVQGIPRVHELKIEE YVQRLQVRGLDPQLPLNLAALQAHLAQEN RVVAFFSLALLAPLVETLILLDRLLYLQEQA LSPAGFHAELLPISPELSPRNLVLVATKMLPLG QALSVLETDS
819	2169	A	6661	65	2686	SGSGHCLAEASMGPGWGWKLRTVALLLA AAGTAVGDR CERNEFQQDGKCSYKWVCD GSAECQDGSDESQETCLSVTCKSGDFSCGGR VNRCPQFWRCDDGQVDCDNGSDEQGCPPKTC SQDEFRC HDGKCISRQFVCDSDRCDLGSDE ASCPVLTGCPASFCNSSTCIPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEH CLSGECIHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCS DGNCHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTC SQLCVNLEGGYKQCCEGFQLDPH TKACKAVGSIAYLFFTNREVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDL SQRM CSTQLDRAHGVSSYDTVISRDIAQPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVDPVHGFMWTDWGTPAKIK KGQLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWDIINEAIFSANRLTGSDV NLLAENLLSPEDMVL FHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARNDMRSCLT EGAAVATQETSTVRLKVS STAVRTQHTTTRPVDPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGMEKKPSSVRALSIVL PIVLLVFLCLGVFLWKNNWRLKNINSINFNDP VYQKTTEDEVHICHNQDGYSPSRQMVSLIED DVA
820	2170	A	6666	17	4146	ERGISSQIKGMKSGSGGSPTSLSWGLLFLSAA LSLWPTS GEICGPGIDIRNDYQQLKRLNCTVI EGYLHILLISKAEDYRSYRFPKLT VITEYLLLF RVAGLES LGDLFPNLTVIRGWKLFYNYALVIF

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						EMTNLKDIGLYNLRNITRGVAIRIEKNADLCYL STVDWSLILDAVSNNYIVGNKPPKECGDLCP GTMECKPMCEKTTINNEYNYRCWTTNRCQK MCPSTCGKRACTENNECCHPECLGSCSAPDN DTACVACRHYYYAGVCVPACPPNTYRFEGW RCVDRDFCANILSAESSDSEGFVIHDGECMQE CPSGFIRNGSQSMYCIPCEGPCPKVCEEKKT KTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIA SELENFMGLEVVVTGYVKIRHSHALVLSFLK NLRLLGEEQLEGNYSFYVLDNQNLQQLWD WDHRNLTIKAGKMYFAFNPKLCVSEIYRMEE VTGTRKGRQSKGDINTRNNGERASCESDVLHF TSTITSKNRIITWHRYPFDYRDLISFTVYK EAPFKNVTEYDQDAGCSNSWNMVDVLDLP NKDVPEPGILLHGLKPWTQYAVYVKAULTM VENDHIRGAKSEILYIRTNASVPSIPDLVLSAS NSSSQLIVKWNPPSLPNGNLSYYTVRWQRQ QDGYLYRHNYCSKDKIPRKYADGTIDIEEVT ENPKTEVCGGEKGPCCACPKTEAEKQAEKEE AEYRKVFENFLHNSIFVPRPERKRDVMOVA NTTMSSRSRNTTAADTYNITDPEELETEYPPF ESRVDNKERTVISNLRPFITYRIDIHSCNHEAE KLGCSASNFFARTMPAEGADDIPGVTWEP RPENSJFLKWPEPENPNGLILMYEIKYGSQVE DQRECVSRQYRKYGGAKLNRNLPNGYTARI QATSLSGNGSWTDPVFFYVQAKRYENFIHLI ALPVAVLLIVGGLVIMLYVFHRRKNNRSLGN GVLVASVNPEYFSAADVVPDEWEVAREKIT MSRELQGSGFGMVYEGVAKGVVKDEPETRV AIKTVNEAASMRERIEFLNEASVMKEFNCHH VVRLLGVSQGPFTL VIMELMTRGDLKSYLR SLRPEMENNPFVLAPPSLSKMIQMAGELADGM AYLNANKFVHRDLAARNCMVAEDFTVKIGD FGMTRDIYETDYRKGKGLLPVRWMSPEL KDGVFITYSDVWSFGVVLWEIATLAEQPYQ GLSNEQVLRVFMEGGLDKPDNCPDMLFEL MRMCWQYNPKMRPSFLEIISIKEMEPEGFRE VSFYSEENKLPEPELDLEPENMESVPLDPS ASSSLPLPDRHSGHKAENGP GPVGLVLRASF DERQPYAHMNGGRKNERALPLPQSTC
821	2171	A	6691	106	825	GRVLFRCGVGHKGQVLMGTFLAQDWLSE SNHVFCVSSMLRLQKRLASSVLRCKKKVW LDPNETNEIANANSRQIRKLIKDLIRKPV VHSRARCCKNTLARRKGRHMGIGKRKG TAN ARMPEKVTWMRRMRILRRLRRYRES/KRYR ESKKIDRHMYHSLYLKVKGNVFNKRLMEH IHKLKADKARKKLLADQAEARRSKTKEARK RREERLQAKKEEIKTLSKEETKK
822	2172	A	6715	772	21	DFRPGLLLPKCKKMFHFHFKPKMYRSIEGCVCI SGAKSSSRFTDSKRYEK\DFQ\SCFGLHETR\ SGD\CNACVLLALKRWKLPAGSKKNWNH VVDARAGPSLKTTLPKKVKTL\SGNRIK\ST QISKLQKEFKR\HNSDAHSTTSASPAQSPLF TVNQFRWTGSDTGVGFPGSNRNHPVFSFLDL\ TYWKRQKICCGNYKGRFGEVLDTLHFKPCC SNKKA\AAEKPEEQPEPLPISTQEWVTEVFM
823	2173	A	6727	3	4063	PYLATLQLDSSLLIPPKYQTPPAAAQGGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSASAPGISQISTSSSGFSGS VGGQNPSTGGISADRTQGNIGCGGDTDPGQS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSQPSQDQGESNVPSVGSADPDYLNTPQMN TPVTLSAAPASNSGAGVLPSPATPRFSVPTP RTRTPRTPRGGGTASGQGSVKYDSTDQGS ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLL SDSVMNIFKDRNFDSCCICACNMNIKADVG LYIPDSSNEDQYRCTCGFSAIMNRKLGYNSSL FLEDELDFGKNSDIGQAAERLLMMQCSFTL PQVEGTTKPKQEPPIISLLLLLQNHQTPFASLN FLDYISSNNRQTLPCVSWSYDRVQADNNDY WTECFNALEQGRQYVDNPTGGKVDEALVRS ATVHSWPHSNVLDISMLSSQDVVRMLLSLQ FLQDAIQKKRTGRTWENIQHVQGPLTWQQFH KMAGRGTYGSEESPEPLPIPTLLVGYDKDFLT ISFFSLPFWERLLDPYGGHRDVAYIVVCPEN EALLEGAKTFFRDLA VYEMCRLGQHKPICK VLRDGMRVGKTVAQKLTDEL VSEWFNQPW SGEENDNHSRLKLYAQVCRHHLAPYLATLQL DSSLLIPFKYQTPPAAAQGGATPGNAGPLAPN GSAAPPAGSAFNPTSNSSSTNPAASSASGSSV PPVSSASAPGISQISTTSSSGFSVGGQNPST GGISADRTQGNIGCGGDTDPGQSSSQPSQDG QESVTERERIGIPTSDSADSHAPPAVVIYM VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD NLFEHMRNSFILQIVPCQYMLQTMKDEQVFI IQYLKSMASFVYQCRRPLPTQIHKSLTGFGP AASIEMTLKNPERPSPIQLYSPFFILAPIKDKQT ELGETTGEASQKYNVLFVGYCLSHDQRWLL ASCTDLHGELLETCVVNIALPNRSRRSKVSAR KIGLQKLWEWCIGIVQMTSLPWRVVIQRLGR LGHGELKDWISILLGECSLQTSKLLKDVCRM CGISAADSPSILSACL VAMEPQGSFVMPDAV TMGSVFGSTALNMQSSQLNTPQDASCTHIL VFPTSTIQVAPANYPNEDGFSNNDDMFVDL PFPDDMDNDIGILMTGNLHSSPNSSVPSPGSP SGIGVGSFHQHSRSQGERLLSREAPEELKQPF LALGYFVSTAKAENLPQWFWSSCPQAQNOQC PLFLKASLHHHISVAQTDELLPARNRQVRPH LDSKTTSDVLRVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTLQYNAMNLL
824	2174	A	6732	2440	365	VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPSSAAAFSSHRHNLCSRRRGGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVVKLRLLKKGRSVDVADNRG WMPITHEAAYHNSVECLQMLINADSSNYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPFLAVENGQIDVLRLLLOHGAN VNGSHSMCGWNSLHQASFQENAEIKLLLRK GANKECQDDFGITPLFVAAQYGKLESLSILIS SGIANVNCQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACL VFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIEFVNHAKAQA KYKEWLPHELLVAGFDPLILLCNSWIDSVSIDT LIFTLEFTNWKTLAPAVERMLSARASNAWIL QQHIATVPSLTHLCRLEIRSSLKSERLRSDSYSIS

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						QLPLPRSLHNYLLYEDVLRMYEVP ELAAIQD G
825	2175	A	6735	277	1252	RIMGLPDRGVQMLLTTVGAFAAFSLMTI AVG TDYWL YSRGVCKTKSVSENETSKKNEEVM T HSGLWRTCCLEGNFKGLCKQIDHFPEDADYE ADTAEYFLRAVRASSIFPILSVLLFMGGCLIA ASEFYKTRHNILSAGIFFVSAGLSNIIGIIVYIS ANAGDPSKSDSKNSYSYGSFYGALSFIIA EMVGVLA VHMFD RHKQLRATARAVTDYLQ ASAITRIPSYRYRQRRSRSSRSTEPSHSRDA SPVGKGFNTLPSTEISMYTL SRDPLKAATTPT ATYN SDRDNSFLQVHNCIQKENKDSLHSNTA NRRITPV
826	2176	A	6744	3	5177	SDDLRTGLFQDVQDAESLKLPGVYEVLFYNE TEDCPGMMLWRYPEPRGLTLVRITPVFNTT EDFDISTADLGDVLQDPCSL EYWDELQKV FV AFREFNLSKVC ELQLPDNL VNDQKKLVSS DLWRIVLNSSQNGADDQSSASESGSQSTCDPL VPTALAACTRVDSCTFPWFVPSLCVSFQFAH LEFHLCHHLDQLGTAAPQYLQPFVSDRNMPS ELEYMIVSFREPHMYLRQWNNGSVCQEIOFL AQADCKLLECRNVTMQSVVKPF SIFGQMAVS SDVVEKLLDCTVIVDSVFVNLGQHVVHSLNT AIQAWQONKCPEVEELVFSHFVICNDTQETL RFGQVDTDENILLASLHSHQYSWRSHKSPQL LHICIEGWNWRWSEPPSVDHAGTFIRTIQYR GRTASLHKVQQLNGVQKQIICGRQIHC SYLSQ SIELKVQHYIGDQGQAVVREHFDCLTAKQK LPSYILENNELTELCVKAKGDEDWSRDVCLE SKAPEYSIVIQVPSSNSSIYVWCTVLTLEPNS QVQQRMI VFSPLFIMRSHLPDPIMHLEKRSGL SETIIPGKGQEKPLQNI EPDL VHHLTFQAREE YDPSDCAVPISTSLIKQIATKVHPGGTVNQILD EFGYGPESLQPIWFPYNNKSDRNEQLSQWDS PMRVKLSIWKPYPVRTLLIELLPWALLINESKW DLWLFEGEKIVLQVPAGKIIIPNFQEAFIGIY WANTNTVHKSVAILVHNLTPKWKDGGNG EVVTLDEEAFVDTEIRLGAFPGHQKLCQCIS SMVQQGIQIQIEDKTTIINNTPYQIFYKPQLSV CNPHSGKEYFRVPDSATFSICPGGEQPA MKSS SLPCWDLMPDISQSVDASLLQKQIMLGSPA PGADSSQCWSLPAIVRPEFPRQSVAVPLGNFR ENGFCTRAJVLTYQELGVTYLTLEDSPRV IHNRCFVKMLIKENIKDIPKFEVYCKKIPSECS IHHELHYHQISSYPDCKTKDLLPSLLLRVEPLDE VTEWSDAIDINSQGTQVVFLTGFYVYVDV VHQC GTVFITVAPEGKAGPILTNINRAPEKIV TF/KMFIITQLSLAVFDDLTHHKASAE LLRTL DNIFLCVAPGAGPLPGEEPVAALFELYCVEIC CGDLQLDNQLYNKS NFHFAVLVCQGEKAEPI QCSKMQSL LISNKELEYKEKCFIKLCITLNEG KSILCDINEFSFELKPARLYVEDTFVYIKTLF DTYLPNSRLAGHSTHLSGGKQVLPQMVTQH ARALVNPVKLRKLVIQPVNLLVSIHASL KLYI ASDHTPLSFSVFERGPIFTARQLVHALAMHY AAGALFRAGWVVGSLDILGSPASLVRSIGNG VADFFRLPYEGLTRPGAFVSGVSRGTTSFVK HISKGTLTSITNLATSLARNMDRLSLDEHYN RQEEWRRQLPESLGEGLRQQLSRLGISLLGAI AGIVDQPMQNFQKTSEAQASAGHKAKGVISG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VGKGMGVFTKPIGGAAELVSQTGYGILHGA GLSQLPKQRHQPSDAVHADQAPNSHVKYVW KMLQSLGRPEVHMALEDVVLVRSGQEHEGC LLLTSEVLFFVSVSEDTQQQAFPVTEIDCAQD SKQNNLLTVQLKQPRVACDVEVDGVRERLSE QQYNRLVDYITKTSCHLAPSCSSMQIPCPVVA AEPFPSTVKTYHYLVDPHFAQVFLSKFTMVK NKALRKGF
827	2177	A	6748	2	1662	FVGAPRRGNPFGSPGNPGRHQGPCCHRPRGK ASGVSPILWRPQAAATGLEMPSSGRALLDSP LDSGLTSLDSSVFCSEGEPLALGDCFTVN VGGSRFVLSQQALSCFPHTRLGKLAVVVAS RRPGALAAVPSPLELCDDANPVDNEYFFDRS SQAFRYVLYHYRTGRHLVMEQLCALSFQEI QYWGIDELSIDSCCRDRYFRRELSETLDFKK DTEDESQHESEQDFSQGPCPTVRQKLWNIL EKPGSSTAARIFGVISIFVGVSIINMALMSAEL SWLDLQLEILEYVCISWFTGEFVLRFLCVRD RCRFLRKVPNIIDLLAILPFYITLLVESLSGSQT TQELAVNGAHCPGCLRLRLALRMLKAWGR HSTGLRSLGMTITQCYEEVGLLLFLSVGISIF STVEYFAEQSIDTITFTSVPCAWWWATTSM TVGYGDIRPDITTKIVAFMCLSGILVLALPI AIINDRFSACYFTLKLKEAAVRQREALKKLTK NIATDSYISVNLRDVYARSIMEMRLKGRER ASTRSSGGDDFWF
828	2178	A	6786	5672	1360	GTHPASSGPVPLPPAAVSAATREELGEPVPFV TASSGFQSMHSSNPKVRSSPSGNTQSSFKSKQ EVMVRPPTVMSPSGNPQLDSKFSNQKQGG ASQSQSPCDKSGGHTPKALPGPGGSMGLK NGAGNGAKGKGKRRERSISADSFDQRDPGTFN DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS TEMANKAAEA VLKQGQVETIVSFHQNISNNK TERSTAPLNTQISALRNDPKPLPQPPAPANQ DQNSSQNTRLQPTPIPAAPKPAAPPRPLDRE SPGVENKLIPSVGSPASSTPLPDGTGPNSTPN NRAVTPVSQGSNSSADPKAPPPPVSSGEPT LGENPDGLSQEQLEHRERLQTLRDIQRMFLP DEKEFTGAQSGGPQNPGLDGPQKPEGPI QAMMAQSQSLGKGPGRDVGAPFGPGGHR DVFPSPDEMVPSPMNSQSGTIGPDHLDHMT EQIAWLKLQOEFYEEKRRKPEQVVVQCSLQ DMMVHQHGRGVVRGPPPPYQMTPEGWAP GGTEPFSQDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVNPASRPGLSGV SWPDDVPKIPDGRNFPQGGIFSGPGRGERFP NPQGLSEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSRHMEPGNNPIFRIPVEGP LSPSRGDFPKGIPPMGPGRELEFGMVPSGM KGDVNLNVNMGNSQMPQKMRAGAGFEE MLKLPGGSDMLPAQKQMVPLPFGHEHPQE YGMGPRPFLPMSQPGSNGSLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSFTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPVGLSAAASFVHLKSPSLPAPSPGWTS PEPPLQSPGIPNHKAPLTMASPA MLGNVESG GPPPTASQPASVNIPGSLPSSTPYTMTPEPTL SQNFLSIMMSRUMSKFAMPSNPGYNHDAI

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						KTVASSDDDDSPFARSPNLPSPMNNMPGMGINT QNPRISGPNPVVPMPTLSPMGMTQPLSHSNQ MPSPNAVGPNIHPHGVPMPGGLMSHNPIMGH GSQEPFMVPQGRMGFPQGFPVQSPQVFPF HNGPSGGQGSFPGMGFPGEGLGRPSNLPQ SSADAALCKPGGPGGDSFTVLGNSMPSVFT DPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ YFPRGEVPGRKQPGGPGFSHMQQMMGEQ APRMGLALPGMGPGVPVGTDPDPLGTAPSM GHNPMRPPAFLQQGMMGPHIRMMSPAQST MPGQPTLMSNPAAAVGMIPGKDRGPAGLYT HPGPVGSPPGMMMSMQGMMGPNRTS
829	2179	A	6797	433	3	ASFFNFSICICKIILEVGPVGHFAHDDVGGRRH GPGGR/GSRSPRSLQCAPGGRRSGCAGSSP ASTCPPSPGGSGADRFGPSPPPSREAAPTAG AAASSTSSGASCPPVPASSRWGVRSTRSGSG GEREPRDRPSEPRLV
830	2180	A	6800	3	1911	LPERAFGPRITPRAPRRRRRLLSPPRPPPL DREPRAPGPWLCPSRAGTAQDPARIRERRGR VAGGAAGPAMELRARGWWLLCAAAALVAC ARGDPASKSRSCGEVRQIYGAKGFSSSDVPQ AEISGEHLRJCQGYTCCTSEMEENLANRSHA ELETALRDSRVLQAMLATQLRSFDDHFQHL LNDSERTLQATFPAGFELYQNAARFDLY SELRLYYRGANLHLEETLAEFWARLLERLFK QLHPQLLLPDDYLDCLGKQAEALRPFGEAP RELRLRATRAVFAARISFVQGLGVAASDVVR KVAQVPLQPECASRAVIEAGSYC/ALHCVGVP GARPCPDYCRNVKGLANQADLDAEWRNL LDSMVLITDKFWGTSGVESVIGSVHTWLAEA INALQDNRLITLAKVIQGCGRPKVNPQGP EEKRRRGKLAFRERPPSGTLEKLVSEAKAQL RDYQDFWISLPGTLCSEKMASTASDDRCWN GMARGRYLPEVMGDGLANQINNPEVEVDIT KPDMTIRQQIMQLKIMTNRLRSAYNGNDVDF QDASDDGSGSGSGDGLDCLCGRKVSRKSS SRTPLTHALPGLSEQEQKTSAASCPQPTFL LPLLLFLALTVARPRWR
831	2181	A	6808	2	1522	ASRHGMPGALLMLLGLGPPLAPGVRGSEA EGRLREKLFSGYDSSVRPAREVGDRVRVSVG LILAQLISLNEKDEEMSTKVYLDLEWTDYRLS WDPAEHDGIDSLRITAESVWLPDVLLNNND GNFDVALDISVVSSDGSVRWQPPGIYRSSCS IQVTYFPFDWQNCMTMFSSYSYDSSEVSLQ GLGPDGQGHQEIHIHEGTIENGQWENIHKPS RLIQPPGDPREGREGQREVFYLIIRKPLFY LVNVIAPCILITLLAIFVFYLPFDAGEKMGSLF ALLTLTVFLLLLADKVPETSLSVPIIKYLMFT MYLVTFVSVLVVVLNLHHRSPHTHQMPWV RQIFIHKLPLYRLKRPKPERDLMPEPPHCSSP SGWGRTDEYFIRKPPSDFLFPKPNRFQPEL SAPDLRRFIDGPNRAVALLPELREVSSISYIA RQLQEEDHDALKEDWQFVAMVVDRLFLW TFIIFTSVGTLVIFLDATYHLPPDPFP
832	2182	A	6824	71	1079	ETMAKNPENCEDCHILNAEAFKSKICKSLK ICGLVFGILALTLVLFWGSKHFWPEVFKKAY DMEHTFYSNGEKKKIYMEIDPVIRTEIFRSGN GTDETLVHDFKNGYTGIFVGLQKCFIKTQI KVIPEFSEPEEIDENEIITTFEQSVIWWPAE KPIENRDLKNSKILEICDNVTMYWINPTLUS

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						GTPAKQLHHNFAPILVSELDQFEEEGEDLHFP ANFKKGHEQNFQWVVPQVKVEKTRHARQAS EEELPINDY TENGIEFDPM LDERGYCCYICRR GNRYCRRVCEPLLGYYPYPYCYQGGRVICRV IMPCNWWVARMLGRV
833	2183	A	6846	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGP GVMESEKEERALNNLIVENVNQENDEKDEKE QVANKGEPLALPLNVSEYCVPRGNRRRFRVR QPILQYRWDIMHRLGEPQARMREENMERIGE EVRQLMEKLREKQLSHSLRAVSTDPPHHDHH DEFCLMP
834	2184	A	6851	3	2024	PNGVALLHLPAAVIPNTNMFQDALGGRSR GSREESPAPSRAPASASLWRRLLVVVEAKMAA HAAAAAQA AAAQAHA EAADSWY LALLGF AEHFRTSSPPKIRLCVHCLQA VFFFKPPQRIEA RTHLQLGSLVYHHTKNSEQARSHLEKAWLIS QQIPQFEDVKFEASLLSELYCQENSVDAAKP LLRKAIQISQQTPLYWHCRLLFQLAQLHTLEKD LVSACDLLGVGA EYARVVGSEYTRALFLLSK GMLLLMERKLQEVHPLLTCGQIVENWQGN PIQKESLRVFFLV LQVTHYLDAGQVKS VKPC LKQLQCCIQTISTLHDEILPSNPADLFHWLP KEHMCVLVYLVTVMHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPILSSFQVILLETIM CRLVTGHKATALQEISQVCQLCQSQSPRLFSN HAAQLHTLLGLYCVSVNCDNAEAQFTTAL RLTNHQELWAFVTNLASVYIREGNRHQEVVA LYSLLERINPDHSFPVSSHCLRAA AFVVRGLF SFFQGRYNEAKRFLRETLMKMSNAEDLNRLTA CSLVLLGHIFYVLGNHRESNNMVVPAMQLAS KIPDMSVQLWSSALLRDLN KACGNAMDAHE AAQMHQNFSSQQLLDHIEACSLPEHNLTWT DGPPPPVQFAQNGPNTSLASLL
835	2185	A	6855	334	1268	PTRRPILPTSPKAISVPSPLQGGKHTLVKSCL SVSGIGGFLVSLSSRMKLQTLAVSVTALKFWS AYVPCQTQDRDALRLTLEQIDLIRRMCA SYSE LELVTSAKALNDTQKLACLIGVEGGHSLDNS LSILRTFYMLGVRYLTLTHTCNTPWAESSAK GVHSFYNNISGLTDFGEKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAPVIFSHSAARGV CNSARNVPDDILQLEERWAFVMVSLFHGE LIQWQPIRPMCSTVADHFDHIKAVUGSKFIGI GGDYDGAGKYRKKTTCKAPWRTSSRMSS
836	2186	A	6862	315	11	PPRSRPSWCRRKVGPRPWWGGTGPPGQG RPEIRLLPLMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSOLANGLAGNPAGHLGLGSSFGT GPGSGRFPF
837	2187	A	6863	2	1615	VLRGQRGPAGGLAEERRRRGRNEWRIHDVTT APFFGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEIIVKLLLSHGANNV AKDNELWTPHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADHICMIAAQ DLDWIDAQAATLLHIAGANGYLRAAELLDDH GVRVDVKDWDGWEPLHAAAFWGQMMAE LLVSHGANLNARTSMDEMPIDLC EEEEFKVL LLELKHKHDVIMKSQLRHKSSLSRRTSRQA S/SVGVVRRTPQVGTGPNLYRKEYE/GEEAI LWQRSAVAEDQRTSTYNGDIRETRTDQENKD

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						PNPRLEKVPVLLSEFPKIPRGELDMPVENGLR APVSAYQYALANGDVWVKVHEVPDYSMAYG NPGVADATPPWSSYKEQSPQTLLELKRQRAA AKLLSHFPLSTHLGSSMARTGESSEKAPLI GGRTSPYSSNGTSVYYTVTSGDPPLLKFKAPI EEMEELVHGCCRIS
838	2188	A	6865	6291	739	AGPLEPRVQAMALQLWALTLLGLLGAGAS LRPRKLDFFRSEKELNHLAVDEASGVVYLGA VNALYQLDAKLQLEQQVATGPVLDNKKCTP PIEASQCHEAEMTDNVNQLLVDPPRKRLVE CGQLLKGNALRALSNISLRLFYEDGSGEKS VASNDEGVATVGLVSSTGPGGDRVLFVKGK NGPHDNGIIVSTRLLDRTDSREAFAYTDHAT YKAGYLSTNTQQFVAAFEDGPYVFFVFNQQD KHPARNRTLLARMCREDPNYYSYLEMDLQC RDPDIHAAAFGTCLAAASVAAPGSGRVLYAVF SRDSRSSGGPGAGLCLFPLDEVHAKMEANRN ACYTGTREARDIFYKPFHGDICGCGHAPGSSK SFPCCGSEHLPYPLGSRDGLRGTAVLQRGGLN LTAVTVAAENNHVAFGLTSDGRILKVYLTP DGTSSSEYDSILVEINKRVKRDVLVSGDLGSLY AMTQDKVFRLPVQECLSYPTCTQCRDSQDPY CGWCVVEGRCTRKAECPRAEASHWLWSRS KSCVAVTSAQPNMSRRACQEVQLTVSPLPA LSEDELCLFGESPPHARVEGEAVICNSPSS IPVTTPGQDHVAVTIQLLLRRGNIFLTSYQYPF YDCRQAMSLEENLPCISCVSNRWTCQWDLR YHECREASPNPEDGIVRAHMEDESCPQLGSP LVIPMNHETDVNFQGNLDTVKGSSLHVGSD LLKFMEPVMTQESGTFARTPKLSHDANETL PLHLYVKS YGKNIDSKLHVTLYDCSFRSDC SLCRAANPDYRCAWCGGQSRVYEAALCNTT SECPPFVITRIQPETGPLGGGIRITLGSNLGVQ AGDIQRISVAGRNCSFQPERYSVSTRIVCIEA AETPFTGGVEVDVFGKLGRSPPNVQFTFQQP KPLSVEPQQGPQAGGTTLTHGTHLDTGSQED VRVTLNGVPCKVTKFQAQLQCVTFGPQATRG QMLLEVSYGGSPVNPFGIFTYRENVPVLAFF PLRSFASGGRSINVTGQGSFSLIQRFAMVIAEP LQSWQPPREAESLQPMTVVGTDYVFHNDTK VVFLSPAVPEEFAYNLTVLIEMDGHALLRT EAGAFEVVPDPTFENFTGGVKKQVKNLIRAR GTNLNKAMTLQEAFAFVGAERCTMKILTET DLYCEPPEVQPPKRRQKRDTHNLPEFIVKF GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM VVVIAVSVCYWRKSQAAREYKIKSLEG LEESVRDRCKEFTDLMIEMEDQTNVHEAG IPVLDYKTYTDRVFFLPSKDGDKDVMITGKL DIPEPRRPVVEQALYQFSNLLNSKSLINFIHT L'ENQPEFSARAKVYFASLLTVALHGKLEYT DIMHTLFLELLEQYVVAKNPKMLRRSETV ERMLSNWMSICLYQYLKDSAGEPLYKLFKAI KHQVEKGPVDAVQKKAKYTLNDTGLLGDD VEYAPLTVSVIVQDEGVDAIPVKVLNCDTISQ VKEKIDQYRGPQPCSWPRPDSVVLEWRPG STAQILSDLDTSQREGRWKRVTNLMHYNVR DGATLLSKVGVSSQPEDSQDLPGERHALL EEENRVVHLVRPTDEVDEGSKRGSVKEKE RTKAITEIYLRLLSVKGTLLQFVDNFFQSVL APGHAVPAPVKYFFDFLDEQAETHNIQDEDTI

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						HIWKTNSLPLRFVWNILKNPHFIFDVHVEVVDASLSVIAQTFMDACTRTEHKLSRDSPSNKLLEYAKEISTYKMKVEDYKGRQMVQVSDQDMNTHLAELISRAHITSLNLTVALHQLYQYTQKYDEIINAL EEDPAAQKMQLAFLRQLQIAAALENKVTDL
839	2189	A	6872	1	1485	RARRLALQCHVCVCALTPGEQSGRRPLPGQTWLMFSCFCFSLQDNSFSSTTVTECEDPVSLHEDQTDCCSLRDENNKENYDAGALVEEHAPPSWEPQQQNV EATVLVDSVLRPSMGNFKSRPKSIFKAESGRSHGESQETEHVSSQSECQVRAGTPAHESQNNAFKQETVRLAQPRIDQRTATSPKDAFETRQDLN EEEAAQVHG VKDPAPASTQSVLA\DGTD SADSPVHKDGGQNEADSAPEDLHSVGTSRLL\YHITDGDNPTAVRHGCSL/SGQSQRFNLD PESAPSPSTQQFMMPRSSRSCSGDGKEPQITITLTKHIQSLKRKRKFEEKFEQEKYRPSHGDKTSNPEVLKWMNDLAKGRKQLKELKLKLS EEQGSAPKGPPRNLLCEQPTVPRENGKPEAAGPEPSSSGEETPDAALTCLKERR EQLPPQEDSKVT KQDKNLKPL YDRYRIKQILSTPSLIPTTVSQDTCMLLLCTDV
840	2190	A	6873	2	2054	FFRFYFSFIRLFAMSLADLTCTNIDEHFFGVALENNRRSAACKRSPGTGDFSRNSNASNKSVDY SRSQCSCGSLSSQYDY SEDFLCDCSEKAINRN YLKQPVVKEKEKKKYNVSKISQSKGQKEISV EKKHTWNASLFNSQIHMAQRRDAMAHRLSARLHKIKGLKNELADMHHKLEALTENQFLKQLQLRHLKAIGKYENSQNNLPQIMAKHQNEVKNLROLRLRKSQEKERTLSRKLRETDQSLLKT KDILQALQKLS EDKNLAEREELTHKLSIITTKMDANDKKIQSLEKQLRLNCRASFRLAIETRKTLAAQTATKTLQVEVKHLQQLKEKDRELEIKNTYSHRILKNLHDTEDYPKVSSTKSVQADRKILPFTSMRHQGTQKSDVPP/TTKGKKGATGNIDHKEKSTEINHEIPHCVNKL PKQEDSKRKYEDLSGEEKHLEVQILLENTGRQDKKEDQEKKNIFVKEEQELPPKIEVIHFERESNQEDVLR EKFKRSMQRNGVDDTLGKGTA PYTKGPLRQRRHYSFTEATENLHHGLPASGGPANAGNMR YSHSTGKHLNREEMELEHSDSGYEPSFGKS SRIKVKDTTFRDKKSSLMEELFGSGYVLKTDQSSPGVAKGSEEP LQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII
841	2191	A	6874	3	2867	SSRTREMEEEKELRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSORAFSARYPRP SRRGYSSHGSPWRKKYSLVNRPPGPSDPFA DHAVRPLHGARGGQPPVQQHVLERQVQLS QGQNVVVKVPKPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEP PRGQLQPSRPTARAG TCSVEDPLLVCQKEPGKPRMVKSVGSGVDSP REPRRTVSES VIAVKASFSSALPRTGVALG RKLGSHSVASCAPQLLDGRRVDAGHTDQFPVPSGSGGPAPASGPRQAREASLVVTCRTNKF RKNNYKWWAASSKSPRVARRALSPRVAAEN VCKASAGMANKVEKPQLADPEPKPRKPATS SKPGSAPSKYKWKASSPSASSSSFRWQSEAG SKDHASQLSPVLSRSPSGDRPALAHSGLKPLS GETPLSA YKVKTRTKIIRRGSTSLPGDKKSG TSPAATAKSHLSLRRRQALRGKSSPVLKKTPTN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KGLVQVTKHRLCRLPPSRAHLPTKEASSLHA VRTAPTSKVIKTRYRIVKKT PASPLSAPPTLS LPSWRARRLSLSRSLVLNRLRPVASGGGKAQ PGSPWWSKGYRCIGGVLYKVSANKLSKTSG QPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRGNR GERCPYIHDPEKVAVCTRFVRGTCKKTDGTC PFSHVSKKMPVCSYFLKGICSNSNCPYSHV YVSRKAEVCSDFLKGYCLGAKCKKKHTLLC PDFARRGACPRGAQCQLLHRTQKRHSRAAT SPAPGPSDATARSRSASHGPRKPSASQRPTR QTPSSAALTAATAVAAPPHCPGGSASPSSSKAS SSSSSSSPASLDHEAPSLQEAALAAACSNR LCKLPSFISLQSSSPGAQPRVRAPRAPLTKDS GKPLHIKPRL
842	2192	A	6898	506	2071	WPDLVHTWSSFFAMGSCCSPDKDTPVDNH RNKFKVINVDDDGNELGSGIMELTDIELILYT RKRDVSKWHYLCLRRYGYDSNLFESGRRRC QTGGQIFAFKCARAEELFNMLQEIMQNNNSIN VVEEPPVERNNHQTELEVPRTPRTPTTPGFAA QNLPNQYPRYPSPGDASSHPSSRHPSVGSARL PSVGEESTHPLLVAEEQVHTYVNTTGQVEER KNRTSVHVPLEARVSNASSTPKKEEPSIEDR DPQILLEPEGVKFVLGPTPVQKQLEMEKELE QLGRDOVSGSGANNTWDTGYDSDERRDAP SVNKLVEENINGLSIPSASGVRRGRLTSTSD TQNNNSAQRRTALLNYENLPSLPPVWEARK LSRDEDDNLOPKTPSLNGYHNNLDPMHNYV NTENVTPASAHKIEYSRRRDCTPTVFNFDIR RPSLEHRQLNYIQVDLEGGSDSDNPQTPKTYT TPLPQTPTRRTELYAVIDIERTAAMSNLQKAL PRDDGTSRKTRHNSDPL
843	2193	A	6919	2	663	AGRPGTTHASGKMAYQSLRLEYLQIPVSR YTTACVLTTAAVQLELITPQLYFNPFLFKHF QIWRLLTNLFFGPVGFNLFNMFYLYRCRM LEEGSFRGRTADFVFMFLFGGFLMTLFGLFVS L/VFLGPGLYNN/GSSMCGAEPLCPHELLRP SQLPGPLSALGAHGIFLVVGLNHCOPFGYCS WTHIFFLGRCSQSTWWNKNSNTIYFESYF
844	2194	A	6928	902	366	HRLCMPIQGACGERME/FSLLPGLECNVIL AHCNLRPLGSSNSPASASQVAGITGVCHHAR LIFVFSVETGFLHAGQAGLELLTSGDPPASAS QSAGITGKSQHTRPGYEFIPYSAQAEDALKA LM
845	2195	A	6939	1660	317	LYPENLGESLFPILLPPWPDPGRPCCVEMS TRAKKLRLRIWRILEEKESVAGAVQTLRLRSQ GGVITSAAASTLSEPPRRTQESRTRTRALGLPT LPMEKLAASTEPOGPRPVLGRESVQVPDDQD FRSFRSECEAEVGNWNTYSRAGVSVWVQAV EMDRTLHKIKRMECCDVPAETLYDVLHDIE YRCKWDSNVIETFDIARLTVNADVGYYSWR CPKPLKNRDVITLRSWLPMGADYIMNYSVK HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT YLAQVDPKGSPLKVVVNKSSQFLAPKAMKK MYKACLYPEWKQKHLPHFKPWLHPEQSP LPSLALSVELSVQHADSLENIDESAVAESREE RIMGAGGEGSDDDSLAEAPHRFRETETG PGAGRALGAAAAPALSPLHPPGTWWHRARP RRVLQPGWTEPQ

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846	2196	A	6944	42	2672	RRKMAGCRGSLCCCCRWCCCCGERETRTPE ELTILGETIQEEDEILPRKDYESLDYDRCINDP YLEVLETMDNKKGRRYEAVKWMVVFAGV CTGLVGLFVDFVRLFTQLKFGVVQTSVEEC QKGLALSLELLGFNLTFVLESLLGLIEPVE AGSGITEGKCYLYARQVPGLVRLPTLLWKAL GVLLTVAAMLLAGLSPMIHSGSVVGAGLPQ FQSISLRKIQFNFPYFRSDRYGKDKRDFVSAG AAAGVAAAAGFAPIGGTLFSLEEGSSFVNQGL TWKVLFCSMSATFTLNFFRSQIGFGSWGFSQ PGLLNFGFEKCSDSKKCHLWTAMDLGFFV VMGVIGGLGATFNCLNKLAKYRMRNVHP KPKLVRLVLESLLVSLVTTVVVFVASMVLGEC RQMSSSSQIGNDSFQLQVTEDEVNSSIKTFFCP NDTYNDMATLFFNPQESAILQLFHQDGTFSVP TLALFFVLYFLLACWTYGISVPSGLFVPSLLC GAAFGRVLAVNLKSYIGLGHYSGTIFALIGAA AFLGGVVRMTISLTVILIESTNEITYGLPIMVT LMVGKWTGDFFNKGIVYDIHVGLRGVPLLEW ETEVEMDKLRASDIMEPNLTYVYPHTRIQSLV SILRTTVHHAFFVVTENRGNEKEFMKGNQLIS NNIKFKKSSILTRAGEQRKRSQSMKSYPSSEL RNMCDHEHASEEPAEKEDLLQQMLERRYTPY PNLYPDQSPSEDWTMEERFRPLTFHGLILRSQ LVTLLVRGVCYSESQSSASQPRLSYAEMAED YFRYPDIHDLDTLLNPRMIVDVTYPMNPSPF TVSPNTHVSQVFNLFRTMGLRHLPPVNAVGE IVGIITRHNLTYEFLQARLRQHYQTI
847	2197	A	6951	3	1994	NTNSSSVTNSAAGVEDLNIVQVTPDNEKER LSSIEKIKQIREQVNDLFSRKFGAIGVDFFVK VPYRKITFNPGCVVIDGMPPGVVFKAPGYLEI SSMRRIEAAEFIKFTVIRPLGLELSNGEYST VGKRKIDQEGRVFQEKWERAYFFVEVQNIST CLICKRSMVSKEYNLRHYQTNHSHKHVDQY MERMRDEKLHELKKGLRKYLLGLSDTECP QKQVFANPSPTQKSPVQPVEDLAGNLWEKLR EKIRSFVAYSIAIDEITDINNTQLAIFRGVDE NFDVSEELLDTPMTGKSGNEIFSRVEKSLK NFCINWSKLVSVASTGTPPMVDANGLVTKL KSRVATFCKGAELKSICCIHPESLCAQKLKM DHVMDVVVKSVMWICSRGLNHSEPTLLYEL DSQYGSLLYYTEIKWLSRGLVLRKFESLEEI DSFMSSRGKPLPQLSSIDWIRDLAFLVDMTM HLNALNISLQGHQSIVTQMYDLIRAFKLCCL WETHLTRNNLAHFPTLKLVSERNESDGLNYIP KIAELKTEFQKRLSDFKLYESELTLFSSPFSTKI DSVHEELQMEVIDLQCNVTKTKYDKVGIFE FYKYLWGSYPKYKHHCALISMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT
848	2198	A	6985	3	289	SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTPTTC CFNAINTKIPIQRLESYTRITNIQCPKEAVM
849	2199	A	6999	963	5	LDLFLCHRDMDGNITSITEFLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHLAVVDIAACNTVPRMLVNLLHP AKPISFAGRMQTFLESTFAVTECLLVVMS YDLYVAICHPLRYLAIMTWRCITLAVTSWT TGVLLSLIHLVLLLPLFCRPQKIYHFFCEILA VLKLACADTHINENMVLGAISGLVGPLSTIV VSYMCLCAILQIQSREVQRKAFCTCFSHLCVI

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						GLFYGTAIMYVGPRYGNPKQKKYLLFHS LFNPMNLPLICSLRNSEVKNTLKRVLGVERAL
850	2200	A	7001	1	1011	MGNDSVSVEYGDYSDLSDRPVDCLDGACLAIDPLRVAPLPLYAAIFLVGVPGNAMVAVWAGKVARRRVGATWLLHLAVADLLCCLSLPLAVPIARGGHWPYGAVGCRALPSILLTMYASVLLLAALSADLCFLALGPAWCLRFSGACGVQVACGAAWTLALLTVPSAIYRRLHQEHFARLQCVVDYGGSSSTENAVTAIRFLFGFLGPLVAVASCHSALLCWAARRCRPLGTAVVGVFFVCWAPYHLLGLVLTVAAPNSALLARALRAEPLIVGLALAHSCNPMFLFYFGRAQLRRSLPAACHWALRESQGQDESVDSSKKSTSHDLVSEMEV
851	2201	A	7011	1	2310	AAASPLRMSRKGPRAEVCADCSAPDPGWASISRGVLVCDECCSVHRSLGRHISIVKHLRHSAPPTLLQMVHTLASNGANSIWEHSLDPAQVQSGPALKQTPKDKVHPKSEFIRAKYQMLAFVHKLPCRDDDGVTAKDLKQLHSSVRTGNLETCRLRLSLGAQANFFHPEKGTTPHVAAKAGQILQAEELVVYGADPGSPDVNGRTPIDYARQAGHHELAERLVEQCVELTDRLAFYLCGRKPDHKNGHYIPQADSLDSELAKAACKKLQALSNRLFEELAMDVYDEVDRREDAVWLATQNHSTLVTERSAVFPFVNPEYSATRNQGRQKLARFNAREFATLIDILSEAKRRQQKSLSSPTDNLELSLRSQSDLDQHDYDSVASDEDTDQEP LRSTGATRSNRARSMDSSDSDGAVTLQEYL ELKKALATSEAKVQQLMKVNSSLSDELRLQREHKLQAENLQLRQPPGPVPTPLPSEAEHTPMAPGGSTHRRDRQAFSMYEPGSALKPFGGPPGDELITRLQPFHSIELEDDAIYSVHVPAGLYRIRKGVASAVPFTPSSPLSCSQEGSRHTSKLSRHGSGADSDYENTQSGDPLLGLEGRFLELGKEEDFHPELESLDGDLDPGLPSTEDVILKTEQVTKNIQELLRAAQEFKHDSFVPCSEKIH LA VTEMASLFPKRPALPVRSSRLNANASAYRLQSECRKTVPPPEPGAPVDFQLLTQQVIQCAVDIAKAAQLVTITREKKQ
852	2202	A	7016	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKORMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP EKDLHEGFHYIHEL TQKTQDLKLSIGNTLFIDQRLQPORKFLEDAKNFYSAETILTQNLQLEM AQKQINDFI/ESKTHGKINNLIENIDPGTVMLL ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS VKVPMFRSGIYQVGYDDKLSCTILEIPYQKNITAFILPDEGLKHLKLEKGLQVDTFSRWKTLSRRVVDVSVPRLHMTGTFDLKKTL SYIGVS KIFEEHGDLTKIAPHRSLKVGEAVNKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPIGK
853	2203	A	7017	1	3293	MTHACNPSTLGGQGRNITRSHGRRRSSRGPV ARHVAAGAGHENKHGGSRRFPAGVAPRRAM ANVSKKVSWSGRDRDDEEAAPLLRRRTARPGGTPLLNAGAGPGAARQSPRSALFRVGHMSSV ELDDELLEFPDMDPPHPPKEIPHNEKLLSLKY ESLDYDNSENQLFLEEERRINHAFRTVEIKR WVICALIGILTGLVACFIDIVVENLAGLKYRVI KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV

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						LVGSVTVAFIEPVAAGSGIPQIKCFLNGVKIPH VVRI.KTLVIKVSGLSVVGGGLAVGKEGPMI HSGSVIAAGISQGRSTSLKRDFFKIFEFRRDTE KRDFVSAGAAAGVSAAGFAPVGGVLFSLLEG ASFWNQFLTWRIFASMISTFTLNFLVLSIYHG NMWDLSSPGLNFGFRDSEKMAVTHIEIPVFI AMGVVGGVLGAVFNALNYWLTMFRIYIHR PCLQVIEAVLVAAVTATVAFVLIYSSRDQPL QGGSM\$YPLQLFCADGEYNSMAAAFFNTPEK SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG AAIWADPGKYALMGAAALGGIVRMTLSLT VIMMEATSNVITYGFPIMLVMTAKIVGDVFIE GLYDMHIQLQSVFPLHWEAPVTSLSLTAREV MSTPVTCLRRREKVGVIQVLDVSDTASNNGF PVVEHADDTQPARLQGLILRSQILVLLKHKVF VERSNLGLVQRRLRLKDFRDAYPRFPFIQSIH VSQDERECTMDLSEFMNPSPTVTPQEASLPR VFKLFRALGLRHLVVVDNRNQVVGLVTRKD LARYRLGKRGLEELSLAQTPKAQATAEGRV AGAAQOPCQLRAVTELDLGLLAGGLASPEP LSLEELSERYESHPTSTASVPEQDTAKHWNQ LEQWVVELQAEVACLREHKQRCERATRSLL RELQVRARVQLQGSSELRLQGEARPAQAP EKEAPEFSGLQNMALDKRLVEVREALTRL RRRQVQGEAERRGAEQEAGRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGGKVFINTW AVRIPGGPAVANSVARKHGFNLGQIFGDYY HFWRHGVTKRSLSPHRHSRLQREPQVQWL EQQVAKRRTRKRDVYQEPDTPKFPQWYLISG VTQARDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRLDGEVTDAREVSLGLNPN HIHTYSASWGPEDDGKTVDGPALAEAEFFR GVSQGRGGLGSIFVWASGNGGREHDSNCND GYTNSIYTLSSSATQFGNVPWYSEACSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGHALTLEANKLNTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCHDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPSS GCKTLTSSQACVVCEEFGSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCRSQS QSSRESPPQQPPRLPPEVEAGQRLRAGLLPS HLPVAVAGLSAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQECCPSD SEEDEGRGERTAFKQDSAL
855	2205	A	7058	3	1441	QRPASQLLAPFAAEALPGAPRAAMAQHFLA ACDVVGFGLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELNVTPEWDFCCKGLALDL EDGNFLKLANNGTVLRASHGKMMITEVLA EAYGKKEWKHFLSDTGMACRSGKYFYFDN

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						YFDLPGALLCARVVDYLTCLNNGQKTFDFW KDIVAAIQHNYKMSAFKENCQIYFPEIKRDPG RYLHSRPESVKKWLRQLKNAGKILLITSSHS DYCRLLCA\YILGNDFTDLFDIVITNALKPGFF SHLPSQRPFRTLENDEEQEALPSLDKPGWYSQ GNAVHL YELLKKMTGKPEPKVVFYFGDSMHS DIFPARHYSNWETVILEELRGDEGTRSQRPE ESEPLEKKGKYEGPKAKPLNTSSKKWGSFFI DSVLGLENTEDSLVTWCKRISTYSTIAIPSI EAIAELPLDYKFTFRSSNSKTAGYYPNPPLV LSSDETLSK
856	2206	A	7082	396	1635	SSPSVFEFEHVAQPVFTMEFLKTCVLRNACT AVCFWRSKVVQKPSVRRISTTSRSTVMPAW VIDKYGKNEVLRFTQNMMPHIIHYPNEVIVK VHAASVNPIDVNMRSYGATALNMKRDPLH VKIKGEEFPLTLGRDVSQVMECGLDVKYFK PGDEVWAAVPPWKQGTSEFVVVSGNEVSH KPKSLTHTQAASLPYVALTAWSAINKVGGLN DKNCTGKRVILGASGVGTFAIQVMKAWD AHVTA VCSQDASELVRKLGADDVIDYKSGSV EEQLKSLKPFDFLDNVGGSTETWAPDFLKK WSGATYVTLVTFLLNMDRLGIADGMLQTG VTVGSKALKHFWKGVHYRWAFMASGPC DDIAELVDAGKIRPVIEQTFPSKVPEAFKLV ERGHARGKTVINVV
857	2207	A	7088	320	2417	LRRRKMTQSLQTLTFLLSLLFLVQGAHGR GHREDFRCSQRNQTHRSSLHYKPTPDLRISIE NSEEALTVHAPFPAHPASRSPDPGRGLYHFC LYWNRHAGRLHLLYGKRDFLSDKASSLLCF QHQUEESLAQGPPLLATSVTSWWSPQNISLPSA ASFTFSFHSPHTGAHNASVDMCELKRDQL LSQFLKHPQKASRRPSAASPASQQLQSLSKLT SVRFMGDMGSFEEDRNATVWKLQPTAGLQ DLHIHSRQEEEEQSEMEYSVLLPRTLFRQTKG RSGEAEKRLLL VDFSSQALFQDKNSSQVLGE KVLGIVVQNTKVANLTPVVLTFQHLQPKN VTLQCVFVVEDPTLSSPGHWSSAGCETVRRE TQTSFCFNHLYFAVLMVSSVEVDAVHKHY LSLLSYVGCVVSAALCLVTIAAYLC SRVPLPC RRKPRDYTIKVMNLLAVFLLDTSFLLSEPV ALTGSEAGCRASAIFLHFSLLTCLSWMGLEG YNLYRL VVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPILA VHRTPGVITYPS MCWIRDSLVSYITNLGLFSLVFLNMAMLAT MVVQILRLRPHTQKWSHVLTLCLSLVLGLP WALIFFSFASGTFQLVVL YLFSIITSFQGLIFI WYWSMRLQARGGPSPLKSNDSARLPISSGS TSSSRI
858	2208	A	7091	185	415	DAGAVKSSDTNIWFRGMCDKKGHRCPG*G QPQHFFVAFHTEAEGAMFYRLHVIHRVMQS QQQLFPSTLFSWLE
859	2209	A	7136	3	302	FFFWRQSLALLPRLECSGATGAHCNLFHPGSS DCPTAS* IAGITGACYHAWLLFVFLAETGFH HVGQGGLELLTSSDPSGSASQSAGITGVSHCT WPI
860	2210	A	7156	23	591	ALSTETRTPDMMRLLVTSLVVVLLWEAGAV PAPKVPIKMVQKHPWSEQDPEKAWGARVVE PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGR GPILPGTKAWMETEDTLGRVLSPEPDHDSLY

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						HPPPEEDQGEERPLWVMPNHQVLLGPEEDQ DHIYHPQ*GSRGHHCPRPVPRLLGLGPSLP CPS
861	2211	A	7161	1220	1003	NYVCTIAF*EKKMGF*LSLSCLVLLFVFLDCI LTTTTRIMFHCTYLFASVCLSLNLTLLSPNCL KSAMILQ
862	2212	A	7211	665	847	LKYYHITMGYKTGKKVIL*KSSMSNRFSVIF YKNIQKLSFSNYVYHONYVFSDDWSYDF
863	2213	A	7212	924	1273	HGSSCALGD LAPG*LPSPGVLSPPAVRL*RPK LVWDSPLPATGPT*GLVLVLGGPDCT*WA RGQHEHKRMRA*SCRVTNLAKKKKKTDQ CIKPNYQSPKCEDYNILANSVA
864	2214	A	7214	845	1619	SDKGGKKADRNHLRHAFLLPHRVRLH DPKVPVDADHVQGDQDGRAAHDIHGEDVTE KYSKDPLAPDEVGDTDEGHDHRHGHREVQGR HGHDOEEVA YEERACEGKFATVEVTDKPV DEALREAMPKVAKYAGGTNDKGIGMGMTV PISFAVFPNEDGSLQKLLKVVFRIPNQFQSDP PAPSDKSVKIEEREGITVYSMQFGGYAKEAD YVAQATRLRAALEGTATYRGDIYFCTGYDPP MKPYGRRNEIWLKT
865	2215	A	7246	559	682	RRLGAVAHAYTSSTLGRRGGWIT*GQELQTS LANMAKPRLY
866	2216	A	7257	641	1310	TCTYKYLGMGWIRGRRSRHSWEMSEFHNYNL DLKKSDFSTRWQKQRCPVVKSCKRENASPPF FCCFIAYAMGIRFIIMVAIWSAVFLNLSFNQEV QIPLTESYCGPCPKNWICYKNNCYQFFDESKN WYESQASCMSQNASLLKVYSKEDQDLLKL KSYHWMGLVHIPTNGSWQWEDGSILSPNLLT IEMQKGDICALYASSFKGYIENCSTPNTYICM QRTV
867	2217	A	7288	151	396	SIKIEAFGSNGPDFWFFRYWSP*LFRQQVFI MPFFQILWLMNANRFCSIFTTNNVANNCW TPYHCWLSVVVCRCESHGI
868	2218	A	7298	3	272	PDTVIGGRGSGGKEFGRWVLW*VFE*RLGTP KGSCPAGGSRMVSESD*EGRGC*ASYPCAC* AGS*WR*GSRPAGRGTPPRLSHARPP
869	2219	A	7332	1223	332	PRRDAEDRDESLNPAFFIGLLHPNSVNSMAR FLTLCTWLLLLGPGLLATVRAECSDCATCS YRLVRPADINFLACVMECEGKLPSLKIWETC KELLQLSKPELPQDGTSTLRENSKPEESHLLA KRYGGFMKRYGGFMKKMDELYPMEPEEEA NGSEILAKRYGGFMKKDAEEDDSLANSDDL KELLETDGNRERSHHQDGSDEEEVSKRYGG FMRGLKRSPLKEKAKELQKRYGGFMRRVG PQKW*MTSPQNRYYGFLKRFABALPSDEEGE SYSKEVPEMEKRYGGFMR
870	2220	A	7382	216	1018	EIHQRLTERTQFLDESRKNPNS*QANLLRGGG AGQGRGREGAESGGSRGEGPGSDGRLPATGD FWSPRSQRGCGRRAPRPEAMENGAVYSPT TEEDPGPARGPRSGLAAYFFMGRLLPLRRVL KGLQLLLSLAFICEEVVSQCTLCGGLYFFEF VSCSAFLSLLLIVYCTPFYERVDTTKVKSSD FYITLGTGCVLLASIIFVSTHRTSAELAAIVF GFIASFMFLDFTMLYEKQESQLRKPENTT RAEALTEPLNA
871	2221	A	7403	3	393	SCAMCSGLL*LLPIWLSWTLGTRGSEPRSVN DPGNMSFVKETVDKLLTGFRCFREREAPRR ALROAALPGESEAGDPESLRSSVNADWIOYS

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						DLWEAEVSTPRCEAGFCQCEFRTPGNQEKDG PFIC
872	2222	A	7413	1061	359	FVDIVSVVEFPHCPPEARFPAQHGDSCRLLTLC PGGS*PQATLHLDRMRVSASPTKEIVKKYK CGLIKPCPANYFAFKICSGAANVVGPTMCFED RMIMSPVKNNVGRGLNIALVNGTTGAVLQQ KAFDMYSGDVMHLVKFLKEIPGGALVLVAS YDDPGTKMNDERSRKLFSDLGSSYAKQLGFRD SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE GWPELLEMEGCMPPKPF
873	2223	A	7429	2242	2394	ILKCAHGGSCL*SQHFGRLRWEDRLRLGVQ DHPGQHCEITPSLLKIERKLF
874	2224	A	7468	146	894	PCTSCVLWATLHLPASTRKAPQAECGMISITE WQKIGVGITGFGIFFILFGTLLYFDSVLLAFGN LLFLTGLSLIIGLRKTFWFFQHRHKLKGTSLFLL GGVVIVLLRWPLLMFLETYGFPSLFKGFPPV AFGLGNVCNIPFLGALFRLQGTSSMV*KTE MSSLNLDHWLKGAKREEWEPPQSPALTHSP TYPGPPQVQKERNGAELTSNPQVDSRGCQE AEMQTPRRLGWGWYHTLTLYL WEEK
875	2225	A	7498	91	251	GEKPVTWLQDEAGQWLLGFVAQPWGWPG SERHEP*HGGVLFRLGPSAPFGKL
876	2226	A	7544	403	587	YSCLCFLFKHITSFKNSVHIWLGTVVHAYNPN ILGGQGGWIA*GOEFKTSLGNTVRPCLYK
877	2227	A	7566	2	940	GCAPDTRFFVPEPGGRGAAPWVALVARGGC TFKDKVLVAARRNASAVVLYNEERYGNITLP MSHAGTGNIVMISYPKGREILELVQKGIPV TMTIGVGRHVFQEFISGQSVVFAIAFITMMII SLAWLIFYIQRFLYTGSQIGSQSHRKETKKVI GQLLLHTVKHGEKGIDVDAENCAVCIEFKV KDIIIRLPCKHIFHRICIDPWLLDHRTCPMCKL DVIKALGYWGEFGDVQEMPAPESPGRDPAA NLSLALPDDDGSDSESPSPASPAESEPCDPSF KGDAGENTALLEAGRSDSRHGGPIS
878	2228	A	7586	315	1232	ERSLLCKVDVRWYVSEGTKTQRRHRQGSRL RGRMQAACWYVLFLLQPTVYLVTANLTNG GKSELLKSGSSKSTLKHIVTESSKDLISIRLLS QTRGKENDTDLRLYDTPEPYSEQDLWDW LRNSTDLQEPRAKRRPIVKTGKFKMFGW GDFHSNIKTVKLNLLITGKIVDHGNGTFSVYF RHNSTGQGNVSVSLVPPTKIVEFDLAQQTVID AKDSKSFNCRIEYKVDKATKNTLCNYDPSK TCYQEQTQSHVSWLCSKPFKVICIYISFYSTD YKLVQKVCPTYNYHSDTPYFSPG
879	2229	A	7605	479	391	TESWKLKWWSPCLDQLNGSAPGNVFIHG
880	2230	A	7612	93	659	DAAVAMTAQGGGLVANRGRFRKWAIELSGPG GGSRGSRDRSGSQGDSLYPVGYLDKQVPDTS VQETDRILVEKRCWDIALGPLKQIPMNLFIMY MAGNTISIFPTMMVCMMAWRPIQALMAISAT FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPHTASDWLAFIEPPERMEFSGGGL LL
881	2231	A	7615	291	1452	SPQKTMRSHTITMTTTSVSSWPYSSHRMRFIT NHSDQPPQNFSAIPNVITCPMDEKLLSTVLTT SYSVIFIVGLVGNIALYVFLGIHRKRNSIQYL LNVAIADLLLIFCLPFRDMYHINQNKWTLGVIL CKVVGTLFYMNMYSIILLGFISLDRIYKINRSI QQRKAITTKQSIYVCCIVWMLALGGFLTMIL TLKKGHNSTMCFHYRDKHNAKGEAIFNFI

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						VVMFWLIFLLIILSYIKIGKNLLRISKRRSKFPN SGKYATITARNSFIVLIIFTICFVPYHAFRTYISS QLNVSSCYWKEIVHKTNEIMLVLSFNSCLDP VMYFLMSSNIRKIMCOLLFRRFQGEPSRSEST SEFKPGYSLHDTSAVAVKIQSSSKST
882	2232	A	7617	67	379	RQMALLKANKDLISAGLKEFSVLLNQVFND PLVSEEDMVTTVVEDWMNFYINYYRQVVTGE POERDKALQELRQELNLANPFLAKYRDFLK SHELPSHPPSS
883	2233	A	7622	400	215	KVKTCRYNPKYSAANDTGVDIPSREKDLAK AVATVGPISVAVGASHVFFQFYKKGKHLSS
884	2234	A	7638	2640	2861	APVLILQMVKLSIVLTPQFLSHDQGLTKELQ QHVKSVCPCPEYLRKVSECRQMGPQGALEQFP GLSCHTSHSG
885	2235	A	7642	201	455	PSRGKMELEAMSRYTSPVNPVAFPHLTIVLL AIGMFFTAWFFVYEVTSIKYTRDIYKELLISL VASLFMGFGVLFLLWVGIVV
886	2236	A	7692	61	569	APENPFSRQHFNSSETKVLSLKTGTWLGNAH HLOEHFSTHHELGLSGKVVGFLVKNILEVIRN GGMETRHPGKVSSWFHRWDSRAEQHNHAE HHEDVPQGEDSKVSEAQQEFPDVVTCAGLP GLLPKALRVLLFQLKVQHRPGIHQQRPQQD VSDHRYGRSVQRNK
887	2237	A	7693	85	315	NPGCCLPVAMRTSYLLFLTCLLLSEMASGG NFLTGLGHRSDHYNCVSSGGQCLYSACPIFTK IQGTCYRGKAKCKK
888	2238	A	7702	242	1298	APSHRRRYLSPRSAGQLGNMALERLCSVLK VLLITVLVVEGIAVAQKTQDQGNIGKHIPAT QCGIWWRTSNGGHFASPNYPDSYPPNKECIYI LEAAPRQRIELTFDEHYIIEPSFECRFDHLEVR DGFFGFSPLIDRYCGVKSPLIRSTGRFMWIKF SSDEELEGFRAKYSFIPDPDFTYLGGLNPPI DCQFELSGADGIVRSSQVEQEEKTKPGQAVD CIWTKATPKAKIYLRFLDYQMEHSNECKRNF VAVYDGSSEIENLKAKFCSTVANDVMLKTOI GVIRMWADEGSRLNRFRMLFTSFGGASPAQA ALSFCCHSNMCINNSLVCGNVQNCAYPWDE NHC
889	2239	A	7707	185	2911	CHYIMNPSTHHPASAGGSILGLDFFGLGLGE MTMDALLARLKLNPDDLREEIVKAGLKCGP ITSTTRFIFEKKLAQALLEQGGRLSSFYHHEA GVTALSQDPQRILKPAEGNPTDQAGFSEDRDF GYSVGLNPPEEEAVTSKTCVPSDPTDYRAG ATASKEPLYGVCPVYEDVPARNERYVVE NKKEALQAVKMIKGSRFKAFSTREDAEKFAR GICDYFPSPSKTSLPLSPVKTAFLFSNDRKDG LCLSESETVNERANSYKNPRTQDLTAKLRK AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIVQ EGCRYNVMHVAAKENQASICQLTLDVLENP DFMRLMYPDDDEAMLQKRIRYVVDLYLNT DKMGYDTPHLFACKFGNADVNVLSHHLI VKNSRNKYDKTPEDVICERSKNKSVELKERIR EYLKGHYVPLRAEETSSPVIGELWSPDQTA EASHVSRYGSPRDPVLTILRAFAGPLSPAKAE DFRKLWKTPPREKAGFLHHVKKSDPERGFER VGRELAEHLGYPWVEYWEFLGCFVDLSSQE GLQRLEEYLTQQEIGKKAQQTGEREASCRD KATTSGSNSISVRAFLDEDDMSLEEIKNRQNA ARNNSPPTVGAFGHTRCSAFPLEQEADLIEAA

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						EPGPHSSRNGLCHPLNHSRTLAGKRPKAPR GEEAHLPPVSDLTVEFDKLNQINIGKSVSKIP DESTKTKDQILTSRINAVERDLLEPSADQLG NGHRRTESEMSARIAKMSLSPSSPRHEDQLEV TREPARRLFLGEEPSKLDQDVLAALECADV DPHQFPAVHRWKSAVLCYSPSDRQSWSPAV KGRFKSQLPDLSGPHSYSPGRNSVAGSNPAKP GLGSPGRYSPVHGSQRLRRMARLAELAAAL
890	2240	A	7711	360	269	RHMPVIPALWEAEVGGLEPRSSRSAWATE
891	2241	A	7721	61	1175	KLPWEPSFLIKMQIRHSEQLTKALISKNPVL VSQYEKLDAGEQRLMNEAFQPADLFGPITL HSPSDWITSHPEAPQDFEQFFSDPYRKTPSPN KRSTYIQSIGSLGNTRIIEEYIKWLTGYCKAYF YGLRVKLLPEVPVSVTRCSFRVNENTHNLQIH AGDILKFLKKKKPEDAFQVVGITMIDLYPRDS WNFVFGQASLTDGVGIFSFARYGSDFYSMHY KGVKVKLKKTSDDSYSDNYIPEITSVLLLR SCKTLTHEIGHIFGLRHCQWLACLMMQGSNHL EADRRPLNLCPICLHKLQCAVGFSIVERYKA LVRWIDDESSDTPGATPEHSHEDNGNLPKPV EAFKEWKEWIKCLAVLQK
892	2242	A	7723	2	1650	SAPTAPARPCRAERGSGGGMALLAASVALA VAAGAQDSPAPGSRFVCTALPPEAVHAGCPL PAMPMQGGGAQSFEEELRAAVLQLRETUVQQ KETLASARAIRELTKLARCEGLAGGKARGA GATGKDTMGDLPRDPGHVVEQLSRSLQTLK DRLESLEPLPAMPMQGGGAQSFEEELRAAVLQ LRETUVQQKETLASARAIRELTKLARCEGL AGGKARGAGATGKDTMGDLPRDPGHVVEQ LSRSLQTLKDRLESLEHQLRANVSNAGLPGD FREVLQQLRGELERQLLRKGAELEDEKSLH NETSAHRQKTESTLNALLQRTVTELRGNSAF KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT ICLWLRSSASPGMGTPFSYAVPGQANEIVLIE WGNNPIELLINDKVAQLPLFVSDGKWHHICV TWTTRDGMWEAFQDGKKGTLGTENLAPWHPI KPGGVLLGQEQDVTGGRFDATQAFVGEISQ FNIWDRVLRAQEIIVNIANCSTNMPGNIPWVD NNVDVFGGASKWPVETCEERLLDL
893	2243	A	7729	3554	2419	LTAGTAMNYPLTLEMDLENLEDFWELDRIL DNYNDTSLVENHLCPATEGPLMASFKAVFVP VAYSILFLGVIGNVLVLILERHRQTRSTET FLFHLAVADLLVFLPFAVAEGSVGVVLGTF LCKTVIALHKVNFYCSLLACIAVDRYLAIV HAVHAYRHRRLLSIHITCGTIWLVGFLLALPEI LFAKVSQGHNNLSLPRCTFSQENQAETHAWF TSRFLYHVAGFLPLVMGWCVYGVVHRLR QAQRRPQRQKAVRVAILVTSIFFLCWSPYHIV IFDLTLARLKAVDNTCKLNGSLPVATTMCEFL GLAHCCNPMPLYTFAGVKFRSRLSLTKLG CTGPASLCQLFPSWRSSISESENATSLTTF
894	2244	A	7738	670	287	FVTRAGRWGAGARVRGGAGGMASGAARWL VLAPVRSGALRSGPSLRKGDVSAAWSGSGR SLVPSRSVIVTRSGAILPKPVKMSFGLLRVFSI VIPFLYVGTLSKNFAALLEHDFVPEDDDDD D
895	2245	A	7753	119	278	APYAHSQVHCLDKVCGLLPFLNPEVPDQFYR LWLSLFLHAGKEAPHCPRTPL
896	2246	A	7754	1	372	SPAWWNSQQRVVSFFLALLTLEPTFHLLPIM

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						QVSTAALAVLLCTMALCNQVLSAPLAADTPT ACCFSTYTSRQIPQNFADYFEISSQCSKPSVIFL TKRGRQVCADPSEEWWQKYVSDLELSA
897	2247	A	7761	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPL RPLSRHPLSSGSPETSAAAMLLTVRHGTVRVY RSSALLARTKNNIQR YFGTNSVICSKKDKQSV RTEETSKETSESQDSEKENTKKDLLGHIKGMK VELSTVNVRTTKPPKRRPLKSLEATLGRLLRA TEYAPKKRIEPLSPELVAAASAVADSLPFDKQ TTKSELLSQLQHEEESRAQRDAKRPKISFSNI ISDMKVARSATARVRSRPELRJQFDEGYDNY GQEKTDLLKKRNIFTGKRLNIFDMMAVTKE APETDTSPLWDVEFAKQLATVNEQPLQNGF EELIQWTKGKLEWEPINNEAGFDDGSEFH EHIFLEKHLESFPKQGPRIHFMELVTCGLSKNP YLSVKQKVEHIEWFRNYFNEKKDILKESNIQF KLRPWKFLFRNN
898	2248	A	7775	85	496	SCQTTQPPAQSCSTGTMRIMLLFTAILAFSLA QSFGAVCKEPQEEVVPGGGRSKRDPDL YQLL QRLFKSHSSLEGLLKALSQASTDPKESTSPEK RDMHDDFFVGLMGKRSVQPDSPD VNQENV SFGILKYPPRAE
899	2249	A	7785	179	703	PFHLGASSNTFRLQVQTQESKAQKEVKMGFI FSKSMNESMKNQKEFMLMNLRLQLERQLIM QSEMRERQMAMQIAWSREFLYFGTFFGLA AISLTAGAIAKKKKPAFLVPIVPLSFILTYQYDL GYGTLLERMKGAEADILETEKSKLQPRGMIT FESIEKARKEQSRFFIDK
900	2250	A	7789	1465	300	VWLPLKSYKIRSPSLHCQCEIFREEFLFSSLOE GRDKDTFSKMAMVSEFLKQAWFIENEEQY VQTVKSSKGGPGSAVSPYPTFNPSDDVAALH KAIMVKGVDEATIIDLTKRNNAQORQKIAAY LQETGKPLDETLKKALTGHLEEVVLLALLKTP AQFDADELRAAMKGLGTDEDTLIELASRTN KEIRDINRVYREELKRDIAKIDTSDTSGDFRN ALLSLAKGDRSEDFGVNEDLADSDARALYEA GERRKGTDVNVFNTILITRSYPQLRRVFQKY TKYSKHD MNKVLDELKGDIECLTAIVKCA TSKPAFFAEKLHQAMKGVGTRHKALIRIMVS RSEIDMNDIKAFYQKMYGISLCQAILDETKGD YEKILVALCGGN
901	2251	A	7796	2	807	VEFHPQARARAGARAPSMGVLLTQRTLLSLVL ALLFPSMASMAAIGSCSKEYRVLLGQLQKQT DLMQDTSRLDPYIRIQGLDVPKLEHCRERP GAPPSEETLRGLGRRCFQLTLNATLGCVLHRL ADIFQRLPKAQDLERSGLNIEDLEKLQMARP NILGLRNINCYMAQLLDNSDTAEPTKAGRGA SQPPTPTASDAFQKLEGCRFLHGYHRFMH SVGRVFSKWGESPNRSRRHSPHQALRKGVRR TRPSRK GKRLMTRGQLPR
902	2252	A	7802	2	721	TAARRRQKGTAAARRLQKGTAAARRRQKGTAA RRRQKGTAAARRPQKGTAAARRRQKGTAAARR QKGTAAARRRQKGTAAARRPQKGTAAARRRQK TAARRRQKGTAAARRRQKGLAIASRGCPASR AGGVRGAGSRLRAMAPKVRQYWDIPDGT CHRKAYSTTSIASVAGLTAAAYRVTLNPPGTF LEGVAKVGQYTFATAAVGAVFGLTTCISAHV REKDDPLNYFLGGCAGGLTLGARTHNYGIG AAACVYFGIAASLVKMGRLGWEVFAKPKV

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903	2253	A	7807	1	584	PWLPWSDGRAARSSRKCPRSRFPVQVGKMA VSTVFSTSSMLALSRHSLSPLLSVTSFRFY RGDSPTDSQKDMIEIPLPPWQERTDESIEIKR ARLLYESRKRGMLENCILLSFAKEHLQHMT EKQLNLYDRLINEPSNDWDIYYWATEAKPAP EIFENEVMALLRDFAKNKNKEQRLRAPDLEY LFEKPR
904	2254	A	7813	40	821	GAGRALGHLETGAGDVAAALPARKFPRSLG AGARLTGWTMNVFRILGDLSHLLAMILLGK IWRSKCKCKGISGSKQILFALVFTTRYLDLFTNF ISYNTVMKVVFLLCAYVTVMYKFRKTF DSENDIFRLEFLLPVIGLSFLENYSFTLLEIL WTFSTYLESVAILPQLFMISKTEAETITTHYL FFLGLYRALYLANWIRRYQTENFYDQIAVVS GVVQTFYCDFPYLVYTKGRSWDDSNADTGL RSYSSI
905	2255	A	7817	1399	881	LSNKDVLSPQLKDENSEKLRRLNEVQSFSEA QTEMVRTLKLEAKMKEESDYHDLESVVQ QVEQNLELMTKRAVKAENHVVKLKQEISLL QAQVSNFQRENEALRCQGASLTVVKQND VALQNLRVVMNSAQASIEQLVSGAETLNLVA EILKSIDRISEVKDEEDS
906	2256	A	7822	3	1462	DSPRNRFEILGRPTRTPTPRPGPRPAMEDLDAL LSDLETTTSHMPSRGAPKPAEPLTPPSYG HQPQTGSGESSGASGDKDHLYSTVCKPRSPK PAAPAAPFSSSSGVLGTGLCELDRLQELNA TQFNITDEIMSQFPSSKVASGEQKEDQSEDKK RPSLPSSPSPGLPKASATSATLELDRLMASLSD FRVQNHLPASGPTQPPVVSSTNEGSPSPPEPTG KGSOLDTMLGLLQSDLSRRGVPTQAKGLCGSC NKPIAGQVVIAGRAWHEHFVCGGCSTAL GGSSFFEKDGAPFCPECYFERFSPRCGFCNQPI RHKMVTALGTHWHEHFCVSCGEPFGDEG FHEREGRPYCRRDFLQLFAPRCQGCQGPILDN YISALSALWHPDCFVCRECFAPSGGSFFEHE GRPLCENHFHARRGSLCATGLPVTGRCVSA LGRRFHPDHFTCTFLRPLTKGSFQERAGKPY CQPCFLKLF
907	2257	A	7828	1792	1671	FIYVNSQSFAPSPDQEVGTLCEFGSDGKLVH YCKSQAWG
908	2258	A	7842	110	1172	KLSCPCSHGTRVTAVRGPRLKAGVQWHDLG SLQPPPSGLKQSSHLSSSWDFRHAPTHPET YTCPKMIEMEQAEQLAELDLLASMFGENE LIVNDQLAVAEKDCIEKKTMEGRSSKVYFTI NMNLDVSDEKMAMFSLACILPFKYPAVLPEI TVRSVLLSRSQQTQINTDLTAFLQKHCHGDV CILNATEWVREHASGYVSRDTSSSPTTGSTVQ SVDLIFTRLWIYSHHIYNCKRKNILEWAKEL SLSGFSMPGKPGVVVCVEGPQSACEFWARLR KLNWKRILIRHREDIPFDGTNDETERQRKFSIF EEKVFSVNGARGNHMDFGQLYQFLNTKCGG DVFQMLWV
909	2259	A	7870	3067	2923	EGICVYTFIYVHMYTRTCMHITYPYMYMNSV LISSEILLIPSKYLFESK
910	2260	A	7884	212	4874	GALTWSHPLLAVCPQGVWLGSTPSGSPALLP PSHRVNAEPGCYVTNACASGPCPPHANCRL WQTFSCCTCPGYGPGCVDACLLNPQCNQ SCRHLPGAPHGYTCDVGGYFGHHCEHRMD QQCPRGWWGSFTCGPCNCDVHKGFDPNCNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						<p>TNGQCHCKEFHYRPRGSDSCLPCDCYPVGST SRSCAPHSGQCPCRPGALGRQCNSCDSFFAEV TASGCRVLYDACPKSLRSGVWWPQTKFQVL ATVPCPRGALGLRGAGAAVRLCDEAQQWLE PDLFNCTSPAFRELSLLLDGLELNKTALDTME AKKLAQRLREVTGHTDHYFSQDVRVTARLL AHLAFESHQQGFGLTATQDAHFENLLWA GSALLAPETGDLWAALGQAPGSPGSAGLV RHLEEYAATLARNMELTYLNPMLVTPNML SIDRMEHPSPRGARRYPHYHNLFRGQDAW DPHTHVLLPSQSPRSPSEVLPTSSSIENSTSS VPPPPAPPEPEPGISIIILLVYRTLGGLLPAQFQ AERRGARLPQNPVMNSPVVSVAVFHGRNFLR GILESPISEFRLQLTANRSKAICVQWDPGLA EQHGVTWARDCELVHRNGSHARCRCRSTGT FGVLMASPRERLEGDLELLAVFTHVVAVS VAALVLTAAILLSLRSLKSNVRGIHANVAAA LGVAELLFLLGIHRTHNQLVCTAVVILLHYFF LSTFAWLFFVQGLHLRYMQVEPRNVDRGAMR FYHALGWGVPVLLGLAVGLDPEGYGNDP CWISVHEPLIWSFAGPVVLVIVMNGTMTLLA ARTSCSTGQREAKKTSALTSSFLLLLVSA SWLFGLLAVNHSILAFHYLHAGLCGLQGLAV LLFCVLNADARAAWMPACLGRKAAPEEAR PAPGLGPGAYNNTALFEESGLIRITLGASTVSS VSSARSGRTQDQDSQGRSYLRDNVLVRHGS AADHTDHSQAHAAGPTDLVAMFHRDACA DSDSDSDLSLEERSLSIPSESEDNGRTRGRF QRPLCRAAQSERLLTHPKDVGNDLLSYWPA LGECEAAPCALQTWGSERRLGLDTSKDAAN NNQPDPAITSGDETSLGRAQRQRKGLKNRL QYPLVPQTRGAPELSWCRAATLGHRAVPAAS YGRJYAGGGTGSLSQASRYSSREQLDLLRR QLSRERLEEAPVLRPLSRPGSQECMDAAPG RLEPKDRGSTLPRRQPPRDYPGAMAGRFGSR DALDLGAPREWLTLPFRTRDLDPOPPPLP LSPQRQLSRDPLPSRPLDSLRSSNSREQLDQ VPSRHSREALGPLQLLRAREDVSGPSHGP STEQLDILSSILASFNSALSSVQSSSTPLGPH TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDRLRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYVPFIY FLFGTSRHSVESLCVPGPVD</p>
911	2261	A	7890	21	806	<p>EFGTSRSSRMAEDLGLSFGETASVEMLPHEG SCRPKARSSARWALTCCLVLLPFLAGLITTYL LVSQLRAQGEACVQFQALKGQEFAPSHQQV YAPLRADGDKPRAHLTVVRQTPTQHFKNQFP ALHWEHELGLAFTKNRMNYTNKFLIPESGD YFIYSQVTFRGMTSECSEIRQAGRPNKPDSTV VITKVTDSYPEPTQLLMGTKSVCEVGSNWQF PIYLGAMFSLQEGDKLMVNVSDISLVDTYKE DKTFFGAFL</p>
912	2262	A	7891	1263	111	<p>ACGIRHEGALPGLTATPEAMLRFLPDLAFSFL LILALGQAVQFQYVFLQLGLDKAPSPQKQF PVPIYLLKKIFQDREAAATTGVSRLDCYVKELG VRGNVLRFLPDQGFLLYPKKISQASSCLOKLL YFNLSAIKEREQLTLAQLGLDLPNSYYNLGP ELELALFLVQEPHVWGQITPKPGKMFVLRV</p>

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PWPOGAVHFNLLDVAKDWNNDNPRKNFGLFL FLLVKEDRDSGVNFQPEDTCARLRCSI.HASLL VVTLPNDQCHPSRKRRRAIPVKLSCKNLCH RHQLFINFRDLGWHKWIIAPKGFMANCHGE CPFFSLTISLNSSNYAFMQALMHAVDPEIPQAV CIPTKLSPISMLYQDNNNDNVILRHYEDMVVD ECGCG
913	2263	A	7892	15	849	ASRLPRGPGCGADMRLPLGLLVFAGCTFAL YLLSTRLPGRRLGSTEAGGRSLWFPSDLAB LRELSEVLREYRKEHQAYVFLFCGAYLYKQ GFAIPGSSFLNVLAGALFGFWLGLLCCVLTS VGATCCYLLSSIFGKQLVVSYPDKVALLQR KVEENRNSLFFLLFLRFPMTNWFNLNLSAPI LNIPIVQFFSVLIGLIPYNFICVQTGSILSTLS LDALFSWDTVFLLALAMVALIPGTLIKFSQ KHLQLNETSTANHIHSRKDT
914	2264	A	7893	815	959	KSGVYWWLTLPLPALWEAQTEGSLRPEVKN RLSNITRPFFSKKKKILV
915	2265	A	7909	3	641	HASGPGGLRRRRGSGANMPVARSWVCRKT YVTPRRPFESRLDQELKLGEGYGLRNKREV WRVKFTLAKIRKAARELLTLDKDPRLFEF NALLRRLVRIGVLDEGKMKLDYILGLKIEDFL ERRLQTVFKLGLAKSIHHAHVLIQQCHIRVR EQVVNILFFTIVRLDSQKHDFSLCFPIGVANPS HVKRKNASKGQGGAGARDDEEEE
916	2266	A	7914	3	967	VAHTQWHTCQRLSQLTHRSILKYLLIDTHAC QVLILKHTHASLSLPSQCQECFPSSIPSASHMVS HPHPPSPRWGQTPEGLPAASPCGPGPRSCFS SILPTGDSWGMCLACTVLWHLPAVPALNRT GDPGPGSIQKTYDLTRYLEHQLRSLAGTYLN YLGPPFNEPDNPPRLGAETLPRATVDLEVW RSLNDKLRLTQNYEAYSHLLCYLRGLNRQAA TAE LRRLAHFCTSLQGLLGSAGVMAALGY PLPQPLPGTEPTWTPGAHSDFLQKMDDFWL LKLQTLWLRSAKDFNRLKKKMQPPAAAVT LHLGAHGF
917	2267	A	7921	2	1166	RPRRGQGLVQEVQTEENVTVAEAGVAETCRL HQYDGSIVVIQNPARTLFFNGTRALKDERFQ LEEFSPRRVRIRLSDARLEDEGGYFCQLYTED THHQIATLTVLVAPENPVVEVREQAVEGGEV ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ ENGKVWSVASTVFRVDRKDDGGHICEAQN QALPSGHSKQTQVLDVQYSFTARIHASQAV VREGDTLVLTCVGTGNPRNQIRWNRGNESL PERAEAVGETLTLPLVVSADNGTYTCEASNK HGHARALYVLVVGESRLRPTEGGGGAPDP GAVVEAQTSPYAIVGGILALLVFLICVLVG MVWCVRQKGSYLTHEASGLDEQGEAREAF LNGSDGHRKEEFFI
918	2268	A	7938	3	2653	RRRLPPASPPSSSVSSSLSPSAVVMACRWSTK ESPRWRSALLLFLAGVYNGALAEHSENVH ISGVSTACGETPEQIRAPSGITSPGWPEYPAK INCSWFIRANPGEIITISFQDFDIQGSRRCLND WLTIETYNIESYRACGSTIPPPYISSQDHIWIR FHSDDNISRKGFRLAYFGKSEEPNCACDQFR CGNGKCIPEAWKCNNMDECGDRSDEEICAKE ANPPTAAAFQPCAYNQFQCLSRFTKVYTCLP ESLKCDGNIDCLDLGDEIDCDVPTCGQWLKY FYGTFSNPYPDFYPPGSNCTWLIDTGDHRK

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						VILRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFDUSHAPLTVVSSSGQIRVHFCADKV NAARGFNATYQVDGFCPLWEIPCGGNWGCY TEQQRCDGYWHCPNGRDETNCTMCQKEFP CSRNGVCYPRSDRCNYQNHCPNGSDEKNCFF CQPGNFHCKNNRCVFESWVCDSDDCGDGS DEENCPTVTPTRVITAAVIGSLICGLLLVIALG CTCKLYSLRMFERRSFETQLSRVEALLRREA PPSYGQLIAQGLIPPVEDFPVCSFNQASVLENL RLAVRSQLGFTSVRLPMAGRSSNIWNRIFNFA RSRHSGSLALVSADGDEVVPSQSTSREPERNH THRSLSFVESDDTDENERRDMAGASGGVAA PLPQKVPTTAVEATVGACASSSTQSTRGGH ADNGRDVTSVEPPSVSPARHQLTSALSRMTQ GLRWVRFTLGRSSSLSQNSPLRQLDNGVSG REDDDDVEMLIPISDGSSDFD VNDCSRPLDL ASDQGGQLRQPYNATNPGVRPSNRDGPCCRC GIVHTAQIPDTCLEVLTKNETSDDEALLC
919	2269	A	7951	1674	1839	VVRVTCCPPARSTERTINAYDEEDCVMVAS GGWNDVACHTTMYFMCFFDKKNM
920	2270	A	7953	47	572	GGRASWPEQAKEPRREGHTDKQQTEDVLAA GLRCLPHLPAICARRMSPAFRAMDVPEPRAG VLLEPFVHQVGGHSCVLRFNETTLCPLVPRE HQFYETLPAEMRKFTPYKKGKSQLLEGLPHW RGDVRDRGHGRPWQPSLEPSLPTLCFPSLSS FSSSWPSAQHLTPSVFNPW
921	2271	A	7957	612	812	RSGRTVVTGIGYSKALQSSNRNTKSLQNEF MMVYSFRALSFKESTWATFQHGGEATKSRL SSTQ
922	2272	A	7967	1443	1660	ENITEKWKIWMCRGNKKSCCWTFIKDRHLT VSCCKSKSGEITLICFCNLVGGFFFGIRGFSN WELVKPN
923	2273	A	7981	1	3023	GSAPRAATAMARARPPPPSPPPGLPLPLP LLPLLLPAGCRALEETLMDTKWVTSELAWT SHPESGWEEVSGYDEAMNPIRTYQVCNRES SQNNWLRGTGFIWRRDVQRVYVELKFTVRDC NSIPNIPGSKETIFNLFYEADSDVASASSPFW MENPYVKVDTIAPDESFSRLDAGRVTNKVRS FGPLSKAGFYLAQDQGACMSLISVRAFYYK CASTTAGFALFETLTGAFTSLVAPGTCPN AVEVSVPLKLYCNGDGEWMVPVGACTCATG HEPAAKESQCRPCPPGSYKAKQGEGLPCPP NSRTTSPAASICTCHNNFYRADSDSADSACTT VPSPPRGVISNVNETSLILEWSEPRDLGVRDD LLYNVICKKCHGAGGASACSRCDNVEFVPR QLGLSEPRVHTSHLLAHTRYTFEVQAVNGVS GKSPLPPRYAAVNITTNAAPSEVPTLRHSS SGSSLTSLWAPPERPNGVILDYEMKYFEKSEG IASTVTSQMNSVQLDGLRPDARYVVQVRART VAGYGQYSRPAEFETTSESGGAQQLQEQLP LIVGSATAGLVFVAVVVIAIVCLRKQRHGS DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA VREFAKEIDVSCVKIEVIGAGEFGEVCRGL KQPGRRREVFAIKTLKVGYTEQRDRDLSEA SIMGQFDHPNIRLEGVVTKSFPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNIVHRLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPRWTAPEAI AYRKFTSASDVWSYGIVMWEVMSYGERPY

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						WDMNQDVINAVEQDYRLPPPMDCPTALHQ LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD WLDIAIKMGRYKESFVSAGFASFDLVAQMTA EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT LPVQV
924	2274	A	7985	1	503	FRPRTKKATAMYLEHYLDSIENLPCELRQNF QLMRELDQRTEDKKAIDILAAEYISTVKTLS PDQRVERLQKIQNAYSCKEYSDDKVQLAM QTYEMVDKHRRLDADLARFEADLKDKMEG SDFESSGGRGLKKGRGQKEKGRGRGRRTS EEDTPKKKKHKGG
925	2275	A	7994	447	589	LPCSFCACQMSSFERVWLQQSHFHNPRWNSR SPIRCYQHWPHCVHC
926	2276	A	7996	925	582	GPCKVCCITLAIMLQCHSFYRKDVQVEHPKS LNPKYSQIENFLSADMALKRKLCLLSIDLDFW IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQI RDTQPIPLGGRYTITIQ
927	2277	A	7998	2	353	RIQRPLNSRSPNHSFLVKAELTAKQATMKLSV CLLLVTALCCYQANAEPFALVSELLDFFI SEPLFKLSLAKFDAPPEAVAALGVKRCITDQ MSLQKRSLIAEVLVKILKKCSV
928	2278	A	8004	130	588	LAPLRCQFGTRTQPRSHPAANDPSAAMSAAAG ARGLRATYHRLLDKVELMLPEKLRPLYNHPA GPRTVFFWAPIMKWGLVCAGLADMARPAEK LSTAQSAVLMATGFIWSRYSLVIPKNWSLFA VNFVGAAGASQLFRIWRYNQELKAKAHK
929	2279	A	8007	2	1016	EFARRRVFIAAREMSLLRSLRVFLVARTGSYP AGSLLRQSPQPRHTFYAGPRLSASASSKELLM KLRRKTGYSFVNCKKALETCCGDLKQAEIWL HKEAQKEGWSKAAKLQGRKTKEGLIGLLOE GNITTVLVEVNCETDFVSRNLKFQLLVQVAL GTMHQCQTLKDQPSAYSKGFLNSELGSLPA GPDREGSLKDQLALAIGKLGENMLKRAAWV KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG ALVICETSEQKTNLEDVGRRLGQHVVGMAPL SVGSLDDEPGGEAETKMLSQPYLLDPSITLGG YVPPQGVSVVDFVRFECGEGEEAAETE
930	2280	A	8008	3	1679	NSRVWGPWTEPSAGSLRPMARKQNRNSKEL GLVPLTDDTSHAGPPGPRALLECDHLRSGV PGGRRRKDWSCSLVASLAGAFSGSFLYGYN LSVVNAFTPYKAFYNESWERRHGRPIDPDIL TLLWSVTVSIFAIGGLVGTIVKMGKVLGRK HTLLANNGFAISAALLMACSLQAGAFEMLI GRFIMGIDGGVALSVLPMYLSSEISPKIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLF GVIVVPAVVQLLSLFPDPSPRYLLEKHNEA RAVKAFQTLGKADVSQVEEVLAESEVRS IRLYSVLELLRAPYVRWQVVTIVITMACYQL CGLNAIWFTYNSIFGKAGIPPAKIPYVTLSTGG IETLAAVFSGLVIEHLGRRPLLIGFGFLMGLFF GTLTITLTLQDHAPWVPYLSIVGILAIASFCSG PGGIPFILTGEFFQSQRPAAFIAGTVNWLNS FAVGLLFFFIQKSLDTCFLVFATICITGAIYL YFVLPETKNRTYAEISQAFSKRNKAYPPEKI DSAVTDGKINGRP
931	2281	A	8009	861	300	AAGAVVSAMPKAKGKTRRQKFGYSVNRKRL NRNARRKAAPRIECSHRHAWDHAKSVRQNL AEMGLAVDPNRAVPLRKRKVKAMEVDIEER

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						PKELVRKPYVLNDLEAEASLPEKKGNTLSRD LIDYVRVMVENHGEDYKAMARDEKNYYQD TPKQIRSKINVYKRFYPAEQDFLDSLQKRK MEVE
932	2282	A	8011	412	1	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG DIRGSHFSSPQRQSRQVPGKETARVLRAGK QGRGQIPCPWPPPPPPPPSPGPGCRQFHQ SLEAKARHPASVREMRGKVKMRRLRRAPA STRASSRQPNPK
933	2283	A	8012	147	1077	PPVPPASRSDMAQNLKDLAGRLPAGPRGMGT ALKLLL GAGAVAYGVRESVFTVEGGHRAIFF NRIGGVQDQDTILAEGLHFRIPWFQYPIYDIRA RPRKISSPTGSKDLQMVNISLRVLSRPNAQEL PSMYQRLGLDYEERVLPSIVNEVLKSVVAKF NASQLITQRAQVSLIRRELTERAKDFSILDD VAITELSFSREYTAAVEAKQVAQQEAQRAQF LVEKAKQEQRQKIVQAEGEAAAKMLGEAL SKNPGYIKLRKIRAAQNISKTIATSQNRIVLTA DNLVLNLQDESFTRGSDSLIKGKK
934	2284	A	8023	255	982	SQFSLSQVLVDSABEGSLAAAAELAAQKREQ RLRKRELHLMRNEARKLNHQEVVEEDKRL KL PANWEAKKARLEWELKEEEKKKECAARG EDYEKVKLLEISAEDAERWERKKKRNPD LG FSDYAAAQLRQYHRLTKQIKPDMETYERLRE KHGEEFFPTSNLLHGTHVPSTEEIDRMVIDLE KQIEKRDKYSRRRPYNDDADIDYINERNAKF NKAERFYGKYTAIEKQNLERGTAV
935	2285	A	8027	59	310	LVSSTVNLLTEKAPWNSLAWTVTSYVFLKFL QGGGTGTGTMRDALTLGLIGPSHRHSLSRL SQHSSPAPMYSQTFHILVLG
936	2286	A	8032	1	639	SGRECNAKTYDYLFKLLIGDSGVGKTCVL FRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKQ JWDTAGQERFRITITAYYRGAMGIMLVYDIT NEKSFDNIRNWRNIEEHASADVEKMILGNKC DVNDKRQVSKERGEKLALDYGIKFMETSAK ANINVENAFFTLARDIKAKMDKKLEGNSPQG SNQGVKITPDQQRSSFFRCVLL
937	2287	A	8039	393	311	EETIHSENSYILEKYIPISANLTLTIA
938	2288	A	8052	675	1334	LHPAATSTAWLHVPPGLSMALSWVLTVL SLL PLLEAQIPLCANLVPVPITNATLDRITGKWFYI ASAFRNEEYNKSVQEIATFFYFTPNKTEDTIF LREYQTRQDQCIYNTTYLNVQRENGTISRIV GGQEHFAHLLILRDTKTYMLAFDVNDEKNW GLSVYADKPETTKEQLGEFYALDCLRIKSD VVYTDWKDKCEPLEKQHEKERKQEEGES
939	2289	A	8055	12	1039	SSVAEFPERVQLSQPNWNFSGAGGAWSLDF AEQLKWSAELARLGESIMDGKQGGMDGSKP AGPRDFPGIRLLSNPLMGDAVSDWSPMHEAA IHGHQLSLRNLISQGWAVNITADHVSPLEHA CLGGHLSVCVILLKHGAQVNGVTADWHITPL FNACVSGSWDCVNL LLQH GASVQPESDLASP IHEAARRGHVECVNSLIAYGGNIDHKJSHLGT PLYLACENQQRACVKKLLESGADVNQGGKQ DSPLHAVARTASEELACLMDFGADTQAKN AEGKRPVELVPPEPLAQLFLEREGPPSLMQL CRLRIKCFGIQQHKKITKL VLPEDLKQFLHL L
940	2290	A	8058	2	1203	KVLSIREPAHSTARKASEPSQPSQSPQGGHLI ARLRTMDLHLFDYSEPGNFSDISWPCNSSDCI

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						VVDTVMCPNMPNKSULLYTLSTFYIFIVIGMI ANSVVVWVNIQAKTTGYDTHCYILNLAIDL WVVLTPVWVSVLVQHNQWPMGELTCKVTH LIFSINLFGSIFLTCMSVDRYLSITYFTNPSS RKKMVRVRVVCILVWLLAFCVSLPDTYYLKT VTSASNNETYCRSFYPEHSIKEWLIGMELVSV VLGFAVPFSIIAVFYFLLARAISSDQEKHSS RKIIFSYYVVFVLCWLPYHVAVLDDIFSILHYI PFTCRLEHALFTALHVTQCLSLVHCCVNPVL YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA SRVSETEYSALQSTK
941	2291	A	8059	73	432	DMAGLMTITVTSLLFLGVCAHHIPTGSVVLPF PCCMFFVSKRIPENRVVSQYLSRSTCLKAGV IFTTKKGQFQCGDPKQEWVQRYMKNLDAKQ KKASPRARAVAVKGPVQRYPGNQTTTC
942	2292	A	8067	278	1262	GGIGEIKQRPSCLOGLDPSLSVLMNISLGLGS VFSAVISQKPSRDICQRGTSITQCQVDSQVT MMFWYRQPPGQSLTLIATANQSEATYESGF VIDKFPISRPNLTFSTLTVSNMSPEDSSYLCSA GRQGTYEYFGPGTRLTVTEDLKNVFPPEVA VFEPSEAEISHTQKATLVCLATGFYPDHVELS WWVNGKEVHSGVSTDPQLKEQPALNDSRY CLSSRLRVSATFWQNPVRNHFRQVQFYGLSE NDEWTQDRAKPVTVQVSAEAWGRADCGFTS ESYQQGVLSATILYEILLGKATLYAVLVSAIV LMAMVKKRDKSRG
943	2293	A	8070	1	879	MVKVVPATRGNLPRSQLTGTHQHCQPREPKI TASERLRRRPRATARLRAHAAPPEPLAVFAP PSDRKELLALPACDPVIASVMSWVQAASLI QGPDKGDFVDEADESLAQREWQSNMQR RVKEGYRDGIDAGKAVTLQQGFNQYKKGGA EVILNYGRLRGTLALLSWCHLHNNNSTLINK INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL DSIEDMDLCHVVPAAKKIDEAKDERLCENNA EFNKNCSKSHSGIDCSYVECCRTQEHASGK PKPHMDFGTDTSQF
944	2294	A	8073	1	797	ESARWSRQLRRLIRLSFPISCGRSHAFGGCK MAATSGTDEPVSGELVSAHALSLPAESYGN DPDIEMA WAMRAMQHAEEVYKLISSVDPQF LKLTKVDDQIYSEFRKNFETLRIDVLDPEELK SESAKEKWRPFCLKFNGIVEDFNYGTLRLD CSQGYTEENTIFAPRIQFFAIEIARNREGYNKA VYISVQDKEGEGVNNNGEKGKADSGEEENT KNGGEKGADSGEKEEGINREDKTDKGGEK GKEADKEINKSGEKAM
945	2295	A	8074	2	505	GAATLLRSASSAARKAAEAQVWLHLHRYL SADRRVLGLREWGRPASERECSLCQRLKREL NMGDVEKGKKIFIMKCSQCHTVEKGKKHKT GPNLHGLFGRKTGQAPGYSYTAANKNKGITW GEDTLMEYLENPKKYPGTMIFVGIKKKEER ADLIA YLKKAATNE
946	2296	A	8081	42	590	EORRGKFGGKLCNLFYFHSNSAESRMDVLF VAIFAVPLILGQEYEDERLGEDEYYQVYVY YTVTPSYDDFSADFTIDYSIFESEDRLNRLDK DITEAIIETTSLETARADHPKPVTVKPVITEPQ SPRSEAMPCPVLRSPILPVRVPLFRWGCISC KKVGRRLMLTWLWGVWQEEIGR
947	2297	A	8084	322	549	GGGSSPRELAGAAGLTVTSQAVARRQPSF SRARAPAHSLRAALSASSARSWGAVSRDRG

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						PCPPAIMYQSSNKC
948	2298	R	8093	3905	846	MEPGEVKDRILENISLSVKKLQSYFAACEDEI PAIRNHDKVLQRLCEHLDHALLYGLQDLSSG YWVLVVFHTRREAIAKQIEVLQHVATNLGRSR AWLYLALNENSLESYLRLFQENLGLLHKYYV KNALVCSHDHLTLFLTLVSGLEFIRFELDLDLDA PYLDLAPYMPDYKPYLLDFEDRLPSSVHG SDSLSLNSFNSVTSTNLEWDDSAIAPSSSEDYD FGDVFFPAVPSVPSTDWEDGDLTDTVSGPRST ASDLTSSKASTRSPTQRQNPFFNEEPAETVSSS DTPPVHTTSQEKEEAQALDPPDACTELEVIRV TKKKKIGKKKSRDEEASPLHPACSQKKCA KQGDGDSRNGSPSLGRDSPDTMLASPOEAGE GPSSTTESSERSEPLLIPEMKDTSMERLGQPL SKVIDQLNGQLDPSTWCSRAEPDQSFRTGSP GDAPERPLCDFSEGLSAPMDFYRFTVESPT VTSGGOHHDPAQLGQPLHVPSSPEAAGQEEE GGGGEGQTPRPLEDTTREAQLEAQLSLVRE GPVSEPEPGTQEVLCQLKRDQPSCLSSAEDS GVDEGQGSPEMVHSSEFRVDNNHLLLLMIH VFRENEQLFKMIRMSTGHMEGNLQLLYVLL TDCYVYLLRKGATEKPYLVEEA VSYNELDY VSVGLDQQTVKLVCTNRRKQFLDADVAL AEFFLASLKSAMIKGCREPPYSILTDATMEK LALAKFVAQESKCEASAVTVRFYGLVHWED PTDESLGPTPCHCSPPEGTITKEGMLHYKAGT SYLGKEHWKTCFVVLNGLYQYPDRDTPVIP LLSVNMGGEQCGGCRANTTDRPHAFQVILS DPPCLELSAESAEMAEMWQHLCQAVSKGVI PQGVAPSPCIPCLVLTDDRLFTCHEDCQTSF FRSLGTAKLGDISAVSTEPGKEYCVLEFSQDS QQLLPPWVIYLSCTSELDRLLSALNSGWKTIY QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRD*PWC*
949	2299	A	8095	9	2374	ARRADTVLLESPSMLQGLLPVSLLSVAVSAI KELPGVKKYEVVYPIRLHPLHKREAKEFEQQ EQFETELKYKMTINGKIAVLYLKNKNLLAP GYTETYNSTGKEITTSQIMDDCYQGHILN EKVSDASISTCRGLRGYFSQGDQRYFIEPLSPI HRDGOEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKNLTHVALVGMEIWTDDKDKIT PNASFTLENFSKWRGVSLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPPYSGVVQDHSD NLLRVAGTMAHEMGHNFOMFHDDYSCKCPS TICVMDKALSFIPTDFSSCSRLSYDKFFEDKL SNCLFNAFLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICDAKTCKIKATFQCALGECCEK CQFKKAGMVCRAKDECDLPEMCNGKSGNC PDDRFBQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWOPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCCKLFCQGGSDNLFW KGRJVTFLTCTKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSCKGHAV CDHELQCQCEGWIPDCDDSSVVFHFSIVVG VLFPMVAVFVVVAMVIRHQSSREKQKQDQRP LSTTGTRPHKQKRKPQMVKA VQPQEMSOMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD NPMSTPKDSNPKA

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950	2300	A	8100	1	1251	MGLLLMLASAVLGSFLTLLAQFFLLYRROPE PPADEAARAGEGFRYIKPVPGLLREYLYGG GRDEEFGAAPEGGATPTAAPETPAPPTRET YFLNATILFLRELRTALTTRWVTKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRRLRVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIKRKHLPNY KIRFKPFFPYQTLQGFEEDEHHIQQWALTE GRLKVTLLCSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDDGGLLTVPLRQ CPG
951	2301	A	8108	1612	839	EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLQRTEDLKAIDKLATEYMSSAR SLSSEELALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDLDLAREADLKEKQI ESSDYDSSSSKGGKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGWFC PRCSQERKKK
952	2302	A	8112	595	291	PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQNMKKQSDSVKCK RRDDGLSAAARKQRDSTPRDSEMQQKQKK ANEKKEPK
953	2303	A	8118	1	669	VCAGIRDPCTPLAKPAAGGAENLSFGKQPG LETNLLKMTTPNKTPGADPKQLERTGTVREI GSQAVWSLSSCKPGFGVDQLRDDNLETYVQ SDGSQPHLVNIQFRRKTI'VKTL'CIYADYKSDE SYTPSKISVRVGNFHNQEIQLLELVEPSGW IHVPLTDNHKKPRTTFMIQIAVLANHONGRD THMRQIKIYTPVESSIGKFFRCTTIDFMMYRS IR
954	2304	A	8133	66	1015	PPLPPRSFPNLSRPEPLPEPGRRGCNRSREPA ARAPSPPPFEGAPGRAMVKVTFNSALAQKE AKKDEPKSGEELIIPDAVAVDCKDPDDVV PVGQRRAWCWCMCFGLAFMLAGVILGGAY LYKYFALQPDVVYCGIKYKDDVILNEPSAD APAAALYQTIENIKIFEEEEVEFISVPVPEFADS DPANIVHDFNKKLTAYLDLNDKCYVPLNT SIVMPPRNLELLINIKAGTYLPQSYLIEHBMV ITDRIENIDLGFYIYRLCHDKETYKLQRRETI KGIQKREASNCFAIRHFENKFAVETLICS
955	2305	A	8143	35	1171	VESRSAWHEGEDQIDRLDFIRNQMNI.TL.DV KKKIKEVTEEVANKVSCAMTDEICRLSVLVD EFCSEFHPNPDVLKIYKSELNKHIEDGMGRNL ADRCTDEVNALVLQTQQEIIENLKPLLPAGIQ DKLHTLIPCKKFDLSYNLNYHKLCSDFQEDIV FRFSLGWSSLVHRFLGPRNAQRVLLGLSEPIF QLPRSLASTPTAPTTPATPDNASQEELMITLVT GLASVTSRTSMGIIVGGVWKTIGWKLLSVS LTMYGALYLYERLSWTTHAKERAFKQQFVN YATEKLRMTVSSTSANCSSHQVKQIATTFARL CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS KLLRNKAVQLENELENFTKQFLPSSNEES
956	2306	A	8157	1854	798	ASGSFAPSSSSAMAAACGPGAAGYCLLLGLH LFLLTAGPALGWNDPDRMLLRDVKALTLHY

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						DRYTTSRRLDPIQLKCVGGTAGCDSYTPKVI QCQNKGWGDGYDVQWECKTDLDAIYKFGKT VVSCEGYESEDQYVLRGSCGLEYNLDYTEL GLQKLKESGKQHGFAFSDYYKWSADSC NMSGITIVVLLGIAFVYKFLSDGQYSPPP YSEYPPFSHRYQRFTNSAGFPFPGFKSEFTGPQ NTGHGATSGFGSAFTGQQGYENSGPGFWTGL GTGGILGYLFGSNRAATPFSDSWYYPSPSY PGTWNRAYSPLHGGSGSYSVCSNSDTKTRTA SGYGGTRRR
957	2307	A	8159	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSL VYSMPSRNLSLRLEGLQEKDSDGSPYSCSVNQ DKQKSRGHSIKTLELNLVPPAPPSCRLOGV PHVGANVTLSQSPRSKPAVQYQWDRQLPSF QTFFAPALDVIRGSLSLTNLSSMAGVYVCKA HNEVGTAQCNVLEVTOPGAAYVAGAVVG TLVGLLOLAGLVLLYHRRGKALEEPANDIKE DAIAPIRLPWPKSSDTISKNGTLSSVTSARAL RPPHGPFRPGALTPTPSLSSQALPSPRLPTDG AHPQIPISIPGGVSSSGLSRMGAVPVMVPAQS QAGSLV
958	2308	A	8161	2340	1192	ELARRPKQSSSEKSRNMIRNWLITIFLPLKL EKCESSVSLTVPPVVKLENGSSTNVSLTRPP LNATLVITFEITFRSKNITILELPDEVVPPGVT NSSFQVTSQNVGQLTVYLHGHNHNTGTGPRIR FLVIRSSAISDQVIGWYFVAWSISFYQVIM NWRKRSVIGLSDFVALNLGTFVAYSFNI LWVPYIKEQFLKYPNGVNPVNSNDVFFSLH AVVLTLLIIVQCCLYERGGQVSWPAIGFLVL AWFVAFVMTVAAGVITWLQFLCFYSYTKL AVTLVKYFPQAYMNFYKSTEGWSIGNVLL DFTGGSPSLLQMFQSYNNQDQWTLIFGDPTK FGLGVFSIVFDVVFIFQHFCLYRKRPGYDQLN
959	2309	A	8163	521	1345	GERAGRRRGRGVWAQFPQLLPRFVGSRR MQPPGPPPAYAPTINGDFTFSSADAEDLSGSI ASFDVKLNLGDFIKESTATTFLRQRGYGL LEVEDDDPEDNKPLLEELDIDLKDIYYKIRCV LMPMPSLGFNRQVVRDNPDFWGFLAVVLFSS MISLYGQFRVVSIIITWIFGSLTIFLLARVLG GEVAYGQVLGVIGYSLLPLIVAPVLLVVGSP EVVSTLKLFGVFWAAYSAASLLVGEEFKTK KPLLIYPIFLLYIYFLSLYTG
960	2310	A	8167	1	2921	MTCFKGQKGEQRSHAFEANKDHKAKVPSPN LYSQNALQFTVDESRILWLNQFLDLKQSL NQFMAVYKLNDSKSDHEVDVVRVDGLMLK FVIPSEVKSECHQDQPRASISQSEMIATNTRH CPNCRHSDLEALFQDFKDCDFFSKTYTSFPKS CDNFNLLHPIFQRHAHEQDTKMHEIYKGNITP QLNKNTLKTSAATDVWAVYFSQFWIDYEGM KSGKGRPISFVDSFPLSIWICQPTRYAESQKEP QTCNQVSLNTSQSESSDLAARLKRKLLKEY YSTESEPLTNGGQKPSSTDTFRFSPSSSEADI HLLVHVHKHVSQMNIHYQYLLLLFLHESLLL SENLRKDVEAVTGSPASQTSICIGILLRSAELA LLLHPVDQANTLKSVPSESVSPVVPDYLPTEN GDFLSSKRKQISRDINRISVTVNHMSDNRS SVDLSHPLKDPFLFKSASDTNLQKGISFMDY LSDKHLGKISEDESSGLVYKSGSGEIGSETSD KKDSFYTDSSSVLNRYEDSNLSFSDSDGNQNI LSSTLTSKGNETIESIFKAEDLLPEAASLSEN

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						DISKEETPPVRTLSQSSLSGKPKERCPPNLAP LCVSYKNMKRSSSQMSLDITSLDSMILEEQLL ESDGSDSHMFLEKGNKKNSTTNYRGTAEVSN ACANLQNYGETSPDAISTNSEGAQENHDDL SVVVFKITGVNGEIDIRGEDTEICLQVNQVTP DQLGNISLRHYLCNRPVGSQDKAVIHSKSSPE ISLRFESGPGAVIHSLLAEKNGFLQCHIEFST EFLTSSLMNIQHLEDETATVMPMKIQVSN KINLKDDSPRSSTVSLEPAFVTVIDHLVVER SDDGSFHIRDHMLNTGNDLKENVKSQSVLL TSGKYDLKKQRSVTQATQTSQGPVWPSQSAN FPEFSDFTREQLMEENESLKQELAKAKMAL AEAHLEKDALLHHIKKMTVE
961	2311	A	8172	1442	682	TAAMSIFTPTNQRILTNAVVRMKRAGKRFEI ACYKNKVVGWRSQVEKDLDEVLTQHSVFVN VSKGQVAKKEDLISAFGTDDQTEICKQILTKG EVQVSDKERHTQLEQMFRIATIVADKCVNP ETKRPYTVILIERAMKDIHYSVKTNKSTKQQA LEVIKQLKEKMKIERAHMRLRFLPVNEGKKL KEKLKPLIKVIESEDYGGQLEIVCLIDPGCFREI DELIKKETKGGKSLEVLNLKDVEEGDEKFE
962	2312	A	8175	286	587	NISNKAESVSHPSVISHSMDSFGQPRPNDQS VLRMRQKKYWKTKQVFIKATGKKEDEHLVA SDAELDAKLEVFHSVQETCTELLKHEKYQLR LNGMKS
963	2313	A	8181	13	2215	AEGCAERRGTEPVVELSMSWESGAGPGLGSQ GMDLVWSAWYGKCVKGKGSPLSAHGIVV AWLSRAEWDQVTYVLFCDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEDQEEDKNIVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIAWNNPSRPRVECVLAELKGVTCENREA VLD AFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPSQFWQPLLRLGLHSQNFQALLE RMLSELPALGISGIRPTYLRTWTVELIVANTKT GRNARRFSAGQWEARRGWLFNCASLDWP RMVESCLGSPCWASPOLLRIFKAMGQGLPD EEQEKLLRICSIYTSQGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEEEKEKEVLPDQVEEEEENDDQE EEEEDEDEDEDEEDRMEVGPFTGQESPTA ENARLLAQKRGALQSAWQVSSDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQQLHLGLKTGLQLF
964	2314	A	8184	6	1393	EPRRNFRDDSTRPRTGRTRGRRRACRS GTGLRSLLLPRLQLPAGPFSRCRWDPVSSPR PSTMPPKGGDGKPPPIGRFTSLKIGIVGLP NVGKSTFFNVLTNSQASAEFPFCTIDPNESR VPVPDERFDLQYHKPASKIPAFNLNVDIAG LVKGAHNGQLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIHHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKLHFLT KPMVYL VNLSEKDYIRKKNKWLKIKEWVD KYDPGALVIPFSGALELKLQELSAEERQKYLE

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						ANMTQSALPKIIRKAGFAALQLEYFFTAGPDEV RAWIIRKGTAKAPQAAGKIHTDFEKGFIKAEV MKYEDFKKEGSENAVKAAGKYRQQGRNYIV EDGDIIFKFNTPQPKKK
965	2315	A	8195	1437	594	RSFSLSFSLSPSEMMALGAAGATRVFVAMV AAALGGHPLLGVSATLNSVLNSNAIKNLPPPL GGAAGHPGSAVSAAPGILYPGGNKYQITDNY QPYPCAEDDEECGTDEYCAPTRGGDAGVQIC LACRKRKRRCMRHAMCCPGNYCKNGICVSS DQNHFRGEIETTTESFGNDHSTLDGYSRRTT LSSKMYHTKGQEGSVCLRSSDCASGLCCARH FWSKICKFVLKEGQVCTKHRRKGSHGLEIFQ RCYCGEGLSCRIQKDDHHQASNSSRLHTCQRH
966	2316	A	8207	416	4082	KFKLIKIMLLTLIILLPVVSKFSFVLSAPQHW SCPEGTLAGNGNSTCVGPAPFLIFSHGNSIFRI DTEGTNYEQLVVDAGVSVIMDFHYNEKRY WVDLERQLLRVFLNGSRQERVCNIEKNVSG MAINWINEEVIWSNQEGHITVDMKGNNNSHI LLSALKYPANVAVDPERFIFWSSEVAGSLY RADLDGVGVKALLETSEKITAVSLDVLDRKL FWIQYNREGSNSLICSDYDGGSVHISKHPTQ HNLFAMSLFGDRIFYSTWKMKTIVIANKHGT KDMVRINLHSSFVPLGELKVHPLAQPKAED DTWEPEQKLCKLRKGNCSSTVCGQDLQSHLC MCABGYALSRDRKYCEGNDWKYCEDVNEC AFWNHGCTLGCKNTPGSSYYCTCPVGFVLLPD GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF CPEGSVLERDGTCSGCSPPDNGGCSQLCVPL SPVSWECDCFPGYDLQLDEKSCAASGPQFPL LFANSQDIRHMHFDGTDYGTLLSQQMGMVY ALDHDVPENKIYFAHTALKWIERANMDGSQ RERLIEEGVDVPEGLAVDWIGRRFYWTDGK SLIGRSDLNGKRSKIITENISQPRGLAVHPMAK RLFWDTDGINPRIESSSLQGLRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHFFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSLVVHP LAKPGADPCLYQNGGCEHICKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDLSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPASSKCINT EGGYVCRCSEGYQGDGIHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECLSHDGYCL HDGVCMYIEALDKYACNCVVGIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYRTQKLLSKNPKNPYEES RDVRSRRPADTEDGMSSCPQWVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTQGCWIPVSSDKGSCQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ
967	2317	A	8210	3	601	SSAMGSRSSHAAVIPDGDSSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRHIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRMLMVGQVTEEQ ENIADRTVQEADGEDGDGAVSFVEFTKSLEKM DVEHKMSIRILK

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968	2318	A	8211	2	409	ISSCPHTAYEGSMSTLSNFTQTLEDVFRFRIT YMDNWRQNTTAEQEALQAKVDAENFYVIL YLMVMIGMFSFIVAILVSTVKSRRHSNDP YHQYTVEDWQEKYKSQLNLEESKATHENIG AAGFKMSP
969	2319	A	8215	1	1938	GMPSRSGGRAAPGPPPPPPPGQAPRWSRWR VPGRLLLLLLPALCCLPGAARAAAAAGAGN RAAVAVAVARADEAEAPFAGQNWLSYGY LLPYDSRASALHSKALQSAVSTMQQFYGIP VTGVLDQTTIEWMKKPRCGVPDHPHLSRRRR NKR YALTGQKWRQKHITYSIHNYTPKV GELD TRKAIRQAFDVWQKVTPLTFFEEVPYHEIKSDR KEADIMIFFASGFHGDSSPFDGEGFLAHAYF PGPGIGGDTHFDSDEPWT LGNANHDGNDLFL VAVHELGHALGLEHSSDPSAIMAFFYQYMET HNFKLQDDDLQGIQKIYGPPAEFLEPTRPLPTL PVRRIHSPSERKHERQPRPPLGDRPSTPGT KPNICDGNFNTVALFRGEMFVFKDRWFWRL RNNRVQEGYPMQIEQFWKGLPARIDAAAYER ADGRFVFFKGDYVWFEKVTVEPGYPHSLG ELGSCLPREGIDTALRWEVPGKTYFFKGERY WRYSEERRATDPGYPKPITVWKGIPOAPOGA FISKEGYTYFYKGRDYWKFDNQKLSVEPGY PRNILRDWMGCNQKEVERRKERRLPQDDVDI MVTINDVPGSVNAVAVVIPCILSLCILVLYTI FQFKNKGTGPQVPTYKRPVQEWV
970	2320	A	8216	1235	2223	SRSLQFYVFSFRRTGLFTCKLIVEIFFRNYMN DSLRTNVFVRFPETIACACIYLAARALQIPL TRPHWFLLFGTTEBEEIEICIELRLYTRKKPN YELLEKEVEKRKVALQEAALKAKGLNPDGTP ALSTLGGFSPASKPSSPREVKAEKSPISINVK TVKKEPEDRQQASKSPYNGVRKDSKRSRNSR SASRSRSRTRSRSRSHTPRRHYNNRRSRSGTY SSRSRSRSRSHSESPRRHHNHGSPHLKAKHTR DDLKSSNRHGHKRSRSRSQSKSRDHSDA KKHRHERGHRDRRERSRSFERSHKS KHHGG SRSGHGRHRR
971	2321	A	8217	3	3274	DCRLQAAMPTNFTVVPVEAHADGGGDETA RTEAPGTPEGPEPERSPGDGNPRENSFLLN VEVEQESFFEKGK NMFEEEMDSNPMVSSLL NKLANYTNLSQGVVEHEEDEESRRREKAPR MGTFIGVYLPCLQNLGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSALATNGVVP AGGSYYMISRLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLYISPGAAIFQAEAAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGKYN KLALVFLACVLSILAIYAGVIKSAFDPDPDPV CLLGNRTLSSRSFDACVKAYGIHNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDAASFILLVGIYFSPVVG IMAGSNRSGDLKDAQKS IPTGILAI VTTSTFY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSWPVWVIGSFFSTCGAGLQILTGAPRL QAIARDGIVPFLQVFGHGKANGEPTWALLT VLICETGILIASLDSVAPILSMFFLMCYLFVNL ACAVQTLRLTPNWRPRFKFYHWTLSFLGMSL CLALMFICSWYYALSAMLIAGCIYKYIEYRG AEKEWGDGIRGLSLNAARYALLRVEHGPPHT KNWRPQVLVMLNLDAEQAMKHPRLLSFTSQ

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						LKAGKGLTIVGSVLEGTLYLDKHMEAQRAEE NIRSLMSTETKGFQCQLVVSSSLRDGMSHLIQ SAGLGGLKHNTVLMAWPASWKQEDNPPSW KNFVDTVRDTHAAHQALLVAKNVDSPQONQ ERFGGGHIDVWWIVHDGGMMLLPFLLRQH KVWRKCRMRIFTVAQVDDNSIQMKDLQMP LYHLRISAEVEVVMVENDISAFYERTLMM EQRSQMLKQMQLSKNEQEREALIHDRNTAS HTAAARTQAPPTPKVQMTWTREKLIAEK YRSRDTLSGFKDLFSMKPDQSNVRRMHTAV KLVGVVLNKSQDAQLVLLNMPGPPKNRQGD ENYMEFLEVLTEGLNRVLLVRGGREVITYS
972	2322	A	8224	701	246	TSRRVTMKFNPFVTSRDRSKNRKRHFNAPSHV RRKIMSSPLSKELRQKYNVRSMPRKDDDEVQ VVRGHYKGGQIGKVVQVYRKKYVYIYERVQ REKANGTTVHVGIHPSKVIVITRLKDKDRKKI LERKAKSRQVGKEKGKYKEELIEKMQE
973	2323	A	8237	873	4610	GCPHAGGKGRVPTGGTGGRTWSPSAAPRSC PRPGPTPAPGAMDKLPPSMRKLRYSLPQQVG AKAWIMDEEEDAEEEGAGGRQDPSSRSIRLR PLPSPSPSAAAGGTESRSALGAADSEGPARG AGKSSNTGDCRRFRGSLASLGRGGGSGGTG SGSSHGHLHDSAEERRLIAEGDASPGEDRTFP GLAAEPERPGASAPPAASPPPPQPPQPASAS CEQPSVDTAIKVEGGAAGDQILPEAEVRLG QAGFMQRQFGAMLQPGVNFSLRMFGSQKA VEREQERVKSAGFWIHPYSDFRYWDLTML LLMVGNIHPIVGIITFFKIDENTTPWVFNVS TFFLDLVLNFRGTGIVVEDNTEILDPORIKMK YLKSWFMVDFISSIPVDYIFLIVETRIDSEVYK TARALRIVRFKILSLRLRLRLRLIRYHQWE EIFHMTYDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMQLQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSHMLCIGYGRQAPVGMDSV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPDTRQRIHD YYEHRYQGKMFDEESILGELSEPLREEINFC RKLVASMPLFANADPNFVTSMLTKLRFVFO PGDYIIREGTIGKKMYFIQHGVSVLTKGNKE TKLADGSYFGEICLLTRGRRTASVRADTYCR LYSLVDNFNEVLEEYPMRRRAFETVALDRL DRIGKKNISILLHKVQHDNLNSGVFNQENIIQ QIVQHDREMAHCAHRVQAAASATPTPTPTVW TPLIQAFLQAAAATTSVAIALTHFRLPAAIFR PPPGSGLGNLGAQTTPRHLKRLQSLPSALGS ASPASSPSQVDTFSSSSFHQQLAGFSAPAGLS PLLSSSSSPPGACGSPSAPTASAGVAATTIA GFGHFHKLALGGLSSSDSPLLTPLPQGARSPQ AAQPSAPPARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPASGSHGSLLLPPASSPPPPVPPQR RGTPPLTPGRLTQDLKLISASQALPDGAQT LRRASPHSSGESMAAFPLFRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSAGSLPPP LSLFGARATSSGPPPLTAGPQREPGARPEPVR SKLPSNL
974	2324	A	8247	279	468	EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRJCSTLYLLGSHWNNLVVRSFVL G

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975	2325	A	8249	62	1571	LVALKNWKPGTNPAPQSPVFGAEVSGVYMMTKVLGMAPVLGPRPPQEQVGPLMVKVEEEKGKYLPSLEMFRRQFRQFGYHDTGPREALSQRLVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQAWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPNEQKPVWEKISSSGTAKESPSMQPQPLETSHKYESWGPLYIQESGEEQEFADPRKVRDCRLSTQHEESADEQKGEAEGLKGDIISVIIANKPEASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYICAECKGAFSSNSNLTKHRRHTHTGEKPYVCTKCGKAFSHSSNLTLHYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAAPYQCKDCGKAFSGKGSRLRHYRIHTGEKPYQCNECGKSFSQHAQLSSHQRLHTGEKPYKCKECKGAFNHSNFKHHRHTGEKPYWCHHCGKTFCSKSNLSKHQRVHTGEGEAP
976	2326	A	8257	298	7086	GNMACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAMPSAGTLPWWQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFSDARRLLYSQKDTSMKDMRKVLRLTLQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEMIQLGDQEVSELCLGPREKLAARVLRNSMDILKPIRLTLNSTSPFFSKELAEATKTLHSLGTLAQELFSMRWSMDMRQEVMFNTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAE TFYDNSTTPYCNDLMKNLESSPLSRITWKALKPLLVGKILYTPDTPATRQVMAEVNKTFOELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRMECVNLNLEPIATEVWLINKSMELDERKFWAGIVFTGITPGSIELPHHVYKIRMGIDNVERTNKKIDGYWDPGRADPFEDMRYVWGGFAYLQDVVEQAIRVLTGTEKKTGVYMQOMP YPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIGIVYEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAAGLLVVLKLGNNLPYSDPSVVFVFLSVFAVVTLQCFLISTLFSRANLAAACGGIYYFTLYLPYVLCVAWQDYVGFTLKIFASLLSPVAFGFGCEYFALFEEQIGVQWDNLFESPVEEDGFNLTTSVSMMLFDITLYGVMTWYIBAVFPQGYGIPRPWYFPCTKSYWFGESDEKSHPGSNQKRISICMEEETHLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKT TTMSILTGLFPPTSGLAYLKGDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVILDEPTAGVDPYSRRGIWELLKYRQGRITLSTHHMDEADVLDGRIAIISHGKLCCVGSFLKNQLGTGYLYTLVKKDVESSLSSCRNSSSTVSYLKKEDSVSQSSDAGLGSDESHTLTIDVSAISNLIRKHVSEARLVEDIGHELTYVLPYEAAKBAFVELFHEIDRLSDLGISSYGISETTLEIFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLPFFTEDDAADPNDSIDIPESRETDLLSGMDGKGSYQVKGWKLTTQQQFVALLWKRLLIARRSRKGFFAQIV

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						LPAVFVCIALVFSLVPPFGKYPSELEQPMY NEQYTFVSNDAPEDTGTLELLNALTKDPGFG TRCMEGNPDPQPCQAGEEWTAPVPQTIM DLFQNGNWTMQNPSPACQCSSDKKKMLPV CPPGAGGLPPPQKQNTADILQDLTGRNISDY LVKTYVQIAKSLKNKIWNNEFRYGGFSLGVS NTQALPPSQEVNDATKQMKKHLKLAKDSSA DRFLNSLGRFMTGLDTRNNVKVWFNNKGW HAISSFLNVINNAILRANLQKGENPSHYGITAF NHFLNLTKQQLSEVAPMTTSVDLVVICVIFA MSFVPASFVVFVLIQERVSKAKHLQFISGVKPI YWLSNFVWDMCNYVVPATLVIIIFICFQKSY VSSTNLPVLALLLLYGWSITPLMYPASFVFK IPSTAYVVLTSVNLFIGINGSVATFVLELFTDN KLNNDILKSVFLIFPHFCLGRGLDMVKNG AMADALERFGENRFVSPLSWDLVGRNLFAM AVEGVVFLITVLIQYRFFIRPFVNKLSPLN DEDEDVRERQRILDGGGQNDILEIKELTKY RKRKPAVDRICVGIPPGECFLLGVNGAGK SSTFKMLTGDITVTRGDAFLNRNSILSNIHEV HQNMGYCPQFDAITELLTGREHVEFFALLRG VPEKEVGKVGWEAIRKLGLVKYGEKYAGNY SGGNKRKLSTAMALIGGPPVFLDEPTTGM PKARRFLWNCALSVVKEGRSVVLTSHSMEEC EALCTRMAIMVNGRFRCLGSVQHLKNRFGD GYTIVVRIAGSNPDLKPVDFFGLAFPGSVPK EKHRNMLQYQLPSSLSSLARIFSLSQSKRLH IEDYSVSQTTLDQVFVNFAKDQSDDDHLKDL SLHKNTQTVVDVAULTSFLQDEKVKESEYV
977	2327	A	8260	3	1567	IPGSTISFSLCFIPPCVPTMVRKPVVSTISKGG YLQGNVNGRLPSLGNKEPPGQEKVQLKRV TLLRGVSIIGTIGAGIFSPKGVQLQNTGSVGM SLTIWTVCGVLSLFGALSYAELGTTIKKSGGH YTYILEVFGPLPAFVRVWVELLIIRPAATAVIS LAFGRYILEPFIQCEIPELAIKLITAVGITVVM VLNSMSVSWSARIQIFLTFCKLTAILIINPGV MQLIKGQTQNFKDAFSGRDSITRLPLAFYYG MYAYAGWFYLNFTVEEVENPEKTIPLAICISM AIVTIGYVLTNVAYFTTINAEELLSNAVAVT FSERLLGNFSLAVPIFVALSCFGSMNGGVFAV SRLFYVASREGHLPEILSMIHVRKHTPLPAVIV LHPLTMIMLFSGLDLSLLNLSFARWLFGLA VAGLIYLRKCPDMHRPFKVPFLFIPALFSFTC LFMVALSLYSDPFTGIGFVITLTGVPAYYLFI WDKKPRWFRIMSEKJTRTLQILEVVPEEDKL
978	2328	A	8261	2	2165	RGGSLRCLVGLKLLGQLLCFQSERCVRFPEGLL RHRGCGLLSSRLSAGKPPRLTSFPGSWGVLPP LADAASMSGVRAVRISIESACEKQVHEVGDL GTETYLPPLSMSQNLARLAQRIDFSQSGSSEE EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMILDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLO RDNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPFHGTFEVIKNTDLDDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQFFPSLO LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE HNLHLIREFHKQTLSSIMMPHPASAFGHKR

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						MRLSGPQAFDKNEINSLQSSEGLLEKIHKQAK HIFLRSRAAATIDSLASRIEDPQIQAHWSNIND VYESSVKVLITSQGYEQICKSIQLQLNIGVEQI RVVHRDGRVITLSYQEQELQDFLLSQMSQHQ VHAVQQLAKVMGWQVLSFSNVHVLGPISIG NASAITVASPGDYAISVRNGPESGSKIMVQF PRNQCKDLPKSDVLQDNKWSHLRGPFFKEVQ WNKMBGRNFVYKMELLMSALSPCLL
979	2329	A	8289	2	1053	FVWNPRGGRKRRRQAAVTQAATRASGTSPSP RDGTMTOGKLSVANKAPGTEGQQQVHGEKK EAPAVPSAPPSYEEATS GEGMKAGAFPPAPTA VPLHPSWAYVDPSSSSSYDNGFFTGDHFLT FSWDDQKVRVVRKVVYILLIQLLVTLAVV ALFTFCDPVKDYVQANPGWYWASYAVFFAT YLTACCSGPRRHFFWNLLTVFTLSMAYLT GMLSSYYNTTSVLLCLGITALVCLSVTVFSFQ TKFDFTSQCGVLPVLLMTLFFSGLILALLPFQ YVPWLHAYVYALGAGVFTLFLALDTQLLMG NRRHLSPEEYIFGALNIYLDIYIFTFLQLFG TNRE
980	2330	A	8305	59	857	ASQLPDYISIPPSLPRI SFHPSPTLARVMAEAP SEATQSHSISSSSFGAEP SAGGGSGPACPAL GTKSCSSCAVHDLIFWRDVKKTG FVFGTTLI MLLSLAAFSVISVSYLILALLSVTISFRIYKSV IQAVQKSEEGHPFKAYLDVDITLSSEAFHNY MNAAMVHINRALKLIRLFLVEDLVDSLKLA VFMWLMTYVGAVFNGITLLLAELLIFSVPV YEK YKTQIDHYVGIARDQTKSIVEKIQAKLPG IAKKKAE
981	2331	A	8308	186	1337	TRMSRHEGVSCDACLKG NFRGRRYKCLICYD YDLASCYESGATTTTRHTDHPMQCILTRVD FDLYYGGAEAFSVEQPQSF TPCYCGKMGYTET SLQEHVTSEHAETSTEVICICAALPGGDPNH VTDDFAAHLTLEHRAPRDLDESSGVRHVRR MFHPGRGLGGPRARRSNMHTSSSTGGLSSS QSSYSPSNREAMDPIAELLSQLSGVRRSAGGQ LNSSGPSASQLQLQMLQLERQHAQAARQ QLETARNATRRNTNTSSVTITITQSTATNAN TESSQQLQNSQFLTRLNDPKMSETERQSM ESERADRS LFVQELLLSTLVRESSSSDEDDR GEMADFGAMGCVDIMPLDVALENLNLKESN KGNEFPFPL
982	2332	A	8315	1	1004	GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFLFLTRSRGAASAGQEPLHNEEL AGAGRVAQPGPLEPEEP RAGGRPRRRDLGS RLQAQRRARVAWAEADENEEAVILAQEE EGVEKPAETHLSGKIGAKKLKLEEKQARKA QREAEAEEREERKLESQREAEWKKEERLR LEEEQKEEEKKAREEQAREHEEYLLKKEA FVVEEGVGETMTTEQSQSFLTEFINYIKQSK VVLEDLASQVGLRTQDTNRIQDLLAEGTIT GVIDDRGKFYITPEELAAVANFIRQRGRVSIA ELAQASNSLIWGRES PAQAPA
983	2333	A	8320	244	1420	RRRWRARGGLVPTLA WAEATGAYVPGRDKP DLPTWKRNFSA LNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPTDNGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPQPLRSPSLDNPTFFPNLGPSENPLKRLVPG EEWEFEVTA FYRGRQVFFQQTISCEGLRLVGS

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						EVGDRTLPGWPVTLDPDGMSLDRGVMSYV RHVLSCLGGGLALWRAGQWLWAQRLGHCH TYWAVSEELLPNSGHGPDPGEVPKDKEGGVF DLGPFTVGSGLGPPDLITFTEGSGRSPRYALWFC VGESWPQDQPWTKRLVMVKVVPCLRALVE MARVGGASSENTVDLHISNSHPLSLTSDQY KAYLQDLVEGMDFGQPGGES
984	2334	A	8321	1	1243	ANMAPVEHVADAGAFRLHAALQDIGKNIY TIREVVTEIRDKATRRRLAVLPYELRFKEPLPE YVRLVTEFSKKTGDYPSLSATDIQVLAITYQL EAEFVGVSHLKQEPQKVKVSSSIQHPETPLHIS GFHLPYKPKPPQETEKGHSACEPENLEFSSFM FWRNPLPNIDHELQELLIDRGEDVPSEEEEEEE NGFEDRKDDSDDDGGGWITPSNIKQIQE QCDVPEDVRVGCLTTDFAMQNVLLQMGHIV IAVNGMIJRFARSYL RCHGCFKTTSDMSRV FCSHCGNKTLLKVS VTVSDDGTLHMHFSRNP KVLNFRGLRYS LPTPKGGKYANPHLTEDQRF PQLRLSQKARQKTNVFAPDYIAGVSPFVENDI SSRSATLQVRDSTLGAGRRRLNPNASRKKFV KKR
985	2335	A	8322	352	529	RNNIRQFIMKVCISGQARWLTPVVPVLWET EAGRSLELKSRLPAWATWGNPISTKINK
986	2336	A	8325	89	1172	KMNPTDIADTTLDSESYNYLYYESIPKCTKE GIKAFGELFLPPLYSLVFVFGLLGNSVVLVL FKYKRLRSM TDVYLLNLAISDLLFVSLPFWG YYAADQWVFGGLCKMISWMYLVGFYSGIF FVMLMSIDRYLAIVHAVFSLRARTLYGVITS LATWSVAVFASLPGLFSTCYTERNHTYCKT KYSLNSTTWKVLSSLEINILGLVPLGIMLCY SMIIRTLQHCKNEKKNKAVKMIFAVVVLFLG FWTPYNIVLFLETLVEVLQDCTFERYL DYA IQATETLAFVHCCLNPIIYFFLGEKFRKYILQL FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS TMDHDLHDAL
987	2337	A	8326	3	470	SLSAMRFLAATFLLLALSTAAQAEVPQFKDC GSVDGVIVKEVNVSPCTQPCQLSKGQSYSVN VTFTSNIQSKSSKAVVHGILMGVVPFPPIPED GCKSGINCPIQDKTYSYLNKLPVKSEYPSIK LVVEWQLQDDKNQSLFCWEIPVQIVSHL
988	2338	A	8335	1205	323	VKMALAAARLLPQFLHSRSLPCGAVRLRTPA VAEVRLP SATLCYFCRCRLGLOAALFPRSAR ALAASALPAQGSRWVPLSSPGLPAAFASFPAC PQRSYSTEEKPQHQKTKMIVLGFSNPINWV RTRIKAFIWAYYFDKEFSITEFSEGAQAFAH VSKLLSQCKFDLLEELVAKEVLHALKEK VTS LPDNHKNALAAANIDEIVFTSTGDISIYYDEKG RKFNILMCFWYLTANIPSETLRGASVFQVK LGNQNVETKQLLSASYEFQREFTQGVKPDWT IARIEHSLLE
989	2339	A	8349	67	185	MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS
990	2340	A	8361	210	1115	ASFLLRPQGHDSGEREPFSQTPGLMQPFSIPVQ ITLQGSRRRQGRTAFPASGKKRETDYSDGDL DVHKRLPSSGTEDRAVMLGFAMMGFSVLMF FLGTTILKPFMLSQREESTCTAIHTDIMDDW LDCAFTCGVHCHGQGYPCLVFVNL SHPG QKALLHYNEEA VQINPKCFYTPKCHQDRNDL LNSALDIKEFFDHKNGTPFSCFYSPASQSEDVI

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						LIKKYDQMAIFHCLFWPSLTLGGALIVGMV RLTQHLSLLCEKYSTVVRDEVGKVPYIEQH QFKLCIMRRSKGRAEKS
991	2341	A	8369	9	921	SSVVEFSALSVMACLSPSQLQKQFQDGLVL EGFLSAEECVAMQQRIGEVAEMDVPLHCRT EFSTQEEELQRAQGSTDYFLSSGDKIRFFFEK GVFDEKGNFLVPPEKSINKIGHALHAHDPVFK SITHSFKVQTLARSLGLQMPVVVQSMYIFKQP HFGGEVSPHQDASFLYTEPLGRVLGVWIAVE DATLENGCLWFIPGSHTSVSRMRMRAPVGS APGTSFLGSEPARDNSLFVPTPVQRGALVLIH GEVVHKSQNLSDRSRQAYTFHLMASGTT WSPENWLOPTAELPFPQLYT
992	2342	A	8370	906	4	MALSGNCSRYYPREQGSAPVNSFPEVVELNV GGQVYFTRHSTLISIPHSLLWKMFSPKRD TAN DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVV LPDHFPEKGRLLKREAEYFQLPDLVKLLTPDEI KQSPDEFCHSDFEDASQGSSTRJCPPSSLLPAD RKWGFITVYRGSCITLREGQADAKFRVRPR ILVGRISLAKEVFGETLNESTRDPDRAPERYS RFYLKFKHLMGAPASNFLGFWGLGQNGQDK HPVNIYLQQRSVIRPDLTSKKAGDLKKGKDA QEVSRRRRWLGDPEHL
993	2343	A	8379	1	2794	MRMQRHKNMTMDFGDSGKRIGGGVLCCLHQ SNTSFKLNNNGFEDIVVIDPSVPEDEKIEQIE DMVTTASTYLFEATEKRRFFKNVSLIPENWK ENPQYKRPKHENHKKHADVIVAPPTLPGRDEP YTKQFTECGEKGEYIHFTPDLLLOKKQNEYG PPGKLFVHEWAHLRWGVFDEYNEDQPFYRA KSKKIEATRCASIGSGRNRVYKCGGSCLSRA CRIDSTTKLYGKDCQFFPDKVQTEKASIMFM QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRST WEVISNSEDFKNTIPMVTTPPPPVFSLKIRQRI VCLVLDKSGSMGGKDRLNRMNQAAKHLLQ TVENGSWVGMVHFDSTATIVNKLIQIKSSDER NTLMAGLPTYPLGGTSICSIGKYAFQVIGELH SQLDGEVLLLTGDGENTASSCIDEVKQSGAJ VHFIALGRAADEAVIEMSKITGGSHFYVSDEA QNNGLIDAFGALTSGNTDLSQKSLQLESKGLT LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPP SISLWDPSTIMENFTVDATSKMAYLSIPGTA KVG TWAYNLQAKANPETLTITVTSRAANSSV PPITVNAKMNDVNSFSPMIVYAEILQGYVP VLGANVTAFIESQNGHTEVLELLDNGAGADS FKNDGVYSRYFTAYTENGRYSLKYRAHGA NTARLKLRPPLNRAAYIPGWVVNGEIANPP RPEIDEDTQTILEDFTASGGAFFVSVQVPSL PLPDQYPPSQITDLDTVHEDKILTWAPGD NFDVGKVQRYIIRISASILDRDSFDDALQVN TTDLSPKEANSKESFAFKPENISEENATHIFIAI KSIDKSNLTSKVSNAQVTLFIPQANPDDIPT PTPTPTPTPKSHNSGVNISTLVLSVIGSVVIV NFIISTII
994	2344	A	8385	231	644	INSSPRTGRDHQELNLHTRDSRSQRAVLKIP RQNP GIFYWIFLPSRSHSASHGSRQVSCQG TQDEILKMRNTFAELKNSLEALSSRMDQAE RIGTQAGVQWRDHGSLQPQPEFKQCFHLSL PSSWDYRACLS
995	2345	A	8390	194	3421	AWRKSSVVPFRGTRRGEKSDQDKSGQKNKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DFLSMKQSPALAPEERCRRAGSPKPVLRADD NNMGNCGCSQKLATANLLRFLLLVLPICALV LLLLEILLSYVGTLOKVYFKSNGSEPLVTDGEI QGSDVILNTITYNQSTVVSTAHPDQHVPAWT TDASLPGDQSHRNTSACMNITHSQCQMLPYH ATLTPLLSVVRNMEMEKFLKFFTYLHRLSCY QHIMLFGCTLAPECIIDGDDSHGLLPCRSECE AAKEGCESVLGMVNYSWPDFLRCSQFRNQT ESSNVSRICFSPQENGKQLLCGRGENFLCAS GICIPGKLQCNQYNDCCDWDEAHNCNSEN FHCHTGKCLNYSLVCDGYDDCGDLSDEQNC DCNPTTEHROGDGRCLAMEWVCDGDHDCVD KSDEVNCSCHSQGLVECRNGQCIPSTFQCDG DEDCKDGSDEENC SVIQTSCQEGDQRCLYNP CLDSCGGSSLCDPNNSLNNCSCPEITLCLCM NLPYNSTSYPNYFGHRTQKEASISWESSLFP LVQTNCKYLMFFSCTILVPKCDVNTGEHIPP CRALCEHSKERCESVLGIVGLQWPEDTDCSQ FPEENSNDQTCLMPDEYVEECSPSHFKCRSGQ CVLASRRCDGQADCCDDSDENCGCKERDL WECPSNKQCLKHTVICDGFPCPDYMDKCN CSFCQDDELECANHACVSRDLWCDGEADCS DSSDEWDCVTLNINVNSSFLMVHRAATEHH VCADGWQEILSQLACKQMGLEPSVTCLIQE QEKEPRWLTLSHNWESLNGTTLHELLVNGQS CESRSKISLLCTKQDCGRPAARMNKRLGGR TSRPGRWPWQCSLQSEPSGHICGVLIKKW VLTVAHCFEGRENAAVWKVVLGINNLDHPS VFMQTRFVKTIHLPYRSRAVVDYDISIVELSE DISETGYVRPCLPNPEQWLEPDYCYITGW GHMGNKMPFKLQEGEVRIISLEHCQSYFDMK TITTRMICAGYESGTVDSMCGDSGGPLVCEK PGGRWTLFGLTSWGSVCFPSKVLGPGVYSNV YFVEWIKRQIYIQTFLN
996	2346	A	8392	199	3085	KVLSSSEMSKTNKSKSGSRSSRSASRSRSRS FSKSRSSRSLSRSRKRRLLSSRSRSRSYSPAHN RERNHPRVYQNRDFRGNHNGYRPFYFRGR NRGFYWPWGQYNRGGYGNYSNWNQYRQAY SPRRGSRSSRSPKRRSPSPRSRSHSRNSDKSSS DRSRRSSSSSSNHSRVESKRKSAKEKKSSS KDSRPSQAAGDNQGDVEKQTFSGGTSQDTK ASESSKPWPDATYGTGSASRASVSELSPRER SPALKSPLQSVVRRRSFRPSVPKPSPLSST SQMGSTLPSGAGYQSGTHQGQFDHGSGSLSP SKKSPVGKSPSTGSTYSSQKEESAASOGAA YTKRYLEEOKTENGKDKEQKQNTNDKEKIKE KGSFSDTGLDGMKSDSFAPKTDSEKPFGRG SQSPKRYKLRDDFEKFMADFHEEMDDQDK DKAKGRKESEFDDPEKFMKVIGANKNQEEE KSGKWEGLVYAPPGKEKQKTEELEEESEFPE RSKKEDRGKRSEGGHGRGFVPEKNFRVTAYK AVQEKSSPPPRKTESRDKLGAKGDFPTGKS SFSITREAQVNVNRMDSFDEDLARPSGLLAQER KLCRDLVHSNKKEQEFRSIFQHIQSAQSQSP SELFAQHIVTVHHVKEHHFGSSGMTLHERFT KYLKRGTQEAANKKKSPEIHRRIDISPSTFRK HGLAHDEMKSREPFGYKAEKGYKDDPVDLR LDIERKKHKERDLKRGKSRESVDSRDSHRSR ERSAEKTEKTHKSGKQKQKRRARDRSRSSS SSSQSSHSYKAEYTEETEEREESTGFDKSRL

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						GTKDFVGPSEGGGRARGTFQFRARGRGWG RGNYSNNNNNSNNDFOKRNREEEWDPEYT PKSKKYLLHDDREGESDKWVSRGRGRGAF PRGRGRFMFRKSSSTSPKWAHDKFSGEEGEIE DDESGTENREEKDNIQPTTE
997	2347	A	8398	202	552	CPALGGRQDLQGTLLWAHDSGVGGQKAKS KQENLESLEATGREEEGGQPPVTTKGVLLA LLMAGLALQPGTALLCYSCKAQVSNEDCLQ VENCTQLGEQCWTARIREWGDDSRQA
998	2348	A	8400	697	301	NPPSACTPGSCDSCSGRGRDLAFDSVWSTNN MSDPRRPKNKVLRYKPPSECNPALDDFTPDY MNLGMIFFSMCGLMLKLKWCWVAVYCSFI SFANSRSSSEDTKQMMSSFMLSISAVVMSYLQ NPQPMTPPW
999	2349	A	8401	93	1126	ASASHITSGHLRCFPGSEGVGTMARCFSLVLL LTSIWTTLLVQGSRAEELSIQVSCRIMGITL VSKKANQQLNFTEAKEACRLLGLSLAGKDQ VETALKASFETCSYGWVGDFVVISRISPNPK CGKNGVGVLIWKVPVSRQFAAYCYNSSDTW TNSCIPEIITTKDPIFNTQTATQTTEFVSDSTYS VASPYSTIPAPTTTTAPASTSIPRRKKLICVTE VFMEITSTMSTETEPFVENKAFAKNEAAGFGG VPTALLVLALLFFGAAAGLGFYVVKRYVKAF PFTNKNQKQEMETKVVKEEKANDSNPNEES KKTDKNPEESKSPSKTTMRCLEAEV
1000	2350	A	8406	2	777	KERCQFVVKPMLSTVGSFLQDLQONEDKGIKT AAIFTADGNMISASTLMDILLMNDFKLVINKI AYDVQCPKREKPSNEHTAEMEHEMKSIVHRL FTILHLEESQKKREHHLLEKIDHLKEQLQPLE QVKAGIEAHSEAKTSGLLWAGLALLSIQGGGA LAWLTWVYVSWDIMEPVITYFITFANSMVFF AYFIVTRQDYTYSVAVKSRQFLQFFHKKSKQQ HFDVQYQNKLEKDLAKAKESLKQARHSCL QMQUEELNEKN
1001	2351	A	8410	1400	264	VGFWERPLRSSRWFRSLRRWEMLARAARG TGALLRGSLLASGRAPRRASSGLPRNTVVLF VPQBEA WVVVERMGRFHRILEPGLNILIPVLD IRYVQSLKEIVINVPEQSAVTLDNVTLQIDGV LYLRIMDPYKASYGVEDPEYAVTQLAQITM RSELGKLSLDKVFRERESLNASIVDAINQAAD CWGIRCLRYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKKQAQILAS EAEKAEQINQAAGEASAVLAKAKAKAEAIRI LAAALTQHNGDAAASLTVAEQYVSFAFSKLA KDSNTILLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTDAASLDEELDR VKMS
1002	2352	A	8421	134	941	NRENLESRMMDPCSVGVQLRTTNECHKTY YTRHTGFKTLQELSSNDMLLLQLRTGMTLSG NNTICFHHVKIYIDRFEDLQKSCDPFNHKKL AKKNLHVLDLDDATFLSAKFGRLVPGWKLC PKCTQINGSVDDVTDROKRPESDGRITAK ALRSLQFTNPGRQTEFAPETGKREKRRLTKN ATAGSDRQVIPAKSKVYDSQGLLIFSGMDLC DCLDEDCLGCFYACPAACGSKCGAECRCRDK WLYEQIEIEGGELIHNKHAG
1003	2353	A	8427	3	1416	TEWGLSGSCPGCSPLPESRGRGAAAWRILR CRLPEPSPLTQPNLAQSQPAPVPVTDPSVT MHPAVFLSLPDLRCSLLLVTVWVFTPTTEIT

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						SLDTENIDEILNNADVALVNFYADWCRFSQM LHPIFEEASDVIKEEFPNENQVVFARVDCDQH SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ RSVKALADYIRQKSDPIQEIRDLAEITLDRS KRNIIGYFEQKDSNRYRVFERVANILHDDCAF LSAFGDVSKPERYSGDNIIYKPPGHSAPDMVY LGAMTNFVDVTYNWIQDKCVPLVREITFENGE ELTEGLPFLILFHMKEDTESLEIFQNEVARQL ISEKGTINFLHADCDKFRHPLLIHQKTPADCP VIAIDSFHMYVFGDFKDVLPGLKQFVFDL HSGKLHREFHHGPDPTDTAPGEQAQDVASSP PESSFQKLAPSEYRYTLLRDRDEL
1004	2354	A	8432	910	387	GLSRKLRAGFLPGFCRVSPCGSWVVEVLVKM ACAAARSPADQDRFICTYPAYLNNKKTIAEGR RIPISKA VENPTATEIQDVCSAVGLNVFLEKN KMYSREWNRDQYRGRVRVQLKQEDGSLC LVQFPSPRSVMLYAAEMIPKLKTRTQKTGGA DQSLQQGEGSKKKGKGGKKK
1005	2355	A	8453	90	530	QSHETKMMSGTHWRVLGLCLLSVGWVGQD GNEEMGGITQTPYKVSISGTTVILTCPQYPGSE ILWQHNDKNIGGEDDDKNIGSDEDLHLSEKEP SELEQSGYVVCYPRGSKPEDANFYLYLRARG NPGLOQNRHYHRLFREDHSGHSHQ
1006	2356	A	8458	3	307	AVQRIHEMNIFRLTGDLSHLAAIVILLKIKW KTRSCAGISGKSQLLFALVFTTRYLDLFTSFIS LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC QLCIFN
1007	2357	A	8459	43	553	GAGAGGDWAAMDKLLKVLSGQDTEDRSGL SEVVEASSLSWSTRIKGFACFAIGLCSLLGT VLLWVPRKGLHLFAVFYTFGNASIGSTIFLM GPVKQLKRMFEPTRLIATIMVLLCFALTCSA FWWHNKGLALIFCILQSLALTWYLSLSPFAR DAVKKCAFVCLA
1008	2358	A	8462	487	150	AQDIRSVHSLGQKSTPVKHFRTLSHLHGLPDP PPHWPPQERSPPSHPCMPSHRPQIPQLSNSGPS DPRWGCVGPSMPTSTCLPGAVEASTTKASLP KCPVDSSLTPTEACFL
1009	2359	A	8465	134	954	ETRVKTSLELLRTQLEPTGTGNTIMTSQPVP NETIIVLPNSVINFSQAQKEPTNQGDLSLKKH LHAEIKVIGTIQILCGMMVLSLGILASASFSFN FTQVTSILLNSAYPFIGPFFIISGSLSIATEKRL TKLLVHSSLVGSLSALSALVGFILSVKQATL NPASLQCELDKNINIPTRSYVSFYHDSLYTTD CYTAKASLAGTSLMLICTLLEFCLAVLTAVL RWKQAYSDFPGSVLFLPHSYIGNSGMSSKMT HDCGYEELLTS
1010	2360	A	8468	2	473	KYRYRRPYPVMRKICQVGPAGLAFILNISPVA HRVALCHLAGCQEQAAYHTLQILFFLVSA FFSCPVEKYFPFGSCDIVGHGHQIFHAFSLICT LSQLEAILLDYQGRQEIFLQRHGFLSVHMACL SFFFLAACSAATAALLRHKVKARLTKKDS
1011	2361	A	8478	5	409	TELSQLEKAHPADMGRRKSKRKPPIKKKMT GILETQFTCPFCNEHESCDVKMDRARNITGVI SCTVCLEEFQTPITCILGNLFFQVRVGRGLES PCSSGPLCALVQGQSRPEEQVPPSDFCGVRR RAGFQCQ
1012	2362	A	8481	2810	1652	RTSTQKWQSVFNDSQEHLERFYCNPENDRM RMKYGGQEFWADLNAMNVYETTEFDQLRR LSTPPSSNVNSIYHTVWKFFCRDHFGWREYPE

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						SVIRLIEEANSRGLKEVRFMMWNNHYILHNS FFRREIKRRPLFRSCFILLPYLQTLGGVFTQAP PPLEATSSSQIICPDGVTSAFYFETWVYMHF SQDFIQVPVSAEDKSYRIYNLFHKTVPFMYR ILQILRVQNFLEWKYKRKKEYMNRKMFGR DRINERHLFHGTSQDVVDGICKHNFDPVCG KHATMGQGSYFAKKASYSHNFSSKSSKGV HFMFLAKVLTGRYTMGSHGMRRPPVNPVS VTSDLYDSCVDNFFEPQIFVFNDDQSYFYVI QYEEVSNVTSL
1013	2363	A	8488	2	517	IENCRTLRQAWHEVCGNKMAAPIQGFSC SRFLGWVFRQPVLTQSAAIYVPTKKRFT PIYQPKFTEKEFMQHARKAGLVIPPEKSDRS IHLACTAGIFDAYVPEGDARISLSKEGLIER TERMKKTMAQSIRRIKDYDANFKIKDFPE KAKDIFIEGSPY
1014	2364	A	8501	363	17	YIRTYVYICIIYAQLMYTYIYRTAYVYICILY AQLMYTYVLYTHSLCIHMYISRTAYVYICIIY AQIMTYVYFYTHRLCIHMYISRTDYVYICILY AQLMYTYVYFYTHSYMSDE
1015	2365	A	8504	3	2190	NSSEHFSQAPQRLSFYSWYGSARLFRFRVPPD AVLLRWLLQVSRESGAECTDAEITVHFRSGA PPVINLGTSPDDTAQPSFQVGVPLSTTPRS NASVNVSHAPGDWFWAAHLPPSSQKIELKG LAPTCAVVFQPELLVTRVVEISIMEPDVPLPQ TLLSHPSYLKVFPDYTRELLLELRDCVSNCS LGCPVRLTVGPVTLPSNFQKVLCTGAPWPC RLLLPSPFWDRWLQVTAESLVGPLGTVAFSA VAALTACRPSVTIQLLQSSQNSQSFNASSGL LSPSPDHQDLGRSGRVDRSFFCLTNYFVTRED MDVVSVHFQPLDRVSVRVCSDTSPVMRLRL NTGMDSGGSLTISLRANKTEMNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGYPGQCLLLRRHS YLYASCSCKAGWRGWSCITDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRRFFLVEASVY AYTMFFSTFYHACDQPGEAFLCISYDTLQY CDFLGSGAAIWVTLCMARKTVLKYVLFLL GTLVIAMSLQDRRGMWNLGPCLFAFVIM ASMWAYRCGHRRCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYTYTHSIWHILL AGSAALLPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT
1016	2366	A	8511	1	453	KWYPSGPVRIPGRFYKLPAGHRRCRM KGGKKKGRSAINVVTREYTNHKKRIHGVG FKKRAPRALKEIRKFAKMGTPDVRIIDTRL NKAIVWAKGIRNVPIRIRVLSRKRNEDSDP NKLTYLTVYVPVITFKNLQTVNVN
1017	2367	A	8513	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINT LSAKWADNFMAEGCGGSKEHSFOHPFLQAV GMFLGEFSCLAAYLLRCRAAGQSDSSVDPQ QPFNPLFLPPALCDMTGTSMLYVALNMTSA SSFQMLRGAVIIFTGLPSVAFLGRRLVLSQWL GILATIAGLVVVGGLDLLSKHDSQHKLSEVIT GDLLIMAIQIVAIQMVLEEKFYKHNVHPLR AVGTEGLFGFVLSLLLVPMYIYIPAGSFGNP RGTELDALDAFCQVGGQPLIAVALLGNISSIA FFNFAGISVTKELSATTRMVLDSLRTVVIWAL

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						SLALGWEAFHALQILGFLILLIGTALYNGLHR PLLGRLSRGRPLAESESEERLLGGTRTPINDA S
1018	2368	A	8518	324	694	SPFWTEKRRMEKPLFPLVPLHWFGFGYTALV VSGGIVGYVKTGSPVSLAAGLLFGSLAGLGA YQLYQDPRNVWGFLAATSVTFVGVGMGRS YYYGKFMPVGLIAGASLLMAAKVGVRMLM TSD
1019	2369	A	8526	2	1787	VSAAAVNMEPPDAPAQARGAPRLLLLAVLL AAHPDAQAEVRLSVPPLEVMRGKSVILDCT PTGTHDHYMLEWFLTRSGARPLASAEHQ GSELQVTMHDTRGRSPPYQLDSQGRVLAEA QVGDERDYVCVVRAGAAGTAEAAARLNVF AKPEATEVSPNKGTLSVMEDSAQELATSNRN GNPAPKITWYRNGQRLEVPVEMNPEGYMTS RTVREASGLLSLTSTLYRLRKDDRDASFHC AAHYSLEGRHGRLDSPTFHLTLHYPTHEVQ FWVGGSPSTAGWVREGDTVQLLCRGGDGPSP EYTLFRLQDEQEVLNVNLEGNLTLEGVTRG QSGTYGCRVEDYDAADDVQLSKTLELRVAY LDPLELSEGVLSLPLNSRAVNVCSVHGLPTP ALRWTKDSTPLGDGPMLSLSSITFDSNGTYVC EASLPTVPVLSRTQNFLLVQSGPELKTAEIEP KADGSWREGDEVTLCSARGHPDPKLSWSQL GGSPAEPGRQGWVSSSLTKVTSALSRDGI SCEASNPNGKRVHVFHFGTVSPQTSQAGVAV MAVAVSVGLLLLVAVFYCVRRKGGPCCRQ RREKGAP
1020	2370	A	8530	2	1200	PRVRLRPSRSRSCRGLLSTRAPGPSFPRSLHS SPLLPHAMKSPFYRCQNTTSVEKGNSAVMGG VLFSTGLLGNLLALGLLARSLGWCSRRPLR PLPSVFYMLVCGLTVTDLGKCLLSPVVLAA YAQNRSLRVLAPALDNSLCAFAFFMSFFGL SSTLQLLMALECWLSLGHFFFYRRHTLRLG ALVAPVVSFAFLAFCALPFMGFGKFVQYCPG TWCFIQMVHEEGSLSVLGYSVLYSSLMALLV LATVLCNLGAMRNLYAMHRLQRHPRSCTR DCAEPADGREASQPPELDHLLLLALMTV LFTMCSLPVIYRAYYGAFKDVKEKNRTSEEA EDLRALRFLSVISIVDPWIFIIFRSPVFRIFHFI FIRPLRYRSRCSNSTNMESL
1021	2371	A	8536	1	237	RRGEIDMATEGDVELELETETSGPERPPEKPR KHDSGAADLERVTDYAEKEIQSSNLETAMS VIGDRRSREQKAKOER
1022	2372	A	8537	94	541	RKERRRRRRMEAVVFVFSLLDCCALIFLSV YFIITLSDLECDYNARSCCKLNKWWVPELIG HTTIVTLLMSLHWFIPLNLPVATWNTYRYI MVPNGMGMVFDPTIHNRGQLKSHMKEAMI KLGPHLLCFFMYLYSMILALIND
1023	2373	A	8540	26	431	RMNKKCPQALLAFWLLSWVSSDKVVQSPL SLVVHEGDTVTLNCSYEVTNFRSLLWYKQEK KAPTFLFMLTSSGIEKKSGLSSILDKKELSSIL NITATQTGDSATYLCAVEAQCSLVTCSLYSNS TAEALQL
1024	2374	A	8544	1731	743	GVRLRYSPIAVVMVGEAGRDLRRRRRAVAVT AEKMAVLAPLIALVYVPRLSRWLAQPYLL SALLSAAFLVRKLPPLCHGLPTQREDGNPCD FDWREVEILMFLSAIVMMKNRRSITVEQHIGN IFMFSKVANTILFFRLDIRMGLLYITLCIVFLM

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						TCKPPLYMGPEYIKYFNDKTIDEELERDKRVT WIVEFFANWSNDCQSFAPYADLSLKYNCTG LNFGKVDVGRYTDVSTRYKYSTPLTKQLPT LILFQGGKEAMRRPQIDKKGRAVSWTFSEEN VIREFNLNELYQRAKLSKAGDNPEEQPVAS TPTTVSDGENKKDK
1025	2375	A	8546	2194	1707	TVSFHKTMA SLK CSTVVCICLEKPKYRCPA CRVPYCSVVCFRKHKEQCNPETRPVEKKIRS ALPTKTVPVENKDDDDSIADFLNSDEEEDR VSLQNLKNLGESATLRSLLLPHLRQLMVNL DQGEDKAKLMRAYMQEPLFVEFADCCLGIV EPSQNEES
1026	2376	A	8547	1078	594	VGMELPAVN LK VILLGHWLLTTWGCTVFSGS YAWANFTILALGVWAVAQRDSIDAISMFLGG LLATIFLDIVHISIFYPRVSLTDTGRFGVGMAL SLLLKPLSCCFVYHMYRERGELLVHTGFLG SSQDRSAYQTIDSAEAPADPFVPEGRSQDAR GY
1027	2377	A	8557	1	340	DFLGPASPQEEGGSESSTMTLETAMGMIDV FSRYSGSEGSTQTLTKGELKVLMEKELPGFLQ SGKDKDAVDKLLKDLANDANGAQVDFSEFTVF VAATSACHKYFEKAGLK
1028	2378	A	8569	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLL LLLLGSGGQPQOVGAGQTFEYLKREHLSKSP YQGEAPRPCFLRDWELQVHFQKHGQGGKNL HGDGLAIWYTKDRMQPGPVFGNMDKFVGLG VFVDTPNEEKQQRVFPYISAMVNNGSLSY DHERDGRPTLGGCTAIVRNHLYDTFLVIRY VKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG YYFGTSSITGDLSDNHDVISLKL FELTVERTPE EEKLHRD VFLPSVDNMKLPMTAPLPPLSGL ALFLIVFFSLVFSVFAIVIGILYNKWQEQRK RFY
1029	2379	A	8572	1	578	AAAASHRSRARSRRRVSSGPAPRRAQSSAG RVASGLDSAPLCTMARALCRLPRRLWLLA HHLFMTTACQEANYGALLRELCLTQFQVDM EAVGETLWCDWGRITRSYRELADCTWHMAE KLCQFWPNAEVD RFLAVHGRYFRSCPISGR AVRDPGSLYFPFIVPITVTLVTALVWQVS KRTEGIV
1030	2380	A	8574	1352	372	DSSTVKGSESRLCLIPDLKGKARTREASSG SRTCGRRTSLCTSAKSSWTYRSGLSWQSIKG THLTTTQALRQPLHRAPLLPQQLCWSRPLEK NKAMGRPLLLPLLLLQPPAFLQPGGSGTSGP SYLYGVTPQPKHLSASMGGSV EIPFSFYYPWEL AIVPNVRISWRRGHFGQSFYSIRPPSIHKDY VNRLFLNWTEGQESGFLRISNLRKEDQSVYF CRVELDTRSGRQQLQSIKGTKLTTQAVTTT TTWRPSSTTIAGLRVTESKGHSES WHLSLD AIRVALAVAVLKT VILGLLCLLLWRRRK SRAPSSDF
1031	2381	A	8580	905	340	RRTAGIYPCFPKPGRTRHALCSVVL LLLTGQL AFDDFQESCAMMWQKYAGSRRSMP LGARIL FHGVFYAGGFAIVYYLIQKFHSRALYYKLAV EQLQSHPEAQEALGPPLNIHYLKLIDRENFDI VDAKLKIPVSGSKSEGLLYVHSSRGGPFQRW HLDEVFLELKDGGQIPVFKLSGENGDEVKKE
1032	2382	A	8593	2558	961	RRRPRLLPGAEPCEPRVGP RRADMGC SAKAR WAAGALGVAGLLCAVLGAVMVMVPSLKKQ

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						QVLKNVRIDPSSLSFNMWKEIPIPFYLSVYFFD VMNPSEILKGEKPQVRERGPYVYREFRHSNI TFNNNDTVSFLEYRTFQFQPSKSHGESDYIV MPNILVLGAAMMENKPMTLKIMTLAFTTL GERAFMNRVTGEIMWGYKDPLVNLINKYFP GMFFFKDKFGLFAELNNSDSGLFTGFTGVQNI SRIHLVDKWNGLSKVDFWHSQCNMNGTS GQMWPFFMTPESSLEFYSPEACRSMLMYKE SGVFEGIPTYRFVAPKTLFANGSIYPPNEGFCP CLESQIONVSTCRFSAPLFLSHPHFLNADPVL AEAVTGLHPNQEAHSLFDIHPVTGIPMNCVS KLQSLYMKSVAGIGQTKIEPVVLPVLLWFA ESGAMEGETLHTFYTLVLMPKVMHYAQYV LLALGCVLLVPVICQIRSQEKCYLFWSSSKK GSKDKEAIQAYSESMTSAPKGSVLQEAEL
1033	2383	A	8595	595	767	AHLPTDLLPPHSPTVPTPKSFQCSQKACFSRS FCLLLSLVSSSLVSLSLCPPLTQA
1034	2384	A	8597	640	164	VITSCIPFAFGLGVRASERLAIDMPYLLKYQ PMMQTIGQKYCMDPAVIAGVLSRKSPGDKIL VNMGDRSMVQDPGSQAPTSWISQVFQTT EVLTRITELQRRPPTWTPDQYLRGGLCAYSG GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F
1035	2385	A	8603	936	204	AMASTLEYSPLRLRVLGPAAGFSRAARADL SWDPMMAFFTGLWGPFCTVSRVLSHHCFSTTG SLSAIQKMTVRVVDNSALGNSPYHRAPRCI HVYKKNVGVKVGVDQILLAKGQKKALIVG HCMGPGRMTPRFDSNNVVLIEDNGNPVGTRI KTIPTSLRKREGEYSKVLAIQNFV
1036	2386	A	8606	1	562	PTRAHSFDLCCSPCRRRLGREGAGEEPTSPV TQYLQPRSPCECKMFACAKLACTPSLRAGSR VAYRPISASVLSRPEASRTGEGSTVFNGAQNG VSQLIQREFQTSAISRDIDTAAKFIGAGAATYG VAGSGAGIGTVFGLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLFLFAM
1037	2387	A	8615	2	2364	SPGFSLPESAESLDGSGQEDKPRGSCAEPFTDT GMVAHNNNSRLKAKGVGQHDNAQNFNGQSF EELRAACLKRGELFEDPLFAEPSSLGFKDLG PNSKNVQNISWQRPKDINNPLFMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKNYAGIFHFQIWQFGQWVNVVDDRL PTKNDKLVFVHSTERSEFWALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGA WSDSAREWEEVASDIQ MQLLHKTEDGEFWMYSQDFLNNFTLLEICNL TPDTLSGDYKSYWHITTFYEGSWRTGSSAGGC RNHPGTFTWNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGPFSEI FTNSREVSSQLRLPPGEYIIPSTTFEPHRADFL LRVFTEKHSESWEDEVNIAEQLEEKVSED DMDQDFLHLFKIVAGGEGEIGVYELQRLNLR MAIKFKSFKTKGFLDACRCMINLMDKDGSG KLGLLEFKILWKLLKWMDFRECDQDHSQT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIUDFDSFISCFRLKTMFTFFLTMDPKNT GHICLSLEQVLGEGWEGICRIAPACPSTPPPS

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						SDVGPASPRLFPWDLLPVSTVAADDHVGI EAL
1038	2388	A	8621	3	1494	RSRMARAPLGVLILLGLGRGVGKNEELRLY HHLFNNYDPGSRFPVREPEDTVTISLKVTLNL ISLNEKEETLTSVWIGIDWQDYRLNYSKDDF GGHETLRVPSELVWLPEIVLENNIDGQFVAY DANVLVYEGGSVTWLPPIYRSVCAVEVTYF PFDWQNCSLIFRSQTYNAEEVEFTFAVDNDG KTINKIDIDTEAYTENGEWAIDFCPGVIRRH GGATDGPGETDVIYSLIIRKPLFYVINIIVPCV LISGLVLLAYFLPAQAGGQKCTVSINVLLAQ VFLFLIAQKIPETLSVPLGRFLIFVMVATLI VMNCVIVLNVSQRTPTTHAMSPRLRHVLEL LPRLGSPPPPEAPRAASPPRASSVGLLRAE ELILKKPRSELVFEGQRHROGTWTAFCQSL GAAAEVRCVDAVNFVAESTRDQEAATGEE VSDWYRMGNALDNICFWAALVLFVSGSSLIF LGA YFNRPDLFPYAPCIQ
1039	2389	A	8636	1	900	PGRERPGGGGARRRPQHLPALLPSEPDCA TL QAMENELPVHTSSACATSTSGASSSSGCN NSSSGGSGRPTGPQISVYSGIPDRQTQVVIQ ALHRQPSTAAQYLQQMYAAQQQHLMLQTA ALQQQHLSSAQLQSLAAVQQASLVSNRQGST SGSNVSAQAPAQSSSINLAASPAQAQLNRA QSVNSAAASGIAQQAVLLGNTSSPALTASQA QMYLRAQMLIFTPTATVATVQPELGTGSPAR PPTPAQVQNLTLRTQQTAAAAAGPTPTQPLV PSLALKPTPGGSQPLPTPA
1040	2390	A	8645	98	1388	ASQLAFGGKLTSTPSRDFQCGRGA VTCESF HEHRHQSGRCLSTGMAPNLKGRPKKKPCPQ RRDSFGVKDSNNNSDGKAVAKVKCEARSA LTKPKNNHNCKKVSNEEKPKVAIGECCRADE QAFVLALYKMKERKTPIERIPYLGFKQNLW TMFQAAQKLGGEYETITARRQWKHIYDELGG NPGSTSAATCTRRHYERLILPYERFIKGEEDKP LPPKPRKQENSSQENENKTKVSGTKRIKHEIP KSKKEKENAPKQDAAEVSSEQEKEQETLISQ KSIPEPLPAADMKKKIEGYQEFSAPKLASRVD PEKDNETDQGSNSEKVAEEAGEKGPTPLPSA PLAPEKDSALVPGASKQPLTSPSALVDSKQES KLCCFTESPESEPEQASFPRLPHHTGHRWQTR MRRRMTNCPWPQITLPTAP
1041	2391	A	8646	113	1492	LLQEMCTKTPVLWGCFLWNLYVSSSQTIYP GIKARJTORALDYGVAQMKMIEQMLKEKK LPDLSGSESLFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGKAI.TNHGTANISTDWGFESP LFVLVNSFAEPMEKPILKNLNEMLCPILASEVK ALNANLSTLEVLTKIDNYTLDDYSLISSPEITE NYLDNLKGVFYPLENLTDPFSPVPFVLPER SNSMLYIGIAEYFFKSASFHFTAGVFNVTL TEEISNHFVQNSQGLGNVLSRIAETIYLSQFFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILQQLVCSLS LNRFRALPESNRSNIEVLRFENILSSILHFGVL PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRW RGKSAP
1042	2392	A	8672	538	170	ARRIARTRESKAAVSQDNVPALQPGKKKKLR LGKKKKKKFKFRLPKFKKQLMYSNPNFKKM

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						TSLAGNTVQCLNKLKYVTYSAQYPAYGNITT LDMITSTDHVLQDFWICFTFYSVKERQI
1043	2393	A	8688	359	17	GLKTRAPATPTFQREVLGPAKQDMQRRCPRI GLMTSLKPIKRRWRDYKRWKSGGFTGESC HHADTLGDRGGLQGDHSELLQWQKRILRTE GEPSPKYISKNIFFICSYITGFL
1044	2394	A	8718	292	1490	GTVKITSVATPITAGHSCSSGGVLQVKSPATQS GFKFTSKMEDFNMESDSFDFWKGEDLSNYS YSSTLPPFLDDAAPCEPESLEINKYFVVIIYAL VLLSLLGNSLVMLVILYSRVGRSVTDVYLL NLALADLLFALTPIWAASKVNGWIFGTFLC KVVSLLKEVNFYSGILLACISVDRYLAIVHA TRILTQKRYLVKFICLSIWGLSLLALPVLLFR RTVYSSNVSPACYEDMGNNANTANWRMLLRIL PQSGFTVPLLIMLCYGFTRTLFKAHMGQK HRAMRVIFAVVLIFLLCWLFPYNLVLLADTLM RTQVIQETCERRNHIDRALDATEILGILHSCLN PLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDS RPSFVGSSSGHISTTL
1045	2395	A	8724	254	3184	FRANLAITVANRRGAQGGKMHTCCPPVTLEQ DLHRKMHSWMLQTLFAVTSVLVSCAETIDY YGEICDNACPCEEKDGILTVSCENRGIISLEIS PPRFPIYHLLLSGNLLNRLYPNEFVNYTGASIL HLGSNVIQDIETGAFHGLRGLRRLHLNNKL ELLRDDTFLGLENLEYLQVDYNYISVIEPNAF GKLHLLQVLILNDNLLSSLFNNLFRFVPLTHL DLRGNRLKLLPYVGLLQHMDKVVELQLEEN PWNCSCELSLKDWDLSISYSALVGDVVCETP FRLHGRDLDEVSKQELCPRLISDYEMRPQTP LSTTGYLHTTPASVNSVATSSSAVYKPLKPP KGTIRQPNKPRVRPISRQPSKDLGYSNYGPSIA YQTKSPVPLECPTACSCNLQISDLGLNVNCQE RKIESIAELQPKPYNPKKMYLTENYIAVVRRT DLLEATGLDLLHLGNRRISMIQDRAFGDLTN LRLLYLNGNRIERLSPELFYGLQSLQYLFLQY NLIREIQSGTFDPVFNLLQLFLNNLLQAMPS GVFSGLTLLRLNLSNHFTSLPVSGVLDQLKS LIQIDLHDNPWDCTCDIVGMKLWVEQLKVG VLVDEVICKAPKKFAETDMRSIKSELLCPDYS DVVVSTIPSSIQVPARTSAVTPAVRLNSTGA PASLGAGGGASSVPLSVLISLLLVFIMSVFVA AGLFVLVMKRRKKNQSDHTSTNNSDVSSFN MQYSVYGGGGGTGGHPAHVHHRGPALPK VKTPAGHVYIEIPHPLGHMCKNPIYRSREGN SVEDYKDLHELKVITYSSNHLQQQQQPPPPP QQPQQQPPQLQLQPGEERRESHHLRSPAYS VSTIEFREDLLSPVQDADRFYRGILEPDKHCST TPAGNSLPEYKFPSPAAAYTFSPNYDLRRPH QYLHPGAGDSRLREPVLYSPPSAVFVEPNRNE YLELKAKLNVEPDYLEVLEKQITFSQF
1046	2396	A	8736	28	452	SPSAAGGLAWVSLALSGSGSRGRDHSGSGVGT AMAGALVRKAADYVRSKDFRDYLMSTHFW GPVANWGLPIAINDMKKSPEUSGRMTFALC CYSLTFMRFAVKVQPRNWLLFACHATNEVA QLIQGGRLIKHEMTKTASA
1047	2397	A	8741	673	924	ALPGTPQQTIVLNTDGKVKSFSPHSNPNLPP AKFFTSLSLQSLNWSSHLPPSPATESVGKRONAK PPTTKLLHSSPLWNFFAQQL
1048	2398	A	8747	3	5054	PEVTKPSLSQPTAASPIGSSPSPVNGGNNAKR

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						VAVPNGQPPSAARYMPREVPPRFRCQQDHK VLLKRGQPPPPSCMLLGGGAGPPPCTAPGAN PNNAQVTGALLQSESGTAPDSTLGGAAASNY ANSTWGSAGSSNNGTSPNPIHIWDKVTVDGS DMEEWPCIASKDTESSENTTDDNSASNPGSE KSTLPGSTTSNKGKGSQCQSASSGNECNLGV WKSDDPKAKSVQSSNSTENNGLGNWRNV GQDRIGPGSGFSNFPNSNPSPAWPALVQEGTS RKGALETDNSSSAQVSTVGQTSREQQSKME NAGVNFVVS GREQAQIHNTDGPKNNTNSL NLSSPNPMENKGMPPFGMGLGNTSRSTDAPSQ STGDRKTGSGVSGWGAARGPSGTDTVSGQSNS GNNGNNGKEREDSWKASVQKSTGSKNDS WDNNNRSTGGSWNFGQDSNDNKWEGENK MTSGVSGGEWKQPTGSDCLKGEWSGPNQPN SSTGAWDNQGHPLLENQGNAPCWGRSS SSTGSEVEGQSTGSHKAGSSDSHNSGRRSY RPTHDPQAVLQTLRTDLDPRLVLSNTGWG QTQIKQDVTVDIEEVPREPKSDKGTEGWES AATQTKNSGGWGDAPSQSNQMKSGWGELS ASTEWKDPKNTGGWNDYKNNSSNWGGGR PDEKTPSSWNEPNSKDQGWGGGRQPNQGS SGKNGWGEVDQTKNSNWESSASKPVSGWG EGGQNEIGTWGNGGNASLASKGGWEDCKRS PAWNETGRQPNWKNQHQQQQPPQPPPPQ PEASGSWGGPPPPPGNVRPSNSSWSSGPQA TPKDEEPSGWEEPSQISRKMDIDDGTSAWG DPNSYNYKNVNLWDKNSQGGPAPREFNLPTP MTSKSASDSKSMQDQGWGESDGPVTGARHPS WEEEDGGVWNTTGSQGSASSHNSASWGQG GKKQMKCSLKGNNDSWMNPLAKQFSNMG LLSQTEDNPSSKMDLSVGLSDKKFDVDKRA MNLGDFNDIMRKDRSGFRPPNSKDMGTDS GPYFEKGGSHGLFGNSTAQSRGLHTPVQPLN SSPSLRAQVPPQFISQVVSASMLKQFPNSGLSP GLFNVPQLSPQQAAMLSQLPQIPQFLACQL LLQQQQQQQLLNQRKISQAVRQQQEQLA RMVSALQQQQQQQRPQGMKHSHPVGP PHLDNMVFNALNVGLPDLQTKGPIPGYGSF SSGMDYGMVGGKEAGTESRFKQWTSMM GLPSVATQEANMHKNGAJVAPGKTRGGSPY NQFDIIPGDTLGGHTGPAAGSWLPAKSPPTNK IGSKSSNASWPEPQPGVPWKGIQNDPESDP YVTPGVLGGTATSPIVDTDHQLLRDNTTGS NSSLNTSLPSPGAWPYASDNSFTNVHSTSAK FPDYKSTWSPDPIGHNPHTLSNKMWNHSS RNTTLPFRPPGLTNPKPSPWSSTAPRSVRG WGTQDSRLASASTWSDGGSVRPSYWLVLHN LTPQIDGSTLTICMQHGPLLTFHLNLTQGT LIRYSTKQEAQAQTALHMCVLGNTTILAEF ATDDEVSRFLAQAPPTPAATPSAPAAQWQS LETGQNQSDPVGPNLNLFGGSTGLGQWSSSA GGSSGADLAGASLWGPFPYSSSLWGVTVED PHRMGSPAPLLPGDLLGGGSDSI
1049	2399	A	8748	200	1387	VPWKRQDEQLSLQVETLYLDSPAVHLLSPTF LPPSSLPPFLQIVDSSSSACTLDSFFFLAPWDS PQDCGFKDHQPLTLQALTVELARWTLMLLS TAMYGAHAPLLALCHVDGRVFRPSSAVLLT ELTKLLCAFSLLVGWQAWPQGPFPWQAA PFALSALLYGANNLVIYLRQYMDPSTYQVL

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						SNLKIGSTAVLYCLCLRHLRSVRQGLALLL MAAGACYAAGGLQVPGNTLPSPPPAAAASP MPLHTPLGLLLILYCLISGLSSVYTELLMKR QRLPLALQNLFLYTFGVLLNLGLHAGGGSGP GLLEGFSGWAALVVLSQLNGLLMSAVMKH GSSITRLFVVSCLVNVNAVLAVLLRLQLTAA FFLATLLIGLAMRLYYGSR
1050	2400	A	8758	3	1660	WVSSMGFEELLEQVGGGFPQLRNVALLALP RVLLPLHFLPIFLAAVPAHRCALPGAPANFS HQDVWLEAHLPREPDGTLSSCLRFAYPQALP NTTLGEERQSRGELEDEPATVPCSQGWEDH SEFSSTIATESQWDLVCEQKGLNRAASTFFFA GVLVGAVAFGYLSDRFGRRRLLVAYVSTLV LGLASAAVSVMFAITRTL TGSALAGFTIV MPLELWLDVEHRTVAGVLSSTFWTGGVML LALVGYLIRDWRWLLLAATLPCAPGILSLWW VPESARWLLTQGHVKEAHRYLLHCARLNGR PVCEDSFSQEA VSKVAAGERVVRPSYLDLF RTPRLRHISLCCVVWFVGNFSYYGLSDVS GLGLNVYQTQLLFGAVELPSKLLVLSVRYA GRRLTQAGTLGTALAFGTRLLVSSDMKSW TVLAVMGKAFSEAAFTTAYLFTSELYPTVLR QTGMGLTALVGRLGGS LAPLAALLDGVWLS LPKLTYYGIALLAAGTALLPETRQAQLPETI QDVERKSAPTSLOEEEMP MKQVQN
1051	2401	A	8759	515	1625	EIRTPVAVSSAPSGDSEGEETQDEVSSHTS EEDGGVVKVEKELENTEQPVGGNEVVEHEV TGNLNSDPLELCQCPLCQLDCGSREQLIAHV YQHTAAVVSASYMCPVCGRALSSPGSLGR HLLIHSEDQRSNCAVCGARFTSHATFNSEKLP EVLNMEISLPTVHNEGPSAEGKDIAFSPPVYP AGILLVCNNCAAYRKLLLEAQTSPVRKVALRR QNEPLEVRLQRLERERTAKKSRDNETPEERE VRRMRDREAKRLQRMQETDEQARRLQRDR EAMRLKRANETPEKRQARLIREREAKRLKRR LEKMDMMLRAQFGQDPSAMAALAE MNFF QLPVSGVELDSQLLGKMAFEEQNSSSLH
1052	2402	A	8763	1106	70	RHGHGGRDRRGGRVARPGGLGRYPGRGAA ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA HGSKHRAAAPPPLFDDTSGGYSSQPGGY PATGADVAFSVNHLGDPMANVAMAYGSSI ASHGKDMVHKELHRFVSVKLYFFAVDTA YVAKKGLLVFPYTHQNWEVQYSRDAPLPP RQDLNAPDL YPTMAFTTYVLLAGMALGIQK RFSPEVLGLCASTALVWVMEVLALLGLYL ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL LFGSDGYVALAWTSSALMYFIVRSRLTAAL GPDSMGGFPVPRQLQLYLTGAAAFQPLIY WLTFLHVR
1053	2403	A	8768	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSVNSSAYTYMGKDKYENEDLIKHW PEDIWFHVDKLSAHVYLRHLKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVYTPW SNLKKTADMDVGQIGFHRQKDVKITVVEKK VNEILNRLEKTKVERFPDLAAEKECRDREER NEKKAQIQEMKKREKEEMKKKREMDLRSY SSLMKVENMSSNQDGNDSDEFM
1054	2404	A	8769	344	527	REATTACRNCSWVFSRCSLGACKPTVC SMP SLSRQGSQTLCLRLAEYCMESVDSQRLLLS

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1055	2405	A	8770	430	1104	QQESPAAGAARMNCKEGTDSSCGCRGNDEK KMLKCVVVGDAVGKTCLLMSYANDAFPEE YVPTVFDHYAVTVVGGKQHLLGLYDTAGQ EDYNQLRPLSYPTNDVFLICFSVVPASVHN QEEWVPELKDCMPHPVYVVLGTQIDLRDDPK TLARLLYMKEKPLTYEHGVLAKAIGAQCYL ECSALTQKGLKAVFDEAILTIFHPKKKKKRC EGHSCCSII
1056	2406	A	8773	261	332	NPRIQLSGNSCCAGSCRVLSEQ
1057	2407	A	8778	3	477	PAGIRHEQARGADRMGKCRGLRTARKLRSH RRDQKWHDKQYKKAHLGTALKANPFGGAS HAKGIVLEKVGVEAKQPNRAIRKCVRVQLIK NGKKITAFVPPNDGCLNFIEENDEVLVAGFGR KGHAVGDPGVRFKVVKVANVSLALYKGG KERPRS
1058	2408	A	8808	171	881	PGLSQEPSSGSMETVVIVAIGVLATIFLASFAAL VLVCRQRYCRPRDLLQRYDSKPIVDLIGAME TQSEPELELDDVITNPHEAILEDWIEDA SGLMSHCIALKICHTLTEKLVAMTMGSGAK MKTSASVSDIIVAKRJSRVDDVVKSMYPP DPKLLDARTTALLSVSHLVVTRNACHLTG GLDWIDQSLSAEEHLEVLREALASEPDKG LPGFEGFLQEQSAI
1059	2409	A	8809	246	757	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWC EGPRMLSWCPFYKVLVLTATVSVVGYASY LVWKDLGGGLGWPLALPLGLYAVQLTISWT VLVLFVTHNPLGALLHLLLYGLVVTAL WHPINKLAALLLPYLAWLTVTSALTYHLWR DSLCPVHQPOFTEKSD
1060	2410	A	8810	304	381	PKLSVYPLOSHHCLSEPFQSLVCCLA
1061	2411	A	8820	1673	848	SCKTENLLEMWWFQQGLSFLPSALVTWTSAA FIFSYYTAVTLHHIDPALPYISDTGTVAPEKCLF GAMLNIAAVLCIATTVRYKQVHALSPEENV IKLNKAGLVGLSCLGLSIVANFQKTLFAA HVSQAVLTFMGSLYMFVQTLTSYQMOPKIH GKQVFWIRLLVWCGVSALSMILTSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI
1062	2412	A	8824	1	763	GGAPPASVPARESPVSGAQSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEEERMETPQEDHLRGQHYH QKQGNGSFDAPNERPYSKIRNTTSCNSGT CTLQDPDQQRNLSGKVLIRVTGCPAQRKEET FKKYRAEIVLLALVIFYLTLIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHGLVTPHKT ELV
1063	2413	A	8826	147	627	CETSTSSAGHAPCRHAAQGPPEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLTAIFQSPGANTGRALH CVLSKEMKSVQSRSLGLSRIHLQSKRKIHFLV TR
1064	2414	A	8835	2982	1869	LKDTLKSQMTQEASDEADMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLDVD TAEYIHKAHEKLMQLTNSRAKAEDALSE MKSQYSKVLNLTQLKQLVDAQENSVSITE HLQVITTLRTAAKEMEESINLKEHLASKEVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						VAKLEKQLLEEKAAAMTDAMVPRSSYEKLQS SLFSEVSVLASKLKESVKEKEKVHSEVVQIRS EVSQVKREKENIQTLTKSKEQEVNELLQKFQ QAQEELAEMKRYSESSSKLEEDKDKKNEMS KEVTKLKEALNSLSQLSYSTSSSKRQSQQLEA LQQQVKQLQNQLAECKKQHQEVISVYRMHL LYAVQGMDEDVQKVLKQLTMCKNQSQK K
1065	2415	A	8841	3	663	AAATAASLSPRGCLRTTPSSDVGPSRAPPPSA APLPTGRAQMSPSGRLCLLTIVGLILPTRGQTL KDTTSSSSADATIMDIQVPTRAPDAVYTELQP TSPTPTWPADETPQPQTQTQOLEGTDGPLYT DPETHKSTKAAHPTDDTTTLSEKPSPTDVQT DPQTLKPSGFHEDDPFFYDEHTLRKRGLLVA AVLFTTGIIIITSGKCRQLSRLCRNHCR
1066	2416	A	8853	3806	2204	FVGEQEGGCEAGAGRGAQTYPGEAGERWFG RRRRRGRVVSRRKMSLKSERRGIHVDQSDLL CKKGCGYYGNPAWQGFCSKCWREYYHKAR KQKIQEDWELAEERLQREEEAFASSQSSQGA QSLTFSKFEEKKTNEKTRKVTTVKKFFSASSR VGSKKIEQAKAPSPSINRQTSIETDRVSKEFIE FLKTFHKTGQETVQTKLFLEGMHYKRDLSIE EQSECAQDFYHNVAERMQTRGKVPPEVEKI MDQIEKYIMTRLYKYVFCPETTDDEKKDLAI QKRIRALRWVTPQMLCVFVNEDIPEVSDMVV KAITDIEMDSKRVPRDKLACITKCSKHIFNAI KITKNEPASADDFLPTLYTVLKGNPRLQSN QYITRFNPSRLMTGEDGYFTNLCCAVAFIE KLDAQSLNLSQEDFDRYMSGQTSRKPQEAES WSPDACLGVKQMYKNLDLLSQLNERQERIM NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI KPPNQPLAADSENVENDKLPPLQPVYAG
1067	2417	A	8855	1372	1513	SNMREVGCGWLVVPVAFWEAEVGGSLARS LROAWATKQDPISKKK
1068	2418	A	8856	1530	1583	PCRPGMECNMISVHCNL
1069	2419	A	8857	1530	1583	PCRPGMECNMISVHCNL
1070	2420	A	8866	293	1675	PYPQGGYPQGPYPQEGYPQGPYPQGGYPQGP YPQSPFPNPFYGGQVFPQGDSPQHGNVQ EEGPPSYDNDQDFPATNWDKSIQAFIRKVF LVLTQLSVTLSTVSVTFVAEVKGFVRENV WTYYVSAYVFFISLIVLSCGDFRRKHPWNL VALSVLTASLSYMGMIASFYNTAIVMAVG ITAVCFVTFVFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRIEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPFEEYVFAALNLYTDINI FIYLTIGRAKF*PSSSSLCPLRWHGWPGPCP WHGSASCTSPSCPAQPREKDALQPCMY TADTSIWTRCGHSMAPLVLPPTPRGTATFPC HLLSTHOCMSFVCQPTPGTGGSTRSRGELSQ EVRVHVFPVPVAPQPGVEHPSPPHPGVLPS GDMRSGGLIPVLSPE
1071	2421	A	8868	2	358	ARGNTLYHLFRLCRKLNLRWFSASTLYDVQH DDKMGSNITFFKRNDCRYVMISCKADMYDN VRHFFMI*SNKLIMEETYLNIKAVIDRPTASII LNGEKLVFPVRSQT*QGCSVWP
1072	2422	A	8870	33	658	MESVLSKYEDQITFTDYLEEYPTDDELVWL GKQHLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMRLCGQMMLAQAALICRH LGRDWSWEKQKEQPKYQRLQCFLDRKDC

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						CYSIHQMAQMGVGEKGKISGEWVLGPNTVAQGV*KNLALFDEWNSLGLVYVSMNDNPSGSIA RFPKKLCRVLP/ASADTAGLTGP
1073	2423	A	8879	146	412	DFSV*GDVDIEVTCPICLQLLTPSLNCGRLR*QVCITA*IKESVVISGG*SSSPVCHTTFQPANLRTSRVLP*SIKSLGPDEPQEG
1074	2424	A	8884	67	435	HLQGRSIRTLQLTGENEKNCEVSEIRRRSGPWKEISFGDYICHTFQGDWCADRSLPEAAAHGRLLALKTLIAQGVNVNLWTL/DRVSSLHEACL*GPVACAKPYWKMPVRHGGTVTGPLLMLV
1075	2425	A	8896	1294	248	RSGDRNGLTHQLGGLSQGSRNQSYRSRSRSRERPSAPRGIPFASASSSVYGYSRPYGSDKPWPSLLDKEREESLRQKRLSERERIGELGAPEVWGLSPKNPEPDSDEHTPVEDEEPKSTTSASTSEEEKKKKSSRSKERSKKRRKKKSSKRKHKKYSESDSDSDSETDSSDEDNKRRAKAKKKK EKKKKHRSKKYKKRKRKSKESDSSSKESQEEFLENPWKDRTKAEPSDLIGPEAPKLTLSQDDKPLNYGHALLPGEGAAMAEYVKAGKRI PRRGEIGLTR*RNCHHLNAQVM**VVSRRHRRMEAVRTAKREPESTVLMRREPLHFPNPRRET KERE
1076	2426	A	8899	146	789	GRSTEAEKEPAFDETRTGKQRRRLPRAGEFHG*E*APGPGPRSFQVSRKMPEEPGARKHPFSGKSFYLDLPAGKNLQFLTGAIQQLGGVIEGFLSKEVSYIVSSRREVKAESSGKSHRGCPSPSPSEVRVETSAMVDPKGSHPRPSRKPVDSPVLSRGKELLOKAI RNQK**CTVQQLSHCRLYGKETTAKRSQREHVQQSQEHGKWPDLKGPR
1077	2427	A	8901	352	3	AKIGAYKYIQELWRKKQSDVMHFLLRVRCWQYPALHRAAGTEWQSLAHRAPRSTQPDKACRLGYKAKQGYIIRICVRRGGWKCPVPKAVTYGKPVHHGVN*LKFAQSLQSVAAEQ
1078	2428	A	8905	536	781	ACPAENREVPFEMAAGQAPHAGPGAGPGQPA PALPFAATPGSRGQALCRGRRRQHLHGPLH RP*QAAPALHAGCOLAPHPPT
1079	2429	A	8912	121	376	NLIWKLCTVTERRLVILDNYDLASE/YEANKYI CNRIQFKPGQDKYFTLGLPTGSTPL*CYPKLI EYNKNGHLSFKYVKTFMSDEY
1080	2430	A	8920	381	1788	SSESPSDPGRMAMTWIVFSLWPLTVFMGHIGHSLFSCEPITLRMCQDLPYNTTFMPNLLNHYDQQTAAALAMEPFHPMVNLDSCRDFRPFLCALYAPICMEYGRVTLPCRRLCQRAYSECSKLME MFGVPWPEDMECSRFPDCDEFPYRLVDNLNAGEPTEGAPVAVQRDYGFWCPRELKIDPDLGY SFLHVRDCSPPCPNMYFRREELSFAFYFIGLIS IICLSATLFTFVTFIDVTRFRYPERPIKCYAV WHMMVSLIFFIGFLLEDRVACNA/SIPAQYKASTVTQGSHNKACTMLFMLYFFTMAGSVWWVILTTTWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTILLAMNKIEGDNISGVCVGLYD VDALRYFVLAFLCLYVVVGVSLLLAGIISLNR VRIEPL*KENQDKLVKFMIRIGVFSILYLVP LLVIGCYFYEQAYRGIWETTQIQC
1081	2431	A	8922	56	420	EERTKMSTGPDYKATVGDSSDGNLNVAQEE CSRKGIVDEFFPILLSN*CIWTQPGQYPQSSYG TLANFVFCSVRHGLALILQLCNFSIYTQQMNLSIAIPAMVNNTAPPSQPNASTERPST
1082	2432	A	8923	355	1079	PFGTSPSTMAVVKNKCLMKGGKKGVKKKVV

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						GPFSKKDQYDYKAPAMFNIRNTGK/TLVART QGTQIASDGLKGLLFEVSLADLQNDVAFRK FKLITEDVQDKNCLTNFYGMDLTCDKICSMV EKWSTMIEAHVDVKT TDGYFFHLFCVGFITK HNNQILKTSYA*HQQS/RQIQKKMMEIMT*EV QTNDLKEVVNKLIPDNIGKDTEK V/CPIYPLH DVFIKRVKMLENPGFERMELRGGSSS
1083	2433	A	8948	28	385	LTWQPPIHPCPAMSEETLQSKLAAAKKKLP WGA VQGSRAMSDLLLLLDLTL LLLMLLGF AGYSGQLAGVAVSAGSPPIRYKFHVEPYGET GWLLT/ESCSISPKLCSIAVH*DNPAWF
1084	2434	A	8950	156	318	HYTPINTDTIENSENNKCW*GY*EVGLIHHW WGGKRVPQFFWKRVWQKRTLNLRV
1085	2435	A	8956	16	413	HMGQLGYFIQCWWECKRLISFWKTI*QSPAK *TTYTSYDTAIPIS/GI/YPKRMSSKCHQETCAR MFLAPFTATIKGKQLTCLPVEERIDYMWYS HKYYIKVKRNL*VTITHTWVNLNLMFEILW YSHKYY
1086	2436	A	8962	868	1026	H*KILQVGRAQRAHXSRL*SQLRRLRHESHL NPGARGCSEARLHRCPTAWTT
1087	2437	A	8985	58	330	LHVKHLGHFQLVPSEVICHILMPVS*ELQRL *ERSVCAFHVICITVYVCLQVYACMCVYICM FVYSVYGCGLCTCVCMDVYICVVCQVEFL
1088	2438	A	8989	394	404	N*KWLHVNVRIQSIFF/KRNQK/INSHELKLD KKFLDMMSNA*STKKHDKLD/LIKFKT/LCSA KYTVKRIKIHPTDLEKMLRNHLSDDK*YS/GV YKDL SKLNRRKTE/S*/VKKWVKDL SRYFIKE VISMENKHKIKIFTS
1089	2439	A	8991	60	329	MALTPESPSSFPGLAATGSSVPEPPGGPNATL NSSWDSPTPESSLEDLEATGTIGTLLSDMGVV GVEDNAYTLEVNSRYMRAVGIM*IHL
1090	2440	A	8996	2	351	SNITITLT*MKKYDNTFCW*GCGQIGT/LIYC WQESKFIAFWSKIQQYLA*ISIHILFDP AFLFL GGYPGGTQSVFLTGVLVSSVFYNNMKMLHTR LLIAALFIIVQYWKQSKDHYI
1091	2441	A	8997	97	456	YPLPVCSYLSGPRGEHWNLSGGKSSCPLPLPT LVSSRFKISKVIVVGDLSVGKTC LINR*GGAG AELGRVGP SLARWAGRSQHLVPSQIVCKDS FDKNYKAPIGADFEMERFEVLGIF
1092	2442	A	8999	548	811	SSFIKRHILIFEDDWHQITCCHPHHPF*RCQ FHIFYVSVQNSISPSLSVSSSHDPDRPDHEVHQH RAAHHHQHGQGPLGHGLVARVG
1093	2443	A	9002	3	2745	ALLGLQOFAQSLILSRSSVMQVRGLQGFVGS TCPHICTV/VNFKELAEHRSKYPGCTPTIVVD AMCCLRYWYTPESWICGGQWREYFSALRDF VKTFTAAGIKLIFFDGMVEQDKRDEWVKRR LKNREISRIFHYIKSHKEQGRNMFFIPSGLA VFTRFALKTLQGETLCSLQEADYEVASYGLQ HNCLGILGEDTDYLIYDTC PYFSISELCLES LD TVMLCREKLCESLGLCVADLPLLACLLGNDII PEGMFESFRYKCLSSYTSVKENFDKGNILA VSDHISKVLYLYQGEKKLEILPL/VTQSSFL *RNGIISFTRT/INLHGFSKNPKV**LWTK*YP RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCH/PEPRQEVPTCSDEPRQEVPTCTG PESRREVP MCDPEPRQEVPMCTGPEPRQEV MCTGPEARQEVPMCTDSEPRQEVPMCTDSEP RQEVPMYTGSEPRQEVPMYTGSEPRQEVPMY TGSEPRQEV LRTDPESRQEVPMCTGHESKQEV

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						PICTDPISKQEDSMCTHAEINQKLPVATDFEFK LEALMCTNPEIKQEDPTNVGPEVKQVMTVS DTEILKVARTHHVQAESYLVYNMSSGEIECS NTLEDELQALPSQAFIYRPIRQVYSLLED CQDVTSTCLAVKEWVYPGNPLRHPDLVRPL QMTIPGGTPSLKILWLNQPEIQVRRDLTLA CFNLSSSREELQAVESPFQALCCLLYLFVQV DTLCLDELHAFIAQALCLOGKSTSQLVNLQP DYINPRAVQLGSLVRGLTTLVLVNSACGFP WKTSDFMFWNVFDGKLFHQKYLQSEKGYA VEVL/CRTK*ISAHQIPQEGSRLQGLHEGEQT HHWPSPLGLTPRREVKGKTLQPLQDGLWV
1094	2444	A	9021	97	834	AREACRAKTDFFPGRFRLLWPSCCCRVIVGAE T*HMAEPVSPLKHFVLAKKAITAFDQLLEFV TEGSHFVEATYKNPELDRIATEDDLVEMQGY KDKLSIIGEVLSRRHMKVAFFGRTSSGKSSVI NAMLWDKVLPSGIGHITNCFLSVEGTGDGKA YLMTEGSDEKKS VKTVNQLAHLHMDKDLK AGCLVRVFWPKAKCALLRDDLVLDGPGTD VTTELDSWIDKFCTKSSSTREITNSGSDT
1095	2445	A	9022	1	537	LVLNSRVEDFVPEGAGRILPFALRPLAACW LLHRRARRSSALCPRPSWGVSGEGAGARE P*ITSSSCLSA/SHLISQSPNMGARRRIRPQ LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF DYVFDIDSQQEQVIQIEKLEIGCFEGYNATV FAYGQTGAGKTYTMTGTGFD
1096	2446	A	9029	1	285	FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL GQHSETPSLKKKLAGYSGMCL*SQVLRRLRQ EDCLSPGGGNCRES*SCPYPATWITERDPV
1097	2447	A	9032	716	357	ARSTGFWEILWCGFLKRLSPRVKCSGAI LAHCNFRHAGFPPLSCLSLNRWEYRRPAPR GKFFLVFLVETGFC/G*DGDLTLTSRACLGL LPKCWDYRREPAASIFQITFFINSK
1098	2448	A	9038	230	652	KVVVMSCEDINISGSFYRNKLYLAFLCKRTS TNPSQGPYHLWVPSHFVQITTCGRPLPHKTKQ G*AALDHLKVFDRIPLPYDKKKQMAVSATLE VVRPKP*RKPAYLGHWAQKVDWKYQAMTA TMGEKRKVYYQKICYQKK
1099	2449	A	9043	185	372	IFYSHQQCMRV/WQCGDIETLIHCW*E*KII HSL/WK/TV*QFLKRLYLHLPNSVIAFLGISP RKIKTCPQNSCTSMNLINAHNDQWKKINI
1100	2450	A	9045	763	584	RQSLALSPRLECSGTISAHCLPLVFTPLSCL SLTSSWDYRRPPHPANFLYFK*RRGF
1101	2451	A	9050	275	2	LFFLRKVSNOFLSPLPVNFQGFVFAFLLLLL FLL/FEMESLPVA/RVECSGTISAHCLPLPGSS DSPASAS*VAGITDMCRYTQILFLHAS
1102	2452	A	9053	449	1224	KTSMFWKFDLHSSSHIDTLEREDVTLKELM DEEDVLQECKAQNRKLIIEFLKAECLEDLVSF I*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLNDSPLNPLASFF SKVLSILSRKPEQIVDFLKKKHDFVDLIKHIG TSAIMDLLRLTLTCEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSL* LLQCVLQWLNEEKIIRLVEIVHPSQEDVSLV
1103	2453	A	9058	403	3	GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GCAGA AGMQH/CWAWCVNVGKFWEMS*YYLLKLSI ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA

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						APFVLA VNC
1104	2454	A	9064	75	393	KWLFSSLNITGRGDIIHGLKWLDRCWNCSSFFPI KRNRQTHSTESNKLKAGHSFGYN*LIH*NSV KTDGCGGANSKGVVVMKVAKTAQQKQTTS YMQIGTTKNSRAT
1105	2455	A	9065	366	778	DLILLRNLAFFPELKRRCISRFYLAHHLKIYS RSILLCNCSGFIYLSL*QYDVFFNFYFFFRDR AWPCCPGWSAAWLTIVILAHYRRPGLERSCC LSLSSSWDHRRVPPCPANF*/YFSMGFTAFFRL VLNS*TOGI
1106	2456	A	9083	673	816	ESGSLIH*WWENKPAQPLWWEI*QHVQKLPT HFPCDPAIPLLGICPED
1107	2457	A	9086	580	18	KPSSGSFIRATYIFLSTAHVPALFSLVRIKLT* AFSQSSVLWAHKQKQKTSLSLVR/ERLQIKTA VRENFLPIRLAKILKLDNVK CWQG/SGSNMSL LHCWWEYNVHIHWN SVTFPRKVEHVITYA PEISVR*IHGGLPTLVHQETHSVFRGAPSVIP ETR/CRPTKESINKLLHIYTMHEYGDENK
1108	2458	A	9093	540	1	GGNDCSVITPTTEPRKEIT*KRKF*EKTDLRP GA/PPSRTPPTPYPCPHGDRLLPPSRPLPAGPA SAFPPAERSRGHRRASL*RARWSAAVPRSA GSASEPVQSRWLRLPVGSDSPPAVPVVRCAP DSRPAAPGSRLPDGLDSPAPSRTPSSVD*GG QRPPPSGDSLSPGCCRY
1109	2459	A	9099	1255	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL GAVAHSCNPSTLVGRGGRITRGQELR
1110	2460	A	9103	242	70	EEQFFFFAVGMFP*VDFLAPASGELWDRRLT CSRPFTRHQSFGLAFLRVCSLSDSLDSDSVVG SALLSSVL/NQGGGRNVLEAREAAKHPTI*RQS LLRKQRNKRAIP
1111	2461	A	9110	189	121	SFLSVRLCNGAIMAHCALPLPG
1112	2462	A	9113	100	910	RRRGGSRRPRTVPAPGPGPSFGMDVRFYP AAAGDPASLDFAQCLGYGYGSKFGNNNNYM NMAEANNAFFAASEQTFHTPSLGDEFEIPPT PPPESDPALGMPDVLLPFQALSDPLSQGSEFT PQFPQSLDLPSTISRNLVEQDGV LHSSGLHM DQSHQVSQYRQDPSLMRPSST*PDAARSG VMPPAQLTTINQSQLSAQLGLNLGGASMPHT SPSPPAKSAATPSPSSSINEEDADEANRAJGEK RAAPDSGKKPKTPKK
1113	2463	A	9120	3452	3051	FLRPSFALVPQAGVQWCAWSLQPPSPRFK*F SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH VGQAGHEPLTSGDPPASASQSAGITGVSHQA WPSFFIFSRDVTLLCCSGWSRTSGLKQSACLS LLKCWDY
1114	2464	A	9122	152	377	NQLPLQQTFFIYETGFCVSAQAGVQCRDHS SLHP*PPGSSDPPAPPS*VLGITGQRVHACLI YLYVQTVPQRV
1115	2465	A	9124	553	981	QRFLLRQQLGSWPTCRSLEGDLASPW**RLPG SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE WRLQHKGRGRGDLHLPDHHLSPSSADHPA QQPSQFNGRNLYFLPLFR
1116	2466	A	9135	48	410	SASHEPAEHDGAGDSLASQPPRPAGRPAGA QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGRGLQ PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPRPAASSA *NSAGS*GLVEGT*PPGAGHGAPSPA VGARLS

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						CPARTSVQGGTWTCT*APAGRPAGLGGWEAE RESAPSCSAGS*DAD*GAEPWAGAGRSWGS
1117	2467	A	9141	380	939	KSGHWAKECLQPRIPRPCICVGPWHKSDCP TCPGAVPRAPGTLPQGSITDSFPDLLSLVAED *CCLMASEASWTTTELWVTLTVEGKSVF/CL NTEATHSTLPSFQGPVSLASITVVGIDGQASKP LKTQQLWCQLGQYSFMHYFLVPTCPVPLLG* GILTCLSAFLTIPRLQPHLIAALSPSS
1118	2468	A	9154	471	2	AAGQVVVEVTSHLVLCITSDAAGLRLLPPAES EREGGHCAPAEAPLPPRPQYCLAKHPLRLKLP EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ LVEGNIGVNLQNTLQKH*INGFLDTTPEAQE TKEKTNKLNFIKKVKRQLAEWEKIFQIA
1119	2469	A	9155	2	3187	ACPRLARRRRRVRSLRRRGWLRARWSRGQ NNMAARRITQETFDVAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSAEMYDDVHS DGRYSLSGSVASHRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDGSSRLIEKECLEK ESRDYDVDPGEADSV/LRGGSQVQARGRAL NVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTSPD VTLGTNPGTEDIQFPIQKPLGLDLKNLRLPRR KMSFDIHKSDVFSRFGIEIKWAGFHTIKDDIK FSQLFQTLFELETETCAKMLASFCKSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFEIKPFDKYIMRLQDRLLKSVTP LLMACNAYELSVKMKTLNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAPPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAEPEPMREEEKMIPPTKPEIQAK APSSLSDAVPQRADHRVVGITDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKLLPWQRRGLLRAQGVLRG WKARRA/TGTGTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAKDCPPDPVGPSPQDPSL EASGSPSPKAGVDISEAPQTSSPCPSADIDMKT METAELARFVAQVGPEIQFSIENSTDNPDL WFLHDQNSSAFKFYRKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEFP PREAELESPEVMPPEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGEAAEDDLGAPALSQ ASSGTCFPRKRISKSLKVGMPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRDRWR HFNPKFECAPLQNVSRHSCFPVV
1120	2470	A	9163	124	207	PPRACRPCRACPCPPT*KCSQPVSWPC
1121	2471	A	9166	272	523	PMSSLQGCFTYFKCHFKGIFLLISNLIAF**EK V/CSHTDSLKFIGKGVGMVTHACNPGTLG G*GOWIA*VREFETSLGNM
1122	2472	C	9170	442	236	MNRRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQENGCLQFDSTHIT FSKRQN*
1123	2473	A	9171	10	423	MVDRSPLLTSVHIFLAJGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTTPGGRLFCGFYGLFGVPFC LTWINALGKFFG

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1124	2474	A	9173	3	374	GPSPLLVLPPQEPGGTGPVRAGAGAGMWL WEDQGGLLGPFSFLMLMLLLETRNPVNACLL TGSFLVLLGVFSFEPVPSCRALQELKPRDRISA IAHRGGRHDPENTLGAIROGS**WSNRR
1125	2475	A	9179	704	188	ESSGILLFQCFQGIHVQKLTQARPTLFSWWL CSKPPKETGELENAESGGDGGRRGGKQDNV AWWRMAQKGDFFWDDDFPQSGPFGGQA LPMGFFLYFRDPGREITWKHFVQYYLARGL VDRLEVNVKQSVRVIPAGTSSEVRGEFRAE YCRHKFISCKNVVFFYFFQ
1126	2476	A	9183	153	233	MEYMAESTDRSPGHILCCECGVPISPNN
1127	2477	A	9185	1	321	LTGQLGSILLRVFSKSRAGLGARKLKAYRTM EYMAESTDRSPGHILCCECGVPISPNNPAAQYICV ACLRSSFHYHCIPKLFHFPSTSSSAFITPSHY LTFSTIS
1128	2478	A	9186	183	847	VLKFLLLQTMDEQSQGMQGPVPQFQPKAL RPDMGYNTLANFRIEKKIGRGQFSEVYRAAC LLDGVVPVALKKVQIFDLMDAKARADCIKEID LLKQLNHPNVIKYYASFIEDNELNIVLELADA GDLSRMKHKFKKQKRLIPERTVWKYFVQLCS ALEHMSRRVMHRDIKPANVFITATGVVKLG DLGLGRFFSSKTTAAHSLVGTPTYMSPERIHD NG
1129	2479	A	9190	1	370	GTSWKIPSAAVSESSPNGAAYASGLPCGVGR PPWAGLALLPSPTLMALLRRPTVSSDLNDIT RATTIKIRVVATITRARIEDMRHSATALTRPD ATTAQIPKLPVTTVCNRRANPGIPPSVL
1130	2480	A	9194	131	487	AYLKRLVPVPSITGFARLTSEWLRLLPFLGV LALLGYLAVRPFPPKKKQKDSLNLKIQKEN PKVYNEINIEDLCLTKAAYCRCWRSKTFPAC DGSHNKHNELTGDNVGFLILKKKE
1131	2481	A	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE PLAFLRALELLFAIFAFATCGGYSGGLRLSYD CVNKTESNLSIDIAFAYPFLHQVTFEGPTCE GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL AATGVYIFFQNKY
1132	2482	A	9206	1	852	GGGRAGAGSRDMGSTDSKLNFRKAVIQLTTK TQPEATDDAFWDQFWADTATSVDVFLV PAAEIRAVREESPNLATLCYKAVEKLVOGA ESGCHSEKEKQIVLNCSSRLTRVLPYIFEDPD WRGFFWSTVPGAGRGQGEEDDEHARPLAE SLLLAJADLLFCPDFTVQSHRRSTVDSAEVDH SLDSCEYIWEAGVGFAHSPQPNYIHDNMRME LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY NHLY
1133	2483	A	9208	1165	1463	GPRARVQGFSGADIVKFMALGSMYLVLTIV AKVLRGAEPCCGPLKNRVLRCPLP/VPLPPP HPQPSRGPNVGLCLPTKYVVYKLLSWPLHSNS NVYFIV
1134	2484	A	9210	66	1586	MAGAGPKRRALSAPVAEEKEEAREKIMAAK RADGAAPAGEGEGVTLQGNITLLKGVAVIVV AIMGSGIFVTPTGLKEAGSPGLALVWVWAC GVFSIVGALCYAELGTTISKSGGDYAYMLDV YGSIPAFLKLWIELIIRPSSQYIVALVFATYL LKPLFPTCPVPEEAAKLVAELCVLLLTAVNC YSVKAATRVQDAFAAAKLLALAILLGFVQI GKGDVSNLDPNFSFEGTKLDVGNIVLALYS LFAYGGWNYLNFVTEEMINPYRNPLAIHSLP

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						IVTLVYVLTNLAYFTTLSTEQMLSSSEAVAVDF GNYHLGVMSWIIPVFGVGLSCFGSVNGSLFTSS RLFFVGSREGLHPLSLMHPQLLTPVPSLVFT CVMTLFYAFSKDIFSVINFFSFFNWLCVALAI GMIWLRHRKPELERPIKVNALPVPFFILACLF LIAVSFWKTTTPWSVASDFTIISGLPVYFFGV WWKNKPKWAPPGLHSPRPSCVRSSCMVVPQ
1135	2485	A	9216	40	410	RDRLPPAYFCRPVVCVVTALDVGSPESQEM DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV MQETLRNLASIGEKWKDONIEDQYKNPRNL RSLGGERVDENTEENHCGETSSQIPDDTLNK
1136	2486	A	9223	3	983	RRRRRSRYRRCRFRPGPLAVSMPHAFKPG DLVFAKMGYPHWPARIDDIADGAVKPPFN KYPIFFFGTHETAFLGPKDLFPYDKCKDKYK PNKRKGFGNEGLWEIQNNPHASYSAPPPVSSD SEAPEANPADGSDADEDEBGRGVMAVTAVT ATAASDRMESDSDSKSSDNSGLKRKTPALK MSVSKRARKASSDLQASVSPSEENSESSSE SEKTSDDQFTPEKKAARAPRRGFLGGRKKK APASDSDSKADSDGAKPEPVAMARSASSSS SSSSSDSDSVKKPPRGRKPAEKPLPKPRGRK PKPERPPSSSSD
1137	2487	A	9229	21	239	LFPRLECRDPVTVNCTNLNPGSKNAPTASQV GSTWNYRGGPLPHTNFFVKTGFRCQAGLKL RGSREPPAWA
1138	2488	A	9231	1664	2	TRSVGVNTECVGVVTEPECLGPCPEPGTSVNL EGIVWHETEGLVNVNVTWRNKTYVGTLLD CTKHDWAPPRFCESPTSDLEMRGGRGRGKR ARSAAAAPGSEASFTESRGLQKNRGGANGK GRRGSLNASGRRTPPNC AEDIKASPSSTNKR KNKPPMEI.DLNSSEDNKPGKVRVTSRSTP TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK YKHINGLRYHQAHALDPENKLEFEPDSEDK ISDCEGLSNVALECSEPSTSVSAYDQLKAPA SPGAGNFPFGTPKGKRELMNNGPGSIGAKAGK NSGKKKGLNNELNNLPVISNMTAALDSCSAA DGLAAEMPKELEAGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPPTPPQLIA IPTATFTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPIVNPALVSLKDKKKKEKR KLKDKGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNENGLANGLSESQESRMAS IKAEADKVYTFIDNAPSPSIGS
1139	2489	A	9234	207	443	TRRGQPWRRRAAAGILPGREAAACLPSCIAS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL
1140	2490	A	9238	248	328	MAQGNNGYQTSNGVADESPNMLVYRKV
1141	2491	A	9242	2	535	FVEAAVKMLGSLVLRKALAPRLILLRLRSP TLRGHGASGRNVTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGFRDTKCLAA ATWGRLPGEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARQ NMQEVSRNRCALLHSAAVQEYGYGN
1142	2492	A	9245	157	466	HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD FALGNDFLNITTKAQA/TKEKLDKLDKFIKIKTC CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF GICKEYSRQ
1143	2493	A	9247	264	115	GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPDG ARDSTSIIRMGPEIPPP

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1144	2494	A	9260	1	401	KKVPGRLSEMSFSLNFTLPANTTSSPVTDCGP SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE AMEESDRPCEISEDDNPKISENPRRSPTHEKN TMGAQEAHIYVKTVAGSEEPVHDIRYRPTIEM ERRR
1145	2495	A	9264	175	411	METIWIYQFRLIEIGDSTVGKSCLLHRFTQGRF PGLRSPACDPTVGVDFFSRLLIEIEPGKRIKLL WDTAGQERFISIT
1146	2496	A	9277	592	814	MFTYLEGREGIKSQPKMEPHSVTRLECSGMI SAHCSLNLPGTSDSPASASR/VAGTTGMRHHA WLIFAFVETGF
1147	2497	A	9279	1255	2	FRRGRRGEEKEEEEEEEGWVNGMENSHPP HHHHQQPPQPGPSGERRNHHWRSYKLMIDP ALKKGHHKLYRYDQGHFLAMSSNRPVEIVE DPRVVGWTKNKELELSPKFKIDEFYVDQV PPKQVTFAKLNDNIRENFLRDMCKKYGEVEE VEILYNPKTKKHLGIAKVVFATVRGAKDAVQ HLHSTSVMGNIHVLDITKGETRMRFYELLV TGRYTPQILPVGELDAVSPVNETLQLSDALK RLKDGGLSAGCGSGSSSVTPNSGGTFFSQDTA YSSCRLDTPNSYG/QGTPLTPRLGTPFSQDSSY SSRQPTPSYLFSDQPAVTFKARRHESKFTDAY NRRHEHHYVHNSPAVTAVAGATAAFRGSSD LPFGTVGGTGGSSGPFFKAQPDSTATTAHTP PAQATPAPGR
1148	2498	A	9302	1026	6	IASIQNADTMPGVGLLVSHFSTLVSRQRCPNY ADPQNLTDSIFLLLEVSGDFELQPVLAGLFL SMCLVTVLGNLLIILAISPDShLHTPMYFFSN LSLPDVAGFTSTTVPKMIVDINQSRSRVISYAG CLTQKSLFAIFGGTEENMLLSVMAYDRFVAI CHPLYHSAIMNPCFCAFLVLLSFFLSLLDSQL HSWIVLQFTIKNVEISNFVCDPSQLLKFAACSD SIINSIFYFHKDPERQLVLAGLFLSMCLVTVL GNLIILDVSPDShLTPMYFFLSNLSLPDIGFT STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAIF GGMEERHAPECDGL
1149	2499	A	9303	1	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE FRLVAADRSMGRYMLFGVINLICTGFLMWC SSINSIALTSYTYLTIFDLFSLMTCLISYWVTL RKPSPVYSFGERLEVLAFASTVLAQLGALF ILKESAERFLEQPEIHTGRLLVGTFFVALCFNLF TMLSIRNKPFAYVSEAASTSWLQEHVADLSR SLCGIIPGLSSIFLPRMNPFFVLIDLAGAFALCIT YMLIEI
1150	2500	A	9308	797	693	DRSTSVTRAGVQWCSLGSQPRTPGLLRSSCL SLP
1151	2501	A	9309	205	406	VAIKELPVLWKWSKPTRITAKEPPQTQQRAG SKTAAPPCQWSRMASEGPNIPCPGARHSDKQ FLICTI
1152	2502	A	9314	913	504	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV QGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRR PPPHRVEIFFVFLAETGFHRASQAGPDLPTS/S/I PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL GTNVSLRAA
1153	2503	A	9315	392	1	HPHRPRPGFRSPARSSRPCVLTSLPPFPSPSP PADDLVKAGRDRKDPQVR/ERRLRPNPGRLG GPR/PRPARARS/CHQPRLTRVCPRSPPEARA PAPAAPARGRGAPKRNRPRTDTRAPRGSSAR PGNS

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1154	2504	A	9321	331	433	MPCI/QAQQYGTAPSPGPRDHSASDPLTPEFIKPT
1155	2505	A	9324	180	275	MEEPQSDPSVEPPLSQETFSDLWKLLSENNVL
1156	2506	A	9326	383	619	MISPSRTEGDPLPLPP/EGEGQEVGRFGGGPAK EAAQRHCRASVSILRMRRPGQGSSRPARVPL RGPDSHRLREPPPSPP
1157	2507	A	9327	152	292	YERRGRSQGGGSHPAGAQPGGRAJGAGWQS KEPLWEGLQRSGLPG
1158	2508	A	9328	1	430	QELKQGNPLAPSPSAPSTSAGLGDNCNHRVD LSKTFVSSSALAMLQERRCLYVVLTDSCRFL VCMCFLTFIQALMVSGYLSSVITTIERRYSLKS SESGLLVSCFDIGNLVVVVFVSFRGRRRRP/ RVAAVGGLLDLEGEMI
1159	2509	A	9334	108	383	KGNQVNGNGNQLKRKHESMCPVSLTQNTVR LMEAGLPQKQAEADELFEAGLVIVVKLDER VLNALYSSVGLQWFKESDLSHLRLLEISFR
1160	2510	A	9338	2	430	FVGRPRQLSDRLEDLFLAGFRVGERLRTAAM KRYVRILLGEGAHEHVADVPVGGRGVPRGEA DHTDQELREEIHKANVERVVHDVSQEATIEKI RTKWIPLV/RWGDHA/EGPVGKSYLPSGRSM EALPIMSQTETIETCVEC
1161	2511	A	9341	1	390	NSRVDDFVAPGLSEAGKLLGLEPPERQRLAA AVG/CSPMSGVISMSAPFLGKIIDAIYTNPTV DYSNLTCLCLGLSGVFLCGAAANAIKVYLM QTSRQVRVVKRLRTSLFSSILGQEVAFSDKAGT GELI
1162	2512	A	9343	84	837	QGRFRAFCWQRDFLQPPGMRLSALLALASKV TLPPHYRYGMSPPGSVADKRKNPWRRRPV VVEPISDEDWYLFCDTVEILEGKDAGKQKQ VVQVTRQRNWWVVGGLNTHYRYIGKTM DYR GTMIPSEAPLLHRQVKLVDPMDRKPTIEWR FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET WIDGPKDTSVEDALERTYVPCCLKTLQEEVME AMGKETR/NTRRSIGIEPGAQLLPNFCPSLE G
1163	2513	A	9346	967	616	DSLALSPRLECSGAISAHCNLTTPPGFTFSCLS LPSSWAYRCASPHPDNFFVFLVESGFHHVGO AGLKLLISSDPPTSAPFKCWDYRRDASSAPAT FSSYQRNPDLLNDTIMPNIK
1164	2514	A	9347	3	1099	SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL FSVLLPLRLDGIQWSYWAFFAPIWLWKLLV VAGASVGAGVWARNPYRTEGEACVEFKA MLIAVGIHLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSAACVWGFRHDSLELEILC SVNIIQFIFIALKLDRIHWPWL VVFVPLWILM SFLCLVVLYYTVSLLFLRSLDVVAEQRRTH VTMAISWITTVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMTTFRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHEKA LPLQNKDRGSWPASRGSPLL
1165	2515	A	9362	547	991	DVSGPPLLRPCSGREQTRSLSFSPDPSSFSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRLRCGRAVLTQKRC TKHAYGRKPIWLSQMACSGPEPTLHDCFRP LGEDTLFHVEYTSVHGRERLSAKD
1166	2516	A	9363	201	387	PPILRWTPPSGKNFFFFFESEFY/SSPRVECS GAISAHLAHCNLCPLGSSDSPASAFQVAS
1167	2517	A	9368	707	1087	AVLTPCLSPCSPSRIPR/SPRPYGGRRSLSTPP

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						PRPLILYAPAPRPAGTAFIPHSHPPPDRLRPT ATPA/TPCPSLPFPPRPLHPTQFSTALLDPFPPW PLPFFPSS/RFPDPDCSTSYSPTFPPPT
1168	2518	A	9375	511	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS PITVTSAVIIVLMLLM/IFSPWLATHDPNAID LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS QQSILAGLVVVATTGMIGSPLECLFGELGGRA DAIFMRVMDIMRS/IPSLVLTMEKTAALGPSL FNAMQASSEH
1169	2519	A	9377	42	410	GNGRVAPRDPGAVASAEPLTTHDSGVNPN NSARRMEAMASGSNWLSGVNVVLVMAYWS LVFVLLFIFAKRQIMRFAMKSLRGPHGPVGH NAPKDLKEEIDILLSRVHNKYEPHLLADDDA
1170	2520	A	9378	302	1303	GVSGFSASVLRQRRMEDELEPSLRPTQIQGR ILLTICAAAGIGGTFQFGYNLSIINAPTLHIQEF TNETWQARTGEPLPDHLVLLMWSLVLSYPL GGLFGALLAGPLAITLGRKKSLLVNNIFVVS AAILFGFSRKAGSFEMIMLGRLASWGVNAGV SMNIQPMPLPGGESAPKELRGAVAMSSAIFTA LGIVMGQVVGLSTTAATGLRGLAGELEELEE ERAACQGCRRARPWELFQHRALRRQVTSLV VLGSAMELCGNDVYAYASSVFRKAGVPEA KIQYAIIGTGSCCELLTAVVSVSLEGALPPPAL WGGTPRSFALNQFTLQKKKK
1171	2521	A	9381	2	412	RGPASAEQEDERARTAPLERVRARGRMTTSSA LFPSLLPCSWSTSNKYLAEFRAGKMSLKGTTE TPDKRKGLAY/IQQTDDSLIHFCWKDRTSGNV EDDLIIFPDDECFKRLPQCPNGRVVYLKFKAG SKRLFFWMQEP
1172	2522	A	9384	20	355	GWNGRSTEAAPAEAPHVPHKETKAAMGTQ CTHGGKVRDPDHDMLTTVVHKIKLFLVCHSL LQLCAIMISDYLKSSIYTVKRLGLFRPTSGLL ASFNEVGNTALIVLESY
1173	2523	A	9393	430	87	LCQCIVPGQKETFSNLNPFSSATVRFYL*LSLQ QRKEDQ*III*YHLNKDCLHIFMSAITLYMKI* KIFVLDFDNIMFETPFYII*FIFLFSQNLKRIRQV IRPPISFSKINNGP
1174	2524	A	9397	77	374	ERLEIGRLGGERGSGFASCLRVIVDSGMWDQ RLVKLALLQLLAFYGIKVKGVVRVHRDCGTF ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF LGML
1175	2525	A	9399	66	397	HESSRADRDKMDTRGSTYTDADPVNKSOGT AKMNKWSKGKVRDKLNNLVFDTATYDKL CKEVPNYKLITLAVVSERLKIPGSLARAALHE LLSRGLI*LVIOHIAQVIY
1176	2526	A	9408	2	299	LDLTHVLSLSISLTVTILGTFGMVIPLLDVVY GERGYAQNGDF*DAQLDDYSFSCYSHAQVN GAPNSLTRAYDDP*VKISGLECQKVGVALVEV KCLNL
1177	2527	A	9416	2	402	CNFLRSSRIRVHSTPAASTMPPKVPNEIKVV YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD FV*ATGDWNVLIISVILTIRLLSHIFVPPFFCF DHLIAFWDLQSLIFLHVIFSLFITLLFCFFSIF
1178	2528	A	9419	142	426	TPLFDLWPRVVLWSLETVLTSLRTRRAASGPP ACRIMPTTVDDVLEHGGEVHFLQKQMLYLL ALI*DTFAPYYGVIVLFGFTPDHRCRSPGVAEL
1179	2529	A	9420	1450	1655	LSSAGTKMNLN*KNYWPGASAHACNPSTLG GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA WWRAP

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1180	2530	A	9422	176	375	HRPQTTRPDWKPRT*PQKG*GRLSSEISPAFP SRFSRSTKPVPKADPPARQKLTGVLHAPLLK L
1181	2531	A	9436	2	274	PIAASLRMYNLQPYTEENLICTAFATMVETVP IARTILDRLTGIPHGVCYFVE*ADWATADKCVH IYNGKPLPGATPLLSLQLHQLAHLGS
1182	2532	A	9442	3	240	VDKCSSKSVLSEYCPHCMCSLSTDPKPFQGL SMILK*MGAGDEKISAMGKARVDHRELVLGL LYPTEDYKLIFRARH
1183	2533	A	9444	384	3	LKDFQFWALHDWPLFCCCTFLFLVLECFTR KGCSGWAPWLSLQCCQHFGRPRWADHLRSGV RDQPGQYSKTTLFKIQKLAGHSGAHL*S*LL ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT ERG
1184	2534	A	9462	391	655	LSGFKSLMPKIPLQYTYVVRVTTWSFCLPLDQ RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV IHTCNPSLGGGRAGWIV*AQEFET
1185	2535	A	9467	215	566	RCPMWQGGQASRMDPAKARDREASTCCSLA WWWGWECWVRALKLSSGPAGPLACWVAK KKSLSLSPVYPSEKAGLYYF*DRVSLCHPG WSAVVQFWLTAASNSCSFLLSSWDYRCA
1186	2536	A	9468	275	452	HIPQLHTKTHYVPTRMVNKI*QIDNSKPVQR GG*TGILTHCW*ESKL VQPLWKIVWHYQ
1187	2537	A	9469	388	3	EVAPGPSQILPRRVTDDGDRPQFSLPGPRLPQ SSRGAEPCLSNCHSPAPRKQRMGDSQ*STP NPASPHPEAPQEPWDSASGVSFSLGRGAK ASS*VPGKGRGPRQGSSELLAETILEFLALAN S
1188	2538	A	9471	124	397	TMDKKNRHNGLDMSLHMTGPMCLIENTT GRLMANPEALKILSAITQPMVEEALAGLYRAC *FYLINNLAGMKKGLCLGSTEQAHTIGI
1189	2539	A	9480	584	769	GHVQSQHFGRRPRADHLRSGDRDHPG*HDET PSLLKIQKISAWWWRAPVVPATWEAEAEW R
1190	2540	A	9483	463	86	VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL PRQHCTLQTHRHLPAPVKV*KT*RLFPGLR GASSCRRRCNPVLAARKAGSPRSHSTRENC RRSRCPDTAHRRRRRGRRRNPSCVRSRWR
1191	2541	A	9489	1	411	LADALCLSAATGAVRPGARAQPTRRRLSP SVRVCCRAAAASNLLYSSCLQRHSEASEEG ERGLSAKCCSLVLRGGCSSNSHSHFRIT*EI MAAFVLLSYEQRLKRPRLGPPDVYPDPKQ KEELTAVNVK
1192	2542	A	9497	389	161	VSFLSMSSGHCIIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEEINTS
1193	2543	A	9509	186	1	IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLGLYPTM
1194	2544	A	9512	58	433	PLQRSKCLTLRCLRAKPWAWSPRACSSAL LKSSRSRASSLNVCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNFTANIIVEGQKLEAFPLRTGTQ
1195	2545	A	9515	595	1223	GHGAPSFQTVPRTP*ASWVVPVPAASESAFAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEP LPRCSAPLRSASAPQVS*CV*AVNLLPHNL* PLHLLLD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAAGSRARRFPGP GTRRTPSGCQNPAAASGG

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1196	2546	A	9518	229	468	RSPTATPAPHAMGPGAPFARGGRPLPLLGAM AERVAPGWDLHTPYLPRTNSRRTPHL**EPHA GYIGALFFMSGGWPGGQ
1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG HAMRHLTGNTSMAIRFL*ADSRFQVQRRYE APNWKYKYG*IPVDMLC
1198	2548	A	9524	204	1	KNKKTTKCLSVTLNISGPNQ*NKRHRVAEWI VKQEPNICHLETHFPFRDTRYLKEREQKKRK SSYS
1199	2549	A	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA V*QRGDGKNPGVTHLNRPVGTGX
1200	2550	A	9548	186	1	VNAKEF*KIQHYFMTKSNKLHIEHTYLPKI KAIYDKWTSIDMLNLQKL*AFRLRVTRQI
1201	2551	A	9549	591	2	SSVVEFRGPRSSLPPLDSTFCGSSPNWTGGC GSCPSGE*LVSFGSEQRKYSNSNVMHETSQ YHVQHLATFIMDKSEAJTSVDDAIRKLVLQSL KEKIWTQEMLLQVNDQSLRLDIESQELEDLF PLPTVQRSQTVLNQLRYPSVLLVCQDSEQSK PDVHFFHCDEVEAEVLVEYMEASALTDCLGK AMRP
1202	2552	A	9552	428	1	KYGNEGHWSRQCPNPGKPIRCPCLCRGPHWK LDCERFPQGPLPSLPELAKTSYSDLTGLATED *WGPGMDAPATTIASSKTRVTLMVAGRPVFF LI*YRATYSALPNFSGPTQSSQVSVVGIDGQV SKPRATPPLFCSLHTF
1203	2553	A	9568	517	738	RRKFERKQKQ*RYREGKQYRQRDKMKEWG EKBKRREKGEREERKMRHREKGESGQRD TMENWRVERLTEKER
1204	2554	A	9573	83	415	EDKRLRLVDGDSRCAGRV*TYHDGFWGTICD DGWDLSDAHVVCQKLGCGVAFNATVSAHFG EGSGPIWLDLNTGTESHLWQCPSRGWGQ HDCRHKEDAGVICSEFTALR
1205	2555	A	9577	64	424	ARGSCPTRPRTANGRMGETKDAPQMLVTFK DVAVTFREEWRQLVLVHRTL*YR*GMLETC GLDITLRLHNPQPDVHLLYHGTQLLVKRE VSHSPCAGDMRELFTEATLTPHPYNNGA
1206	2556	A	9584	38	476	TLGAVLFSEVSKESSTSHSGGQLGRQNRHPL SNFITPSSPRLKP*TASSQRNLGQILNMFITAV NPQPLSTPSWQIETKYSTKVLGTGNWMEERRK GLPYKHLITHHQEPHRYLISTYDDHYNRHG YNPGLPFLRTWNGQKLLWL
1207	2557	A	9586	2	412	LRSSPAALLRALCITVTGTALALRSRVATTN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNNRQKLP THILCLL*EKGFGLTFAFIIGLDGSTGPTRFLL FGILFSICFS
1208	2558	A	9597	122	3	IKNYWPGMVAHACNPSPGLGGRGRWIA*AQK FADAWADAW
1209	2559	A	9611	148	558	KSLRNVWDLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNYYQ RIRDHLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRRESQCT LLNASITETFNC
1210	2560	A	9618	384	2	SLHDMMLLAEQQQKQKQWAVNTQNTAWSNA DSKFGQRLKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNLCQRQETADS***WSPKNSHVGKDS GELSAK
1211	2561	A	9620	316	610	QKHPGGGQLGRSPQEDSRFHNKASSGVSRVR

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						LGRAWWLTPVIPTLWEAKAGGSPE*D*AGRG GSRL*SQHFGRRPRVDHLRSAVQDQPGQHGE TPSLKIQKIN*VWGRRL*SSYSEAEAGESL
1212	2562	A	9623	297	344	QFPVDGDYQKIEKITQLFQAQNLCLAMTR TREL*KGGGKGRHE*AVVPFLKGGYGVKAP AILNTSNCT*CF*ETKMLSDDPKACVFEVSSA DL*NTSFGVIR
1213	2563	A	9624	2	356	AELSLASTACGRNTSGDSLDPDYDRAPISPLA TSGTILSAISCLWDLPTPVLRLVGLSCQPSMSSQ IPRMYSTDVEAAVNSLEDLYLQAYYAYLCVG LYFHRDDMALEGVSRFL*ELAE
1214	2564	A	9634	776	912	SLSRVWRACL*VPYNQENCLNPRGGGCSEPR SHYCTPAWATEKDS
1215	2565	A	9636	220	426	KPGNFVVSSEY*DITSGQLKTAVRG*IEMTST EENFGEKLHDIGFGNGFLDKT*KAQATKAKI DK
1216	2566	A	9637	391	76	CFLEDGCTQAS*AEAAVSPSMAEEEEQGSTSC RERRSIRFKMKNHSPDDTIKENVTISNIRTKI NHLPETERNLLEHGLMYIRLNAAFCSLVAHS LFGILKAT
1217	2567	A	9655	2008	2432	LHCKMGALETQTHPCSQNMLRSLQKCCCKV EEHHLQPVQVLQTLHLSATAGTCRRPARPP PAPPTPTPWRSRQSGKQSERAS*LKGRGRYGL GALGGRGGRALGGSRWPPPLPGETLFGCKH RRRRRGSDAAPGEEAGT
1218	2568	A	9658	3	405	HASARALLSPNLSPNNKMAISGGPVLGFFILA VLMSAQEPWAIKEEHVIIQAEFYLNPDQSGEF MLDFEGEDTFHGDMAKKETVWRLE*LARLD NFEAQRALANIAADQAALIMDMGSDYTLIP NVPPKVTVL
1219	2569	A	9662	3	284	PDWTEKRRMQDTGSILPLHWFGFGYAALVA YGGIIGYVYKAGSVPSLAAGLLFGSLSGLGAYQ LSQDPRNVWVFLATSGTLGIMGMRFYHSG KL
1220	2570	A	9669	200	699	LLLTGYIQTQLNQQLSGNQEQEMQAVDNLTS PGNTSLCTRDKYKITQVLFLLYTVLFFVGLITN GLAMRIFFQIRSKSNFIPLKNTVISDLLMLTF PFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYI SISFLGLITIDRYQKTRPFKTSNPKNLLGAKIL K
1221	2571	A	9676	164	562	KERDSSTFSAAMTTMQGMEQAMPAGPGVP QLGNMAVIHSHLWKGLEKFLKGEKVLGV VQILTALMSLSMGITMMCMASNTYGSNPISV YIGYTIWGSVMFIISGSLIAAGIRTTKGLVRG SLGMNITSS
1222	2572	A	9688	43	412	VAKMVKCCSAIGCASRCLPNSKLKGLTFHFV PTDENIKRKWVLAMKRLDVNAAGIWEPKKG DVLCSRHFKKTFDRSAPNIKLPGVIPSIFDS PYHLQCKREKLHCRKNFLKTVPATNYNH
1223	2573	A	9696	308	564	RTSMGILYSEPICQAAYQNDFOQVWRWVKE DSSYANVQDGFNGDTPLICACRRGHVIRVSFL LKKECLCQPKPERENLLALCCE
1224	2574	A	9700	3	632	DAWASGGELGSLFDHHVQRAVCDTRAKYRE GRRPRAVKVYTINLESQYLLIQGVPAVGVMK ELVERFALYGAIEQYNALDEYPAEDFTEVYLI KFMNLQSARTAKRKMDQSFSGLLHVCYA PEFETVEETRKKLQMRKAYVVKTTENKDH VTKKKLVTEHKDTEDFRQDFHSEMSGFC ALNTSAGNSNPYLPYSCPLCYFSSK

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1225	2575	A	9710	1	163	RSGCVLRMTWETGAPAVAETPDIKLFGKWS TDDVHINDISLQDYIAGVRLILL
1226	2576	A	9713	82	492	QGLPSFLPAFGPSGSLGFPAPITLGSSCNTVDT ICHGYSEIRPLFYLSFCDLLGLCWLTTLLYG ASVANKDIIICYNLQAVGQIFYISSFLYTVNYI WYLYTELRMKHTQSGQSTSPVIDYTCRVQC MAFVFSSLI
1227	2577	A	9720	3	416	GKWKRTQVPLLGEACADMALARKEFLRGNG LAAGKMNISIDLDNYAELVLNVGRVTLGEN NRKKMKDCQLRKQNNVSRVACALLNSGG GVIAEVENKGYSYKKDGIGLDLENSFSNML PFVFNFLDFMQNGNYF
1228	2578	A	9723	278	411	EASSNTVASNVADKTDPHSMNSRVFIGNLN TLVLQKSDVEAVF
1229	2579	A	9725	121	902	LFAMSGFENLNTDFYQTSYIDDDQSQSYDY GGSGGPYSKYAGYDYSQQGRFVPPDMMQP QQPYTGQYQPTQAYTPASPQPFYGNFDEP PLLEELGINFDHIWQKTLTVLHPLKVADGSIM NETDLAGPMVFCLAFGATLLLAGKIQFGYVY GISAIGCLGMFCLNLMSMTGVSFGCVASVL GYCLLPMLLSSFAVIFSLQGMVGILTAGIIG VCSFSASKIFISALAMEGQQLLVAYPCALLYG VFALISVF
1230	2580	A	9739	11	247	TFVLNMNTPKEEFQDWPIVRIAHLPLIVYG HFSPERPMDYFDGVLMFVDISGKCKRDVCL MWMSNRLAWEFTCLA
1231	2581	A	9744	37	1100	TPLDFWPGFVLSWLQPLSASLRARRAASGPP ACRIMPITVDDVLEHGGEFFHFKQMFLLA LLSATFAPYVGVFLGFTPDHRCRSPGVAEIS LRCGWSPAELNNTVPOPGPAGEASPRQCR YFVDWNQSTFDCVDPLASIDTNRSLPLGPC RDGWVYETPGSSIVTEFNLCANSWMLDLFQ SSVNVGFFIGSMSIGYIADRFRKLCCLTTVLI NAAAGVLMASPTYTWMILIFRLIQLVSKAG WLIGYILITEFVGRYRRTVGIFYQVAYTVGL LVLAGVAYALPHWRWLQFTVALPNFFLLY YWCIPESPRWLISQNKNAEAMRIKHIKKNG KSLPASL
1232	2582	A	9753	164	517	PGFGMQGPPFITPSWSLPPWRAYVAAAVLC YINLLNMYMNFIIAGVLLDIQEVFQISDNHAG LLQTVFVSCLLSAPVFGYLGDRHSRKATMS FGILLWSGAGLSSSFISPRYSWLF
1233	2583	A	9757	25	419	LPAPWTERVRKSEGLVGTCLGDFMASPRVT IVALSVALGLFFVMGTIKLTPRLSKDAYSEM KRAYKSYVRALPLLKKMGINSILLRKSIGALE VACGIVMTLVPGRPKDVANFFLLLVLAFLV FHQLV
1234	2584	A	9765	71	456	RLELDWGFSLHFLPVAYLCPLSSGFEMNVQP CSRCGYGVYPAEKISCIDQIWHKACFHCVC KMMLSVNNFVSHQKKPYCHAHNPKNNTFTS VYHTPLNLNVRTFPAISGIHQDEGEQCKSV FHWD
1235	2585	A	9767	52	559	IRSGAMSVDKAELCGSLTLWLQTFHVPSCA SPQDLSSGLAVAYVLNQIDPSWFNEAWLQGI SEDPGPNWKLKVTSGLLIRGQTGEEMTRDGP ARHMSWVMGRKRDCLVINHLFIHSSMEYSP CARPGHSARNNTDKNLPHTAILVTSNTYTTI KINFQAGRSGSCL
1236	2586	A	9770	352	608	FRGEALTVRFLTKRFIGEYASNFESIYKKHLC

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						LERKQLNLEIYDPCSQTQKAKFSLTSELHWA DGFVIVYDISDRSSFATKALI
1237	2587	A	9793	266	515	NLAIYFFPRLFLRLDSQSNPKAFALTCHH QKIKNFQILPVSIDALTPPLVVCFLVSFLTHFS RYKPTRPVCITQFQCS
1238	2588	A	9802	537	967	ELGAGRSREAMEAAVKKEISVEDEAVDKNI FRDCNKIAFYRRQKQWLKKSTYRALLDSVT TDEDSTRFQINEASKVPLLAETYGIEGNIFRLK INEETPLKPRFEVVDLTSPSTVRLISCSGDT GSLILADGKGDLKC
1239	2589	A	9805	105	540	VPGDFAMVRAGAVGAHLPASGLDIFGDLKK MNKRQLYYQVLFAMIVSSALMIWKGLIVLT GSESPVVLSGSMEPAFHRGDLFLTNFRED PIRAGEIVVFKVEGRDIPVHRVIKVHEKDNG DKFLTKGDNNEGDDRGSYK
1240	2590	A	9819	3	305	TDGRDPLPCAARRRGGGGECGAGVVAEWS PQPLDPAMLLWMQGFVLEAVACQDNDYLR YGILFEDLDCNGDGVVDIELQELRNWSSAF DPNSEEHG
1241	2591	A	9834	841	1209	SPARGKSNRTDVMITAPKNKKMTENLAPEA LDSSTHSSSTATQSRKMNTPAPTSTVPAIPR GGSGGPPPCAPHDRVSSVLQCDTQAMDHKTE SSHVSVEFLFKRTKTPSFHFAVRENRN
1242	2592	A	9843	3	589	TISCGPATPEPASLSSASSDDFCCKEDRYR LGSSLDGMRPTPLCRICFQGPQEGELLSPCR DGSVKCTHQCLIKWISERGCWSELCKYKY HVIAISTKNPLQWQAISLTVIEKVQVAAAILGS LFLIASISWLIWSTFSPARWQRQDLFPQICYG MYGFMDVMIVAVDSEDMVQAAKEVGKRWS DIPP
1243	2593	A	9846	198	411	WRISHHAGKMPVMKGLLAPQNTFLDTIATRF DGTHSNFILANAQVAKGPIVYCSDFCEL FARTEVMQ
1244	2594	A	9848	116	650	PICGFLYLCSAMASESSPLLAYRLLGEEGVAL PANGAGGPGGASARKLSTFLGVVPTVLSMF SIVVFLRIGFVVGAGLLQALAMLLVAYFLA LTVLSVCAIATNGAVQGGGAYCILQHRWTG VWPVLPAREVMISRTLGPVGGSIGLMFYLA NVCGCAVSLLGLVESVLDVFGA
1245	2595	A	9849	573	1620	KSKCRFPEGLSEGFPMRKEALSSGSVQAE AMLDEFQEQAEGLTVYVISEHSSLLPQDMM SYIGPKRTAVVRGIMHREAFNIIGRRIVQV AMSLTEDVLAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPKSHDYWDIEGAVRR YVQPFNLALGAAGNFVSQSILYYAMLGVNP RFDSSASSYYLDMHSLPHVINPVESRLGSSAA SLYPVLNLLYVPELAHSFLYIQDKDGAPVAT NAFHSPRWGIMVYNVDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLFLGIAQFQPPKCL LSGPTSEGLMTWELDRLLWARSVENLATATT TLTSLA
1246	2596	A	9850	114	464	PPQLGAQRVREPRHPDVRAFLRVTSPLRSRS ARSLGRRPRIAMVTVGNYCEAGPVGPAWM QDGLSPCFFFTLVPTRMALGTALVLALPCK RRERPAGADSLSWGAGPRISYV
1247	2597	A	9851	2	327	FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF HQFTDTIQRSKWIRAVNRVDPKSKJWIPGP GAILCSKHFQESDFESYGIRRLKKGAVPSVS LYKVFKYSSRCTS

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1248	2598	A	9853	58	444	RVDDFVYSKGGKDAGGADVSLACRRQSIPEE FRGITVVELIKKEGSTLGLTISGGTDKDGKPR VSNLRPGGLAARSDLLNIGDYIRSVNGIHLTR LRHDEIITLLKNVGERVVLEVEYELPPPGGCP WT
1249	2599	A	9856	2	1265	LPPPRPSRHRGRAGTRASAAAAAGPTVSAV RAPVRGQDSGAGTPQGRLAGRGAHLRVGA SGSGVAAGPAARHAPRRRCADAGEAVGASC GRCAVALLSGVCTLVSTHVCVSGCGAAGT PMGAGDAGASAEAVTTAPQEPARPLQAGS GAGPAPGRAMRSTTLLALLALVLLYLVSGAL VFRALQPHQQAQRELGEVREKFLRAHPCV SDQELGLLKEVADALGGGADPETNSTSNSSH SAWDLGSAFFSGTITTTIGGGGDWHVGGGK ELPHGGRCRETEGSQVAPRLPASPLCPGYGN VALRTDAGRLFCIFYALVGIPFGN.I.AGVGD RLGSSLRHGIGHIEADFLKWHVPPELVRVLSA MLFLIGCLLVLTPTFVFCYMEDWSKLEAIY FVIVTLTTVGFQDYVA
1250	2600	A	9873	2	652	FVVPSPCGGIPGRAPNGASRPTMGNSASRND EWVYTDQPHQRRKEILAKYPAIKALMRPDP RLKWAVLVVLVQMLACWLVRLAWRWLL FWAYAFGGCVNHSLTLAIHDISHNAAFGTGR AARNRWLAVFANLPEGVPYAASFKEYHVDH HRYLGGDGLDVPTRLEGWFFCTPARKLL WLVLPFFYSRLPLCVHPKAVTRMEVLNITLV QLA
1251	2601	A	9875	150	1209	PVIMPLHFSPGDIVRPSCCVSSPKLRRNAHSR LESYRPDTLSREDTGCNLQHISDRENIDDLN MEFNPSDHPRASTIFLSKSQTDVREKRKSLFN HHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTI KCVALAIYYHIKNRDPDGRMLLDIFDENLHPL SKSEVPDYDKHNPEQKIYRFVRTLSAAQL TAECAIVTLVYLERLLTYAIDICPANWKRI LGAILLASKVWDDQAVWNVVDCQILKDITVE DMNELERQFLELLQFNINVPSSVYAKYYFDL RSLAEANNLSFPLEPLSRERAHKLEAISRLCED KYKDLRRSARKRSASADNLTLPWSPAIIS
1252	2602	A	9879	6	376	KRPDSRPPAQYRAGPTRPRTRGCELLYWKAT KAVGIKMGSLSTANVEFCLDVFKELNSNNIG DNIFSSLSLLYALSMVLLGARGETEEQLEKV WNSSEVCSEPRSLSCSRSGSAKLILSLYQ
1253	2603	A	9880	180	388	KEQAELLYGLYCQCDLTLSSHPSSVPAMSSC NFTATFVLIIGPLEKAHFVWGFPLLSMYVA AMFGNC
1254	2604	A	9881	19	494	VISFQITDITMDSSTAHSVPVFLVFPPEITASEYE STELSATTFSTQSPLOKLFARKMKILGTIQLF GIMTFSFGVIFLFTLLKPYRPFIFLSGYFPWG SVLFINSAGFLIAVKRKTETETLILSRIMNLSA LGAIAIGILLTFEFHPRSKLHL
1255	2605	A	9896	72	386	RPGREQRDCFQAPPLGLGGRQTDMMHPLT GATCVGLPNVGMCPQLSGALTFMYLQQGNQ EATVAPDTMAQPYASAQFAPPQNGIPGEYTA PHPHPAPEYTGQTT
1256	2606	A	9902	95	399	SGGPAGLLHRFVLPKMGSLLPILVPFILLG DIQEPGHAEGILGKPCPKIKVECEVEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTYH KEELE
1257	2607	A	9905	374	459	EHLKSTPNRLGVVAHTCNPSTLGGRGW

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1258	2608	A	9911	364	1974	AGPGVPAVGGRWASGPGGLGGRTLCSGPPDH QRRGPSCGASGDPQCVGSPHPQARPLAR GARLLPGHLPSPRPRLPTGQPPAAAFRGVPR PQGGGHHPLPTPGGRPCFAVSESGSAILLS YLGECSSTSYVTGAACISPVLCREWFEEAGLP WPYERGFLLHQKIALSRYATALEDTVDTSLR FRSRSLREFEALFCHTKSFPISWDAYWDRND PLRDVDEAAVPVLCICSADDPVCGPPDHTLT ELFHSNPYFLLLSRHGGHCGFLRQEPFAWS HEVILESFRLTEFFRTEERIKGLSRHRASFLG GRRRGALQRREVSSSNLEEFNWKRSTYRL MAAAAGAAAAGSREPQDRPECGAGHPGPR YYRHPRWLLRPEAFGLPLRTRAPSAEDSQR ERPAARSGPEMRVRYFVVAAVLAPYLALSQD PMVKSSASGQSGSYNHVREEMLIKAGGA MSRRVVRQSKFRHVFQGAADQAYEDIRV SKVTWDSSFCVNPCKFLAIVEAGGGGAFIVL FLAK
1259	2609	A	9919	693	935	GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA TLSKAERLRSQPGPEQGGSSYPRTPTAAAIL PPRPGRS.HRKRLVSTK
1260	2610	A	9921	455	1082	QRSLCSAIEKDGGDVKALYRRSQALEKLGR LDQAVLDLQRCVSLEPKNVFQEAALRNIGGQ IQEKVRYMSSTDAKVEQMFQILLDPEEKGT KKQKASQNLVVLAREDAEAKIFRSNGVQLL QRLDMGETDMLAALRTLVGICSEHQSRV ATLSILGTRRVVSILGVESQAVSLAACHLLQV MFDALKEGVKKGFRGKEGAIIV
1261	2611	A	9928	1	438	GFRGAEAPGAAQAPKKKKPRPTEGGPGAGSG RGKDPYRGPILLHQPKPKDEFSSLESYEIAF PTRVDHNGALLAFSPPPQRRGTGATAES RLFYKEASPSHFLNLTRSSRLLAGHVSVEY WTREGLAWQRADRPCLYA
1262	2612	A	9931	168	435	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA PPRLPFCLQELQGRHALHTFSLERTCSYQDFL WADEGRLLHVGAQDLATWHTLSPLGLW
1263	2613	A	9938	247	488	RMSATSVDQRPKGQGNKVSQNGSIHQKDG CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY YAPSIGFPYSLGEAAWSQL
1264	2614	A	9941	61	277	ESIGLTALGPRRRPWHRWSDPITLKMKGWG WLALLGALLGTAWARRSQDLHCGACKAVR RRVRQFNIDY
1265	2615	A	9956	2	522	FVASEVSKMPVPASWPHPPGFLLLTLLGLT EVAGEEELQMIQPEKLLLVTVGKTATLHCTV TSLLPVGPVLWFRGVGPGRELIYNQKEGHFP RVTTVSDLTRNNMDFSIRISSITADVGTY CVKFRKGSFDPHVEFKSGAGTELSVRGEYSVG FLSQVWWLSSHFFMN
1266	2616	A	10002	243	387	PKNNACHLLFTAVCQPRCKHGECIGPNKCKC HPGYAGKTCNQGRKTV
1267	2617	A	10004	36	707	LPAPASTWSVARETMASSSVPPATVSAATAG PGPGFGFASKTKKKHFVQKVKVFRAADPLV GVFLWGVASHNELSQVPPVMLLPDDFKAS SKIKVNNHLFHRENLP SHFKFKEYCPQVFRNL RDRFGIDDQDYL VSLTRNPPSESESDGRFLIS YDRTLVIKEVSSEDIADMHSNLSNYHQVRPLS SPILSLSSLLTYSSAIVSNRCQLGRKLIGREN
1268	2618	A	10005	2	209	GEGYELFVPSNGVPAVCHMVGRPHRAVLSP SQDELEHSLGESAAQGAAGVVLWVSWENTR

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1269	2619	A	10010	245	688	TKVSLGLA FGMLKKNKGHSSKKDNLA VNAVALQDHILHD LQLRNL SVADHSKTQVQKKENKSLKRDTKAI IDTGLKKTTCQPKLEDSEKEYVLDPKPPLTL AQKLG LIGPPPPPLSSDEWEKVKQRSLLQGDS VQPCPICKEEFELRPQVFSIRG
1270	2620	A	10011	2	588	RVDDFVRPLPGLMSRSRASIHRGSIPAMSYA PFRDVRGPSTHRTQYVHSPYDRPGWNPFCII SGNQLLMLDEDEIHPILLIRDRSESSRNKLLR RTVSV PVEGRPHGEHEYHLGRSRRKSVPGGK QYSMEGAPAAPFRPSQGFSLRRKSSIKRTKS QPKLDRTSFRQLPRFRSADHDIRYRGWSMW DEIDV
1271	2621	A	10013	209	363	LPAPFNLSRPLSFGFQFPGGNDNYLTITGPSHP FLSGAEVVSQSCRRRGRA
1272	2622	A	10014	7	388	SAVTISWKWRSVMGIQTSPALLASLGAGLVT LLGLAVGSYLVRSSRRPQVTLDPNEKDLLR LIDKTL S ARSPCKHIYLSRIDGSLSRFPYTPVT SDEDQGYVDIDIKVYLKG VHTPFEGGKMSH
1273	2623	A	10016	1	1339	MAARTLGRGVGRLLGSLRGLSGQPARPPCGV SAPRAASGSPGSAPAVAAAAAQPGSYALS AQAAREPAAFWGPLARDTLVWDTPYHTVW DCDFSTGKIGWFLGGQLNVSVNCLDQHVRS PESVALIWERDEPGTEVRITYRELLETTCLRA NTLKRHGVHRGDRVAIYMPVSPLA VAAMLA CARIGAVHTVIFAGFSAESLAGRINDAKCKVV ITFNQGLRGGRVVELKKIVDEAVKHCPVQH VLVAHRTDNKVHMGDLDPLEQEMAKEDP VCAPEMGSSEDMFLMYTSGSTGMPKGIVHT QAQYLLYAALTHKL VFDHQPGDIFGCVADIG WITGHSYVVYGPLCNGATSVI.FESTPVYPNA GRYWETVERLKINQFYGAPTAVRLLKYG AWVKKYDRSSLRTLGSVGPINCEAWEWLH RVVGDSRCTLVDTWWQT
1274	2624	A	10017	1	3750	FRPQGT PRSPASHVLTMSAPDEGRDPKPKG KTLGSFFGSLPGFSSARNLVANAHSSARARPA ADPTGAPAAEAQPPQAQVAHPEQTAPWTE KELQPEKMMVSGAKDLVCSKMSRAKDAVSS GVASVVDVAKGVVQGGDLTTRSALTGTKEV VSSGVTGAMDMAKGA VQGGDLT SKAVLTG TKDVTSTGLTGAVNVAKGT VQAGVDTTKTV LTGKDTVTGVMGAVNLAKGT VQTGVETS KAVLTGKDAVSTGLTGAVNVARGSIQTGV DTSKTVLTGKDTVCSGVTGAMNVAKGTIQT GVDTSKTVLTGKDTVCSGVTGAMNVAKGT IQTGVDTSKTVLTGKDTVCSGVTGAMNVA KGTIQTGVDTTKTVLTGKNTVCSGVTGAVN LAKEAIQGGDLTTKSMVMGT KDTMSTGLTG AANVAKGAMQTGLNTTQNLATGKDTVCSG VTGAMNLARGTIQTGVDTTKIVLTGKDTVC SGVTGAANVAKGA VQGGDLTTKSVLTGKDT AVSTGLTGAVNVAKGT VQTGVDTTKTVLTG TKDTCVSGVTSVAVNVAKGA VQGGDLTTKSV VIGTKDTMSTGLTGAANVAKGA VQTGVDTA KTVLTGKDTVTGTVGAVNVAKGT VQTGM DTTKTVLTGKDTTSGVTSVAVNVAKGA VQT GLKTTQNLATGKNTFGSGVTSVAVNVAKGAA QTGVDTAKTVLTGKDTVTGMLGAVNVAK GTVQTSVDTTKTVLTGKDTVCSGVTGAAN

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						VAKGAIQGGGLDTTKSVLTGTKDAVSTGLTGA VKLAKGTVQTGMDTTIKTVLTGTDKDAVCSGV TGAANVAKGAVQMGVDTAKTVLTGTDKDTV CSGVGTGAANVAKGAVQTGLKTTQNIATGTK NTLGSVGTGAAKVAKGAVQGGGLDTTKSVLT GTDKDAVSTGLTGAVNLAKGTVQTGVDTSTK VLTGTDKDTVCSGVGTGAVNVAKGTVQTGVDT AKTVLSGAKDAVTTGVTGAVNVAKGTVQTG VDASKAVLMGTGKDTVSGVTGAMSMAGKA VQGGGLDTTKTVLTGTDKDAVSAGLMGSGNVA TGATHTGLSTFQNWLPSTPATSWGGLTSSRT TDNGGEQTALSPQEAFFSGISTPPDVLSVGPEP AWEEAAATKGLATDVATFTQGAAPGREDTG LLATTHGPPEAPRLAMLQNELEGLGDIHFM NAEEQAQLAASQPGPKVLSAEQGSYFVRLGD LGPSFRQRAFEHAVSHLQHGQFQARDTLAQL QDCFR
1275	2625	A	10025	124	415	TILARKKEKTCPCCKEIGRNSRSGMYSRKAM YKRKYSAANTKVEKKKKEKVLAPVTKPVGG DKNGGTRVVKLPTMPRYPTEDVPRKLLSHG KKPFS
1276	2626	A	10030	3	507	GGSLRFPSPRPVPCSRVFCVPPGGCGLSPMS ASRPQSPTTPWCLPRRYMKHKRDDGPEKQED EAVDVTVMTCVFFVMCCSMLVLLYYFYDL LVYVVIGIFCLASATGLYSLAPCVRRLPFGK CRIPNNSLPYFHKRPQARMLLALFCVAVSV VWGVFRNEDQ
1277	2627	A	10035	51	869	YSRFTVPLPATMASSEVARHLLFQSHMATKT TCMSSQGSDDQIKRENIRSLTMSGHVGESL PDQLVNRSIQGGFCFNILCVGETGIGKSLIDT LFNINFEDYESSHFCPNVCLKAQTVELQESN VQLKLTIVNTVGFQDQINKEERQLGRSQSTEN PQKYRSEQHPVEPKCTSFWKALGKWAGIE SSQSAQPYLPINSPPHRLADVADVHLFSSV LSGAFGCYHLDVTVNEFKKQQRDEQEGYS KGDQEQGSWKHGADPLRGEM
1278	2628	A	10036	3	457	RAFDVRRKKSRLRCCPRDFHAGCLTVSGPST VMGAVGESLSVQCRYEEKYKTFNKYWCRRP CLPIWHEMVEVGSEGVVRSQVITDHPGDL TFTVTLENLTADDAGKYRCGIATILQEDGLSG FLPDPFFQVQVLVSSASSTENSVKTP
1279	2629	A	10039	214	435	NDSLVPMSWRSRSCAPSSSAWRRSAATTR SRKCLRTKRKRWSGKGTMQSTLSETPRRA QMPCMWYPPFWG
1280	2630	A	10043	2	344	RATWHNAGKEREAVQLMAGAEKRVKASHS FLRGLFGGNTRIEEACEMYTRAANMFKMAK NWSAAGNAFCQAALKHMQLOSKHDSATSFV DAGNAYKKADPQGKTARHVACYLCV
1281	2631	A	10080	620	818	VYKLDSSLSFYFYFFIFETESHFLPLMKWTG PIMAHCSLKILASRNSADSAFLSAGDTSLSHST
1282	2632	A	10084	3	1640	SASIIIRGDKRASGEVGIAPSSRHILIGESAKY NGTAISLVRGPGLGEVTVFWRIPPSVGEFA ETSGKLTMRDEQSAVIVVIQALNDDIPEEKSF YEFQLTAVSEGGVLSSESSANITVVASDSPY GRFAFSHEQLRVSEAQRVNITIRSSGDFGHVR LWYKTMSTAEAGLDFVPAAGELLFEAGEM RKSLLHVEILDDDYPEGPEEFSLTITKVELQGR GYDFTIQENGLQIDQPPEIGNISIVRIIMKNDN AEGHIEFDPKYTAFEVEEDVGLMIPVVRHLHGT

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						YGYVTADFIQSASSPAGGVVDYILHGSTVTFQ HGQNLSFINISIIDDNESEFEPIELLTGATGG AVLGRHLVSRHIAKSDSPFGVIRFLNQSKISIA NPNSTMLSLVLERTGGLLGEIQVNWETVGP SQAALLPQNRDIADPVSGLFYFGEGEGGVRTII LTYPHIEEIVEETFIKHLVKGEAKLDSRAK DVTLTITQIEFGDPNGVVQFAPETLSKKTYSEPL ALEGPLLITFFVRRVKGTGFEIM
1283	2633	A	10088	316	516	MGSKTLPAPVPIHPSLQLTNYSFLQAVNGLPT VPSDHLFNLGYGSALHAVHLHQWTLGYPAM HLXRS
1284	2634	A	10091	2	569	FVSPSRAMASALIYVSKFKSFVILVVTPLLLP LVILMPAKFVRCAYVILMAIYWCTEVIPLAV TSLMPVLLFPLFQILDSRQVCVQYMKDTNML FLGGLIVAVAVERNLHKRIALRTLWVGA KPARLMLGFMGVTALLSMWISNTATTAMMV PIVEAILQMEATSAATEAGLELVDKGKAKE LP
1285	2635	A	10092	290	728	KQSTRPDVMTLYPLHWQEEMSGESVSSAVP AAATRTTSFKGTSPSSKYVKLNVGGLYYTT MQTLTKQDTMLKAMFSGRMEVLTDSGWL IDRCGKHFGTILNYLRDGA VPLPESRREIEEL AEAKYYLVQGLVEECQAALQV
1286	2636	A	10100	1	574	RPRGRGAWAGPGGDYSGVRRQRRRTRISGS QRGSDAAGTMGCTGRCSLICLCALQLVSAL ERQIFDFLGFWAPILGNFLHIVVLGFGTIQ YRPRYTMVYTVWTALWVTWNVFIICFYLEV GLSKDTDLMTFNISVHRSWWREHGPGCVRR VLPPSAHGMMDDYTYVSVTGCTVDFQYLEVI HSA
1287	2637	A	10103	252	376	RSRMGDKPIWEQIGSSFIQHYQLFDNDRTQL GAIYVSFQL
1288	2638	A	10107	1	478	MEEEDESRGKTEESGEDRGDGPDRDPTLSPS AFTLRAIQQAVGSSLQGDLPNDKDGSRCHGL RWRRCRSPRSEPRSQESGGTDATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESDM LELVAEVRIGDRDPIPLPVPSLLPRLAWRTG KT
1289	2639	A	10113	237	438	LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLF DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG
1290	2640	A	10114	367	856	RGAKAKSAVLPPGPPCSSILSPPAPLTPRSPG TEATRPTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGAENGQFPYLGVEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDLAVI KHCKDPLRLKCVKQGESSGLSVLPGGOTAR GAGQ
1291	2641	A	10116	128	591	RTIRETERRSALSCSVLKSEPLPLQOPQASQQR RRRLPGRROVQVQEGGSGSLRAWVLAMASV LGSGRGSGLSSQLCKSKRRRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAAARPPSPGDRARGGATR
1292	2642	A	10121	1	749	QRRFRAGLWGGHOLTDLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAVVEEMKKHETMP MTEKVEELLRVIGFFYEIVEDKKSGRSSDITS

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						LGNVLTSTPNAKTVNGKAESSDSGAEEEEAC
1293	2643	A	10124	2	989	PLMSLVRVVEFVAASSAQKTPSRLENYYMVC KADEKFNQLVHFLRNHKQEKHLVFFRYSSGL CGRGIRDSARMCSTCACVEYYGKALEVLVK GVKIMCIHGKMKYKRNKIFMEFRKLQSGILV CTDVMARGIDIFEVNVVLQYDPPSNASAFVH RCGR TARIGHGGSALVFLPMEESYNFLAIN QKCPLQEMKQPNRTADLLPKLKSMALADRA VFEKGMKAFVSYVQAYAKHECNLFRLKDL DFASLARGFALLRMPKMPFELRGKQFPDFVPV DVNTDTIPFKDKIREKQRQKLEQQRREKTEN EGRRKFIKNKAWSKQKAKKK
1294	2644	A	10129	91	1042	VTMYKDCIESTGDYFLLCDAEGPWGIIIESLA ILGI VVTILLLLAFLFLMRKIQDCSQWNVLPQ LLFLLSVLGLFLAFAFIELNQQTAPVRYFLF GVLFALCFSCLLAHASNLVKLRGCVSFSWT TILCIAIGCSLLQIIATEYVTLMTGRGMMFVN MTPCQLNVDFVLLVYVFLMALTFVSKAT FCGPCENWKQHGRLLFTVLFSLIIVVWISML LRGNPQFORQPQWDDPVVCIALVTNAWVFL LLYIVPELCILYRSCRQECPLQGNACPVTA YQ HSFQVENQELSRDKWKVLLNSDFLSHSGA
1295	2645	A	10133	376	518	RPRVVTTHNSQWCFLPQDHPGWLPGQSGAPG GRGAPROEGPGSSWRQV
1296	2646	A	10135	3	551	EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE NIQDVL SALPNDDYFLLRWLQARSDLOKS EDMLRKHMEFRKQQDLANILAWQPPEVVRLL YNANGICGHDGEGSPVYHIVGSQDPKGLLL SASKQELLRDSFRSCCELLRECELSQKLGRK VEKIIAIFGLEGLRLDLWKPGLLELQ
1297	2647	A	10138	48	407	MVSSCCGVCSDQCGQDLQCETCRPSCE TTCCRTTCRPSCCVSSCRPQCCQSVCCQPT CSRPSCCQTTCCRTTCYRPSCCVSSCRPQCC QPVCQPTCCRPSCECTTCHPXCC
1298	2648	A	10156	94	453	GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG QEMYLRFDQTTRSPYRMSRLARHQLVTKI QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP INTVAVKNDHDFLEKDLGEPLCRRLLNT
1299	2649	A	10161	1	393	PRFSELVDGRGRV SARFGGSPSKAATVRSQPT ASAQLENMEEAPKRVSALALQLEHGSKDIGN VPGNCSENPQNGGTCPVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFFVWEGG VCHHV
1300	2650	A	10162	98	391	AKIASLERIMPANYTCTRPDGDNTDFRYFIYA VITYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIALDLQVLSLPLRIFYLKHDPWF VPV
1301	2651	A	10165	1	7545	PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPEGRGRASSISDLQGGKFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGAQT RWLGKPDPRKRRRGSPQEEGGLRVSAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCVLAPLRPHDPWVA AKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDVVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRSTPV IMEGVQEETDTRDVKRQVERSEICTEPPQKQ

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						KSTLKNEKHLKKDDSETPHLKSLKKKEVKSS KEKPEREKTTPSEDKLSVKHKYKGDQCMHKTG DETELHSESEKGLKVEENIQKQSQQTKLSSDDK TERKSKHRNERKLSVLGKDGPVSEYIKTDE NVRKENNKERRLSAEKTKAEHKSRRSSDSK IQKDSLGSQKHGHTLQRRSESYSEDKCDMDST NMDSNLKPEEVVHKEKRRTKSLLEEKLVLS KSKTQGKQVKVETELQEGATKQATTPKPD KEKNTTEENDSEKQRKSKVEDKPFEEVGVEPV LETASSAHSTQKDSHRAKLPLAKEKYKSD KDSTSTRLERKLSGDKSRSLKHSSDKIKKKD ENKSDDKDGKEVDSSHEKARGNSSLMEKKL SRRLCENRRGSLSQEMAKGEEKLAANTLSTP SGSSLQRPKSGDMTLIPEQEPMEIDSEPGVE NVFEVSKTQDNRNNNSHQDIDSENKQKTS ATVQKDELRTCTADSKATAPAYKPGRGIGV NSNSEKHADHRSTLTCKMHIQSAVSKMNPGE KEPIHRTTEVNIDSETVHRMLLSAPSENDRV QKNLKNATAEEHVAQGDATLEHSTNLDSSPS LSSVTVVPLRESYDPDVIPLFDKRTVLEGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ GKVMPLGSKLTGVTVENENITKEGGLVDMA KKENDLNAEPNLKQTIKATVENGKKDGLAVD HVVGLNTEKYAETVKLKHKRSPPKVKDISID VERRNENSEVDTSAAGSAPSVLHQRNGQTE DVATGPRRAEKTSVATSTEGDKDKDVTLSPVK AGPATITTSSETRQSEVALPCTSIIEADEGLIIGT HSRNNPLHVGAASECTVFAAAEEGGA VVTE GFAESETFLTSTKEGESGECVAESEDRAADL LAVHAVKIEANVNSVVTEKDDAVTSAGSEE KCDGSLSRDSEIVEGTTTFISEVESDGA VTSAG TEIRAGSISSEVDGSGQNM MRMGPKKETEG TVTCTGAEGRSDFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGITEDGEPASCTGSEDSSEGF AIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENNVDMSGTEKGSKDT DICSSAKGIVESSVTSASVSGKDEVTFVPGGCE GPM TSAASDQSDSQLEKVEDTTISTGLVGG YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNLSAGGKNQOK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEFEAPMPASVSGDSSQLTAS RSEKDEKAMISTSIGEEFELPISSATTIKCAES LQPVAAA VEERATGPVLISTADFE GPMPSAPP EAESPLASTSKEEKDECALISTIAEECEASVS GVVVESENERAGTVMEEKDGSIGIISTSSVEDC EGPVSSAVPQEGDPVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLAENNCRCPGPVR GGKEPGFVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKBCPEIGPFAGRGQKESTL HLINAEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGGTAK DSSVSSIRYLA AVNTGAIKADDMPVQGTVA EHSFLPAEQQGSSEDNLTSTTTK CITQESKIA P

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						SHTMPPATYSVALLAPKCEQDLTIKNDYSYGK WTDQASAEKTGDDNSTRKSFPEEGDIMVTYS SEENVCDIGNEESPLNVLGGLKLANLKMEA YVPSEEEKNGEILAPPESLGGKPSGIAELQRE PLLVNESLNVENSFGRTNEEIHSESYNKGESS GRKDNAEAIJSGHSVEADPKVEVEEERHMPKR KRKQHYLSSEDEPDNDPDVLDRIETAQRQC PETEPHATKEENSRLLELPKTSSETNSTTSRV MEEKDEYSSSETTGKPEQNDDDTIKSQE
1302	2652	A	10167	321	842	EPSLFPLRPSPARPPPPAPFPSPPELAGPEPH FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG NSTVAGRGTSVRCLSPSPRPLPLLPLADLLE DGFGEHPFYHCLVAEVPKEHWTPGPNPSPFP EARETKCYVRSSVGCVEPLTTQAEVTENLDR KNSQQVFKLLKKK
1303	2653	A	10171	206	429	NMILLKKRRLLINSLGEGTINGLLDELLETNV LSQEDTEIVKCNENVTVIDKARDLLDSVIRKGA RACEICITYI
1304	2654	A	10184	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSAQNGF YHEAVVLFQTALKLNPDHRLFGNRSFCHER LGQPAWALADAQVALTLRPGWPRGLFRLGK ALMGLQRFREAAAVFQETLRGGSQPDAAREL RSCLLHLTLQGQGGICAPPLSPGALQPLPHA ELAFSGPLSLRCPSTALRSPGLSPLLH
1305	2655	A	10194	2	394	TDLLGRRFRVDGAAMAACEGRRSALGSSQ SDFLTPPVGGAPWAVATTVMYPPPPPPPHR DFISVTLSPGESYDNSKSWRRRSCWRKWKQL SRLQRNMILFLLAFLFCGLLFYINLADHWKG IRNTCT
1306	2656	A	10195	1	410	IPGSTISLEGPLSKWTNVMKGWQYRWFVLDY NAGLLSYTYSKDKMMRGSRGCVLRGAVI GIDDEDDSTFTITVDQKTFHFQARDADEREK WIHALEETILRHTLQLQVRVFTWFPDSSLVGA FFFWLVSGFFFK
1307	2657	A	10205	85	308	QGLPSTMVKLGCSFSFGKPGKDPGDQGAAM DSVPLISPLDISQLQPLPDQVVIKTQTEYQLS SPDQQNYTKSR
1308	2658	A	10214	2	453	ECGGIRQPGPGPPALASAPAATMNRVGGSPS AAANYLLCTNCRKVLKDKRIRVSQPLTRGP SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL DNITQVMSLHTQYLESFLRSQFYMLRMDGPL PLPYRHYIAIMAAARHQCYSYLNIM
1309	2659	A	10233	45	421	RGWPEQSTGRPRDVARQPRCQKEEGRRLRP RALESRTFQGSERSRWGPPESTKENVQCGH RPAPFNSSWLFFHERLQVQNGECPWQVSIQM SRKHLCGGSILHWWVLTAAHCFRRITLLDM AV
1310	2660	A	10241	243	442	AFQLFNAKCESAFLSKRNPLQRNWTVLVYRRK HKKGQSAEIQKKRTRRAFKQRAITGASLADI MAK
1311	2661	A	10261	751	176	LPGADYGGHLSLRLFHLLLSAAWVPDESQ VTLNSAICVLSTVLIMEFPDLGKHCSEKCKQ LDLFPVKCDACKQDFCKDHPYAAHKCPFAF QKD VHVPCPLCNTPVKKGQIPDVVVGDI DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML QMVCAQCHGNFCIQRHRLDHSRCHGSRPTI KAG
1312	2662	A	10270	3	669	STSSDEGSPSASTPMINKTGFKFSAEKPVIEVP SMTILDKKDGEQAKALFEKVRKFRAHVEDSD

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						LIYKLYVVQTVIKTAKFIFILCYTANFVNAISF EHVCKPKVEHLIGYEVFECHTNMAYMLKKL LISYISICVYGFICLYTLFWLFRIPLKEYSFEKV REESSFSIDIPDVKNDFALLHMVDQYDQLYS KRFGVFLSEVSENKLEISLNHEWTFEKL
1313	2663	A	10287	1221	266	GAHRVLSPAQGAQPRLSAASVEVSMVGQR VLLVAFLLSGVLLSEAAKILTISTLGGSHYLL LDRVSQLQEHGHNVTMLHQS GKFLIPDIKEE EKSYQVIRWFSPEDHQKRIKKHFD SYIETALD GRKESEALVKLMEIFGTQCSYLLSRKDIMDSL KNENYDLVFVEAFDFCSFLIAEKL VKPFVAIL PTTFGSLDFGLPSPLSYVPVPFSLTLDHMDFW GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF PEGSRPVLSHLLKLAELWFVNSDCAFDFARPL LPNTVYIGGLMEKPIKVPQVSEPSAFSLGFT
1314	2664	A	10288	536	1890	NVQLAKFSSITLVFFSCDADPSALAKYVVAL VKKDKSEKELKALCIDQLDVFLQKETQIFVEK LFDVNTKSYLPPPEQSSGSLKVEFFFPQEK DIKKEEITKEEREKKFSRRLNHSPPQSSRYR ENRSRDERKKDDRSRKRDYDRNPPRRDSYRD RYNRRRGRSRSYSRSRSRSWSKERLREDRD RSRTRSRSTRSRERDLVKPKYDLDRDPLEN NYTPVSSVPSISSGHYPVPTLSSTITVIAPTHHG NNTTESWSEFHEDQVDHNSYVRPMPKKRC RDYDEKGFCMRGDMCFDHDGSDPVVVEDVN LPGMQPFPAPPPVVEGPPPPGLPPPPILTPPV NLRPPVFPFGPLPPSLPPVTGPPPLPLQPSG MDAPPNSATSSVPTVTTGIHHQPPAPP SLFT ADTYD TDGYNPEAPSIITNSRPMYRHRVHPR AKLG
1315	2665	A	10293	447	1331	SHPLLSCPEKVS AKLRAAAEAAAEEERRTRGA GSRGICAGLRSVAPGPEPLKQEEGRREW GSSI GTPSPCGSAQAAAAAAEEATEKIPALRPALL WALLALWLCCATPAHALQCRDGYEPCVNEG MCVTYHNGTGYCKCEGFLGEYCQHRDPCE KNRCQNGGTCVAQAMLGKATCR CASGFTGE DCQYSTSHPCFVSRPCLNGGTCHMLSRDTYE CTCQVGFTGRNPKCPGGLNLYQFNGIIVVYS GGSVPPSGTKTSKPAEHNAMGTGSKNFASOT LWVMVSGATSTSTSL
1316	2666	A	10294	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTG YSLVQENGQRKYGGPPPGWDAAPPERGCEIFI GKLPRDLFEDELPLCEKJGKIYEMRMMMDF NGNNRGYAFVTFSENKVEAKNAIKQLN NYEIR NGRL LGVCASVDNCR LFVGGIPKTKK
1317	2667	A	10301	158	1956	LLKSCGVLLSGVCIPCEGKPTVLVIQTA VPQ DRPTKSSMRSAAKPWNPAIRAGGHGPD RVRP LPAASSGMKSSKSTSLAFESRLSRLKRASSE DTLNKPGSTAASGVVRLKKTATAGAISELTES RLRSGTGAFITTKRTGIPAPREFSVTVSRERSV PRGPSNPRKSVSSPTSSNTPTTKHLRTPSTKP KQENEGGEKAALLESQVRELLAEAKAKDSEIN RLRSELKKYKEKRTLNAEGTDALGPNVDGTS VSPGDTEPMIRALEEKKNKFQKELSDLEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ ESSFGSPTGNQLSSDIDEYKKNHGNALRTSG SSSDVTKASLSPDASDFEHITAETPSRPLSSTS NFFKSSKCSTAGSSPNSVSELSLASLTEKIQKM EENHHSTAEEELQATLQELSDQQQM VQELTAE

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						NEKL VDEK TILETSFHQHRERAEQLSQENEKL MNLLQERVKN EPTTQEGKIELEQKCTGILE QGRFEREKL LNIQQQLTCSLRKVEEENQ GAL EMIKRLKEENEKLNEFLELERHNNMMAKTL EECRVTLBGLKMEGSLKSHLQG
1318	2668	A	10303	333	879	GECFIMAAVVQNDLVFEFASNVMEDEQL GDPALFFAVIVEHVPGADILNSYAGLACVEEP NDMITESSLDVAEEIIDDDDDITLTVEASCH DGDETIETIEAAEALLNMDSPGPMLEKRRIN NIFSSPEDDMVVAPVTHVSVTLDGPEVMEQT QVQEKYADSPGASSPEQPKRKKK
1319	2669	A	10322	169	654	MEVRMSGSVAVTRAIVPGLLLLIATLSL LIGAKSLPASVVLEAFSGTCQSADCTIVLDAR LPRTLAGLLAGGALGLAGALMQTLTRNPLAD PGLLGVNAGASFAIVLGAALFGYSSAQEQLA MAFAGALVASLIVAFSGSQGGGQLSPVRLTL AGVXL
1320	2670	A	10323	441	2	KMNQVAVVIGGGQTLGAFLCHGLAAEGYRV AVVDIQSDKAANVAQEINA EYGESMAYGFG ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI AKAAFISDFQLGDFDRSLQVNLVGYFLCARE FSRLMIRDIGIQGRIIQINSKSD
1321	2671	A	10332	1	453	RHRTAGPGSTISSRTDSASAPAARAMPC EYTY AKLTSDCSRPSLQWYTRAQSKMRRPRLLKLD ILKCTLVFGVRILYLKLN YTEECMDKNMH YVDPDHVKRAQKYAQQVLQKESPPKFAKTS MALLFEHRYSDLLPFVQKAPT DSEA
1322	2672	A	10333	25	423	EPSNGPVVYSALGNEDDEILLGKDIIGTFAAS ERKMRAHQVLTFLLLFVITSGASENASTSRGC GLDI.LPQNVYI.CDI.DAIWGVVVEAVAGAGA LITLLMLILLGRLPFKEKEKKSPAVLHFLFL LGTILG
1323	2673	A	10334	52	426	SSLGNEDDEILSLAKDITGMFVASHRKRAH QVLTFLLLFVITSVASENASTSRGCLDLLPQ YVSLCDLDAIWGVVVEAAAGAGALITLLMLI LLVRLPFFKEKEKKSPVGLHFLFLGLTLP
1324	2674	A	10336	1	932	ERLCFPCMQSKTYSYMSPNKCSGMRFP LQEE NSVTHHEVKCQKPLAGIYRKREEKR NAGN AVRSAMKSEEQKIKDARKGPLVPFPNQKSEA AEPKTPPSSCDSTNAIAKQALKKPIKGKQA PRKKAQGKTQQNRKLTDFYPVRRSSRKSKAE LQSEERKRIDELIESGKEEGMKIDLIDGKGRG VIATKQFSRGDFVVEYHGDLIEITDAKKREAL YAQDPSTGCYMYVFQYLSKTYCVDATRET N RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS RDIAAGEBLLYDYGDRSKASIEAHPWLKH
1325	2675	A	10338	3	870	PGSTISCSSELKGTQCRATAGSRGRPPMTCWL RGVTATFGRP AEWP GYL SHLCGRSAAMD LG PMRKS YRGDREA FEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRK GKELDSNPFASL VFYWEPLNRQVRVEGPVKLP EEEAE CYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVL YPQVMEFWQG QTNRLHDIRVFRRLPTGDSPLGPMTHRGEE DWLYERLAP
1326	2676	A	10344	2	984	ARAAAHCGICRLVRWWRKRSSVMGIQTSPV LLASLGVLVTLLGLAVGSYL VRRSRRPQVT LLDPNEKYLLRLLDKTVSHNTKRFRFALPTA

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						HHTLGLPVGKHIYLSRIDGSLVIRPYTPVTSDEQGYVDLVIKVVYLGKGVHPKFPEGGKMSQYLDLSLKVGDVVEFRGPSOLLTYTGKGFNIQPNKKSPPPEPRVAKKLGMIAGGTGITPMLQLIRAILKVPEDPTQCFLLFANQTEKDILREDLEELQARYPNRFKLWFTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY
1327	2677	A	10345	1	968	LQSAGEGVTHVLILLESARPVAAVTQVQRRRYHRLSDMSMLAERRRKQKWA VDPONTAW SNDDSKFGQRMLEKMGWSKGLGAQEQGATDHIK VQVKNHLLGLGATTNEDNWIAHQDDFNQLLAELNTCHGQETDSSDKKEKKSFSLEEKSKISKNRVHYMKFTKGKDLSSRSKTDLDICFGKRQSKKTPEGDASPSTPEENETTTTSAF TIQEFYAKRMAALKNKPVVPVPGSDISETQVE RKRGGKRNKEATGKDVESYLOPKAKRHTEG KPERAEAEQERVAKKKSAPAEELRGPCWDQSSKASAQDAGDHVQPA
1328	2678	A	10346	173	439	GSAAMKVKIKCWNGVATWLWVANDENCGICRMAFNGCCPDCKVPGDDCPLVWGQCSHCFHMHCLKWLHAAQVQVQHCPMCRQEWKFKE
1329	2679	A	10351	3	964	QMEPGNDTQISEFLLGFSQEPGLQPFGLFGLSMYLVTVLGNLLIILATISDSHLHTPMYFFLSNLSFADICVTSTTIPKMLMNIQTQNKVITYIACL MQMYFFILFAGFENFLSVMAYDRFVAICHP LHYMVTMNPFLCGLLVLASWTMSALYSLQLI LMVVRLSFTALEIPHFCELNQVIQLACSDSFLNHMVTYFTVALLGGGPTGILYSYSKISSIH AISSAQGKYKAFSTCASHLSVVSIFYGAILGV YLSSAATRNSHSSATASVMYTVVTPMLNPFYSLRNKDIKRALGIHLLWGTMKGOFFKKCP
1330	2680	A	10352	34	2573	IPFLKSCCCCLFDFFPPPLDQVQEECEVERVTEHGTPKPFKFDVSAFGEQSSEDEQFENDLETDPPNWQQLYSREVLGLKPCIKRQEVINELFYTERAHVRTLKVLDQVVFYQVRSREGILSPSELRKIFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSGPGEELKHAAATFCSNQPFALMIKSRQKKDSRFQTFVQDAESNPLCRR LQLKDIIPTQMQRLLTKYPLLLDNIATYTEWPTEREKVKAADHCRQILNYVNQAVKEAENKQ RLEDYQRRLDTSSLKLEYPNVEELRNLDLTKRKMIHEGPLVWKVNRDKTIDL YTLLEDILVLLQKQDDRLVLRCHSKLASTADSKHTFSPVILSTVLVRQVATDNKALFVISMSDNGAQIYE LVAQTVSEKTVWQDLICRMAASVKEQSTKPIPLPQSTPGEEDNDEEDPSKLKEEQHCISVTGLQSPDRDLGLESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLEKVGEDYQIAIPDHLPVSEERWALDALRNLGLLKQLLVQQLGLTEKSVQEDWQHFPYRTASQGPQTDSVIQNSENIKAYHSGEGHMPFRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDHMIMTPEMPTMEFEGGLDDSGEHFFDAREAHSDENPSEGDQAVNKEEKDVNLRISGNLYLDGYDPVQESSTDEEVASSLTLPMTGIPAVESTHQQHSFQNTSDGSAISFTPEFLVQQRWGAMEYSCFEIQSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTLCLQRLAGSALTDKHSKDS

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1331	2681	A	10353	1	2100	AVEFAEGALTMAPWPELGDAQPNPDKYLEG AAGQOPTAPDKSKETNKTDNTEAPVTKIELLP SYSTATLIDEPTVEDDPWNLPTLQDSGKWSE RDTKGKILCFQIGRLILLGFLYFFVCSLDIL SSAFQLVGGKMAGQFFSNSSIMSNPLGLVIG VLVTVLVQSSSTSTSIVVSMVSSSLTVRAAP IMGANIGTSITNTIVALMQVGDREFFRAFA GATVHDFNWL SVL VLLPVEVATHYLEITQL IVESFHFKNGEDAPDLLKVITKPFKLIVQLDK KVISQIAMNDEKAKNKS LVKIWKCTFTNKQT INVTPSTANCTSPSLCWTGIGNWTKMKNVT YKENIAKQCHIFVNFHLPDLAVGTILLLSLLV LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP PPFAWLTGYLAILVGAGMTFIVQSSSVFTSAL TPLIGIGVITIERAYPLTLGSNIGTTTTAILAAL ASPGNALRSSQLALCHFFFNISGILLWYPIPF RLPIRMAKGLGNISAKYRWFVFFLIFFFLIP LTVFGLSLAGWRVLVGVGVVVFHILVLCRL LLQSRCPRVLPKKLQNWNLPLWMLSLKPW DAVVSKFTGCFQMRCCCCRVCCRAACLLC GCPKCCRCCKCEDLEEAQEGQDVPVKAPET FDNITISREAQGEVPASDSKTECTAL
1332	2682	A	10354	30	1377	SQQGSQPHRQGPSSLTAPHSLDLPALPPGPR GSQGLRRVLVPM SVKPSWGPSEGVTA VP TSDLGEIHNWTELLDFNHTLSECHVELSQST KRVVLFALYLAMFVVLGVENLLVICVNW RG SGRAGLMNLYILNMAIADLGIVLSLPVWMLE VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF LVCLSVDRYVTLTSASPSWQRYQHRVRRAM CAGIWVLSAIIPLPEVVHIQLVEGPEPMCLFM APFETYSTWALAVASTITLGFLLPFPLTVFN VLTACRLRQPGQPKSRRHCLLLCAYVAVFV MCWLPYHVITLLLT LHGT HISHCHLVHLLY FFYDVIDCFM LHCVINPILYNFLSPHFRGRL NAVVHYLPKDQTKAGTCASSSSCSTQHSIIT KGDSQPAAPAAAPHEPSLSFQAHHLLPNTSPISP TQPLTPS
1333	2683	A	10358	2	884	AAGAGADGREPASERASRAEPPAVAMGQND LMGTAEADFADQLRVTKQYLPHVARCLIST FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA SSFVFLNLLGQLTGCVLVLSRNFVQYACGLF GHALQTIAYSILWDLKFLMRNLALGGGLLL LAESRSEKSMFAGVPTMRESSPKQYMQLG RVLLVLMFMTLLHFDASFFSIVQNVGTALMI LVAIGFKTKLAALTLVWVLFANVYFNAFWT IPVYKPMHDFLKYDFFTQMSVIGGLLVVAL GPGGVSMDEKKKEW
1334	2684	A	10367	59	1562	QAWSLQVALSPFFFPASPSNSFAAAVPQLLFP ELPLPHVPGQESAKRRSARRFLIMSELTKELM ELVWGTSKSSPGLSDTIFCRWQTGGVFSESEGS ALEQFEGGPCAVIAPVQAFLKLLFSSEKSS WRDCSQEEQKELLCHTLCDILESACCDHSGS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEELGFERFHAIQKRSFRSLPELKDAV LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASEPLDPVYGHGSQSLINLLTGHA VSN VWDGDRECSGMKLLGIHQAAVGFLLTMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA KDMALVAPEAPSEQARRVFQTYDPEDNGFFP DSLLEDVMKALDLVSDPEYINLMKNKLDPEG

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						LGIIILGPFLLQEFFPDQSSGPESFTVYHYNGL KQSNYNEKVMYVEGTAVVMGFEDPMLQTD DTPIKRCLOQTKWPYIELLWTTDRSPSLN
1335	2685	A	10375	82	2929	TRTKRRLGREKAMASPPRGWCGCELLLPFML LGTLCEPGSGQIRYSMEELDKGSFVGNIAKD LGLEPQELAERGVRIVSRGRTQLFALNPRSGS LVTAGRIDREELCAQSPLCVVNFNILVENKM KIYGVVEIINDINDNFRFRDEELKVKNENA AAGTRLVLPFARDADVGVNSLSYQLSSNLH FSLDVVSGTDGQKYPELVLEQPLDREKETVH DLLLTALDGGDPVLSGTTTHIRVTVLDANDNA PLFTPSEYSVSPENIPVGTLLMLTATDPDE GINGKLTYSFRNEEEKISETFLDNLGEISTL QSLDYEESRFYLMEVVAQDGGALVASAKVV VTVDVNDNAPEVILTSLTSSISEDCLPGTVIA LFSVHDGDSGENGELACISIPRNLFPKLEKSD NYYHLLTTRDLREETS DYNITLTVMDHGTP PLSTESHIPLKVADVNDNPPNFPQASYSTSVT ENNPRGVSIFSVTAHDPDSGDNARVTYSLAE DTFQGAFLSSYVSINSDTGVLYALRSFDYEQ RDLQLWVTASDSGNPLSSNVSLSLFVLDQN DNTPEILYPALPTDGTGVELAPRSAEPGYLV TKVVAVDKDSGQNAWLSYRLLKASEPGLFA VGLHTGEVRTARALLDRDALKQSLVVAVED HGQPLSATFTVTAVADRIDLADLGSIKTP IDPEDLDLTLVAVAAVSCVFLAFVTVLLV LRLRRWHKSRLQAEGRLAGVPASHFVGV DGVRAFLQTYSHVSLTADSRKSHLIFQPNY ADTLLSEESCEKSEPLMSDKVDANKERRV QQAPPNTDWRFSQAQRPGTSGSQNGDDTGT WPNNQFDTEMLQAMILASASEADGSSTLGG GAGTMGLSARYGPQFTLQHVLLQELGSDYR QNVYIPGSNAILTNAAGKRDGKAPAGGN KKKSGKKEKK
1336	2686	A	10379	1	557	RPRRRQPSFSCRVLVLEDPFCFRFTNSMNQEK LAKLQAQVRIGGKGTAARRKKVVRHTATAD DKKLQSSLKLA VNNIAGIEEVNMIKDDGTVI HFNNPKVQASLSANTFAITGHAEAKPITEMLP GILSQLGADSLTSLRKLAEQFPRQVLDSKAPK PEDIDEEDDDVPDLVENFDEASKNEAN
1337	2687	A	10380	1	1263	IPGSTISWSPAAARGLSVCRCRLHPASAMDL FGDLPEPERSPRPAAGKEAQKGPLLFDLPPA SSTDGSGGGPLLFDLPPASSGDSGLATSIQ MVKTEGKGAKRKTSEEKNGSEELVEKKVC KASSVIFGLKGYVAERKGEREEMQDAHVILN DITEECRPSSLITRVSYFAVFDGHGGIRASKF AAQNLHQNLIRKFPKGDVISVEKTVKRCLLD TFKHTDEEFLKQASSQKPAWKDGSTATCVLA VDNLIYANLGDRAILCRYNEESQKHAALS SKEHNPTQYEERMRIQKAGGNVRDGRVLGV LEVSRSIGDQYKRCGVTSVPDIRRCQLTPND RFILLACDGLFKVFTPEEA VNFILSCEDEKIQ TREGKSAADARYEAACNRLANKAVQRGSAD NVTVMVVRIGH
1338	2688	A	10385	3	589	GPSQSMAGELEGKPLSGLLNALAQDTFHG YPGITEELLRSQLYPEVPPEEFRPFLAKMRGIL KSIASADMDFNQLEAFLTAQTKKQGITSQDQ AAVISKFWSHKT KIRESLMNQSRWNSGLRG LSWRVDGKSQSRHSAQIHTPVAIIELELGKYG QESEFLCLEFDEVKVNQILKTLSEVEESISTLIS

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1339	2689	A	10386	50	390	QPN LGAMAKHHPLIFCRKQAGVAIGRLCEKCDG KCVICDSYVRPCTLVRICDECNYGSYQGRCVI CGOPGVSDAYYCKECTIQEKDRDGCCKFJVNL GSSKTDLFYERKKYGFKKR
1340	2690	A	10388	113	3472	SQLRKGASATHSSPSRTDCLAQMMDIYVCLK RPSWMVDNKRMRASNFQWLLSTFILLYLM NQVNSQKKGAPHDLKCVTNLQVWNCWSK APSGTGRGTDYEVCIENRSRSCYOLEKTSIKIP ALSHGDYEITINSLHDFGSSTSFTLNEQNVSL IPDTPEILNLSADFSTSLYLKWNDRGSVFPHR SNVIWEIKVLKESMELVKLVTHNTTLNGKD TLHHWSWASDMPLCAIHFVEIRCYNLHFS GLEEWSWSPVKNISWIPDSQTKVFPQDKVIL VGSDITFCVSEQEVLALIGHTNCPLIHLDE NVAIKIRNISVSASSGTNVVFTEDNIFGTIVF AGYPPDTPQQLNCETHDLKEIICSWNPGRVTA LVGPRATSYTLVESFGKYVRLKRAEAPTNES YQLLFQMLPNQEIYNFTLNAHNPGRSQSTIL VNITEKVYPHTPTSFVKVDINSTAVKLSWHLF GNFAKINFLCEIEIKKSNSVQEQNRVNTIKGVE NSSYLVALDKLNPYTLTYFRIRCSTETFWKW SKWSNKKQHLTTEASPSKGPDTWREWSDDG KNLIYWKPLPINEANGKILSYNVSCSDEETQ SLSEIPDPQHKAEIRLDKNDYIISVVAKNVGS SPPSKIASMEIPNDLKEQVVGMGKILLTW HYDPNMTCDYVIKWCNSSRSEPCLMDWRKV PSNSTETVIESDEFRPGIRYNFFLYGCRNQGY QLLRSMIGYIEELAPIVAPNFTVEDTSADSLV KWEDIPVEELRGFLRGYLFYFGKGERDTSKM RVLESGRSDIKVKNITDISQKTLRIADLQGKTS YHLVLRAYTDGGVGPEKSMYVVTKENS VGL IIAILPVAVAVIVGVVTSILCYRKREWIETFY PDIPNPENCKALQFQKSVCEGSSALKTLEMNP CTPNNVLEVLETRSAFPKIEDTEIVSPVAERPEN RSDAKPENHVVESYCPPIIEEIPNPAADETGG TAQVIYIDVQSMYQPAKPEEEQENDPVGGA GYKPMHLPINSTVEDIAEEDLDKTAGYRP QANVNTWNLVSPDSPRSIDSNSEIVSFGSPCSI NSRQFLIPPKDEDSPKSNGGWSFTNFFQNKPN D
1341	2691	A	10392	1	5057	MLPPKHLSATKPKKSWAPNLYELDSDLTKEP DVIIGEGPTDSEFFHQFRNLIVFVGPRTKL IKLRNLCLDWLQPETRTKEEIELL VLEQYLTH PEKLKPWVRAKFPENCEKLVTLLNYKEMY QPEGESLHGVLVVSAGLRCPGLSASTLLTW SGLDNSLSWAAVGMSCVLWDIELHHDFLGV ATKSVSTHAQGDAAQGLGGTIVRMWARDSEN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICBD ESSHG VIMEKFIKDVSRSSKSGRAESSDRSQ RFPMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRRYHFDTDGK GSIHDQKGCPRKKPFECGSEMRAKMSVSSL SLSSPSFTESQPIDFGAMPYVCDECGRSFVSIS EFVEHQMHNTRENLYEYGESFIHSVAVSEVQK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RKLQGGKLPQLQGVETELCYNVNWTAEALPSA EETKKLMWLFPGCTLLDDVARESWLLPGSN DLLLEVGPRLNFSPTSTNIVSVCRATGLGPV DRVETTRRYRLSFAHPPSAEVEAIALATLHDR MTEQHFPHPQSFSPESMPEPLNGPINLGEGR LALEKANQELGLALDSWDLDFYTKRFQELQR NPSTVEAFDLAQSNSEHSRHWFFKGQLHVDG QKLVHSLFESIMSTQESSNPNNVLKFCNSSA IQGKEVRFLRPEDPTRPSRFQQQGLRHVVFT AETHNFTGVCPSFGATTGTGGRIRDVQCTG RGAHVVAGTAGYCFGNLHIPGYNLPWEDLSF QYPGNFARPLEVAIEASNGASDYGNKFGEV LAGFARSLGLQLPDGQRREWIKPIMFSGGGS MEADHISKEAPEPGMEVVKVGGPVYRIGVGG GAASSVQVQGDNTSDDLDFGAVQRGDFEMEQ KMNRRVIRACVFAKGNPICSLLHDQAGGNG NVLKELSDPAGAIYTSRFLGDPTLNALAIW GAELYQESNALLRSPNRDFLTHVSARERCPA CFVGITITGDRRIVLVDRECPVRRNGQGDAP PTPPPTPVDLEWVLGKMPRKEFFLQRKPP MLOPLALPFGLSVHQALERVLRPAVASKRY LTNKVDRSVGGGLVAQQQCVGPLQTPADVA VVALSHEELIGAATALGEQPVKSLDDPKVAA RLAVAEALTNLFALVTDLRDVKCSGNWM WAAKLPGEGAALADACEAMVAVMAALGVA VDGGKDSLMAARVGTETVRAPGSLVISAYA VCPDITATVTPDLKHPEGRGHLLYVALSPGQ HRLGGTALAQCFSQGEHPDLDLPENLVRA FSITQGLLKDRLLCSGHDVSDGGLVTCLEM AFAGNCGQLQVDVPVPRVDVLSVFAEEPGLV LEVQEPDLAQVLKRYRDAGLHCELGHTGE AGPHAMVRVSVNGAVVLEEPVGLRALWEE TSFQDLRLQAEPRCAEEERGLRERMGPSYC LPPTFPKASVPREPGGSPFRVAILREEGSNGDR EMADAFHLAGFEVVDVTMQDLCGAGLDT FRGVAFVGGFSYADVLGSAKGWAAAVTFHP RAGAELERRFRKRPDTFSLGVCNGCQLLALLG WVGGDFNEDAAEMGPDSPARPGLLLRHNL SGRYESRWASVRVGPALMLRGMEGAVLP VWSAHGEGYVAFSSPELQAQIEARGLAPLHW ADDDGNPTEQYPLNPNPSPGGVAGICSCDGR HLAVMPPHERAVRPWQWAWRPPPDITLTS PWLQLFINARNWTLEGSC
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1346	2696	A	10398	1	718	DDFVRCGPQSAAMGASARLLRAVIMGAPGS GKGTVSSRITTHFELKHLSSGDLRLDNLMTGRT EIGVLAKAFIDQGLIPDDVMTRLALHELKNL TQYSWLLDGFPRTLPAEALDRAYQIDTVNL NVPFEVIKQRLTARWIHPASGRVYVNIENPPK TVGIDDLTGEPLIQREDDKPEVTKRLKAYED QTKPVLEYQKKGVLTFSGTETNKIWPYVY AFLQTKVPQRSQKASVTP
1347	2697	A	10402	153	1969	KHRQENNALDMAPEIHMTPMCLIENTNGEL VANPEALKILSAITQPVVVVAIVGLYRTGKSY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LMNKLAKGNKGFSLGSTVKSHTKGIWMWCV PHPKKPEHTLVLLDTEGLGDVKKGDNDNS WFTLAVLLSSTLVYNSMGTTNQAMDQLYY VTELTHIRSKSSPDENENEDSADFVSFFPDFV WTLRDFSLDLEADGOPLTPDEYLEYSLKLTQ GTSQDKNFNLPRLCIRKFFPKKKCFVFDLP HRRKLAQLEKLODEELDPEFVQQVADFCYI FSNSKTKTLGGIKVNGPRLESVLTYINAISR GDLPCMENAVLALAQIENSAVQKALAHYD QQMGQKVQLPAETLQELDLHRVSEARETEV YMKNSFKDVDHLFQKKLAAQLDKKRD DFC QNQEASSDRCSALLQVIFSPLEEEVKAGIYSK PGGYCLFIQKLQDLEKKYEEPRKGIQAEEL QTYLKSKEVTDAILQTDQILTEKEKEIEVEC VKAESAQASAKMVEEMQIKYQQMMEEKEKS YQEHVKQLTEKMERERAQLEEQEKTLTSKL QEQRVLKERCQGESTQLQNEIQKLQKTLKK KTKRYMSHKLI
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1349	2699	A	10409	59	1184	LRRNCSALGGLFQTHISDMKGSYPVWEDFINK AGKLQSQLRTTVVAAAFLDAFQKVADMAT NTRGGTREIGSALTRCMRHSIEAKLRQFSS ALIDCLINPLQEQMEEWKKVANQLDKDHAK EYKKARQEIKKSSDTLKLQKAKKGRGDIQ PQLDSALQDVNDKYLLLEETEKQAVRKALIE ERGRFCTFISMLRPVIEEISMLGEITHLQITSE DLKSLTMDPHKLPSSSEQVILD LKGS DYSWS YQTPPSPSTTMSRKSSVCSSLNSVNSSDSRSS GSHSHSPSSHYRYRSSNLAQQAPVRLSSVSSH DSGFISQDAFQSKSPSPMPPEAPNQRREKRE PDPNGGGPTTASGPPAAAEAAQRPRSM
1350	2700	A	10410	511	958	AGRGGPGKPVSWSSGFGSPGQTQRRSWVKST RGHSSLLPPSQDFVAGLSVILRGTVDDRLNW AFNLVDLNKDGCTKEEMLDIMKSIYDMMG KYTYPALREEAPREHVESFFQKMDRNKDG VTIEEFIESCQKDENIMRSMQLFDNVI

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

SEQUENCE LISTING

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Tang, Y, Tom et al

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<210> 8
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 8
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 ctccattagg tatgtgctct tttaattatta ggcgtttatg atctgactca tgtatgagag 240
 cagccctaaa tgataggggt ttatatcagg tactaattct tgacggactt gttcagtgtc 300
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<210> 9

<211> 366
 <212> DNA
 <213> Homo sapiens

<400> 9
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 ttaccc 366

<210> 10
 <211> 1249
 <212> DNA
 <213> Homo sapiens

<400> 10
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<210> 11
 <211> 617
 <212> DNA
 <213> Homo sapiens

<400> 11
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 accagatccc taagaagtgt gctgacatct ttaacgcccc cagtgtatgat gaagagtttg 180
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 aagagctaag aagaattttt atagaggaca ctgactcaga gactgaggat tttgcaggat 360
 ttacgcagag tgatctgaat ggaagagacta acccagaagt aatggctcgtg gagtcagatt 420
 tgagtgtatga tggcaaagca tctttggtga gcgagggaaga ggaagatgaa gaagaagata 480
 aggctacccc tagaagaagc aggtctagaa gaagtagtat tggctcttga gtagcctttc 540
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617

<210> 12
 <211> 469
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1) ... (469)
 <223> n = a,t,c or g

<400> 12
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 ttcactttctc tcttttagat gggaaatgtgg gggaaacctga catgtctgag gggttttgcc 180
 caaatcacaa ggcagccatg gttttattcc ttgacagggt ctatgggatt gaggttcaag 240
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<210> 13
 <211> 598
 <212> DNA
 <213> Homo sapiens

<400> 13
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 taaaattaaa agcaaatag caagatagaa ataatacaaaa gttatagcaa cttagggaca 120
 agagtactta cttttttggg agtccctaaa acttggcaaaa ttttaaagat ttcacgacc 180
 tcacttgtcc ctgggaaaaag tggccttaac atatagagtt cagccatgat acttccaaca 240
 gccacacat caatgggaga actataaaact gaagatctca gtaaaacttc aggggcacga 300
 tacctatgaa aatagagaac aaaagaggta attttgattg caatttcaa ggtggatggg 360
 cagtagcatt ctacgctgtg tggcatgca tttccatcaa ggaacaggta ttcagaccct 420
 gttccatctg tgtgtcaggc atttgtacaa tgttctgggg ataataggac acaacacatg 480
 ttcctgatc acagacaatg agtggggctg gagacaaatg tctatgaaat gtccatcaag 540
 cctaagacag gaactcaact gaatagatat ggaaataagt gccatctgat atattaag 598

<210> 14
 <211> 576
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (576)
 <223> n = a,t,c or g

<400> 14
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 gggagacatg aagaccgttt cataactgaa gtggagaatg atattgggac cacagaactg 180
 caagtttgga tacaagatt gttcacttgt gagttcagaa accccatctt gttgggtgca 240
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atggcagcat	agcaggcata	ggtgatggca	gagagcaagc	agccattggt	gccccaaaga	360
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ggaaattctg	cagcatcttg	ggcagtgact	gaggagtaac	atatatctag	gaagaaaaaa	480
tgtccaagga	agaattacat	ggnggtacgg	aggcaagaat	cagcattgat	taccaacagc	540
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<210> 15
 <211> 449
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(449)
 <223> n = a,t,c or g

<400> 15						
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attttatcat	ttgctttact	gggtgttaag	tttcaatggg	ggtaaatggt	actcttcttt	240
tttaaatatt	tttggtata	ttttttcatg	tattctcgca	gataagcttc	agttatgttt	300
tggtcacatt	ccaaaagaaa	ttctattgcc	atttttgttg	gaattgcttt	aacaatatag	360
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tggttcacg	attctgaaga	ccatcttcn				449

<210> 16
 <211> 486
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(486)
 <223> n = a,t,c or g

<400> 16						
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tacagaggaa	gacagaggcg	gggatgactg	tggtgtgtot	gtctggacca	aacagcggaa	180
caacagctgt	gtgaaaagca	aggatgtctt	ctccaagcct	gttaacatat	tttgggcatt	240
agaagaatcc	gtgcttgggg	tgaaggcgag	gcagccaaag	cctttctttg	ctgccggaaa	300
tacatttgag	atgacttgca	aagtatcttc	caagaatatt	aagtcgccac	gctactctgt	360
tctcatcatg	gctgagaagc	ctgtcggcga	cctctccagt	cccaatgaaa	cgaagtacat	420
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ggtttt						486

<210> 17
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 17						
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atgaataaga	aaaaggacaa	acaatccaat	taaactggac	aaaaaatttg	aacactttaa	120

aaatgaagat	atatgaataa	ccagtaagca	cacaaaaatg	tgggtatcat	cattagccat	180
gaaagaaatg	ctcactaaaa	ctacaatgga	atctctactt	catgcctagt	agaatggcga	240
aaattaacgc	agcaacaaac	tcaaatacta	acaagaactg	gggcagaaca	agaccctctc	300
gtatcttgtt	agtggagtat	aaaatgaccc	aacctttc			338

<210> 18
 <211> 903
 <212> DNA
 <213> Homo sapiens

<400> 18						
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cccgggagggt	ggagcttgca	gtgagctgag	attgcgccac	tgccctccag	cctggacaac	120
agagtggaggc	tccgtcttaa	aggaaaaaaa	tttctggaat	gatgtccaat	aaatcagaga	180
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catttatatt	gtcatcatat	gcatataaca	ttttaacatt	taaaaaactag	tttaaacaga	300
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ttgtcccttg	aagaaggaag	cagttctctt	tttctttttt	cccttttcca	ttataggatc	480
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tctactaaaa	atataaaaat	taccggggca	tggtggcggg	tgccgttaat	cccaactact	900
agg						903

<210> 19
 <211> 445
 <212> DNA
 <213> Homo sapiens

<400> 19						
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gctgtggaaa	cgtatgttca	catacattgc	tcttgatat	gcagattacg	accgctcctg	120
tgtagagcag	ttagggata	tctttcaaaa	ttaaaaaatg	cagagttaag	ttttgatcca	180
ggagtctcac	tcctgagaat	ttatgctata	gatatgccta	caagcatttg	agatgaaaaa	240
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gcagtgatcc	aagcattcat	ctttgggact	gggttaaggaa	actatgatgc	tttcacagaa	360
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atgtccaaaa	tatactgtta	aagtt				445

<210> 20
 <211> 1370
 <212> DNA
 <213> Homo sapiens

<400> 20						
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<210> 21

<211> 1812

<212> DNA

<213> Homo sapiens

<400> 21

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<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<400> 22

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gctag						1085

<210> 23

<211> 397

<212> DNA

<213> Homo sapiens

<400> 23

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tcattttact	ootctctg	attctctccc	tgcattttct	cttttctctc	tttctttttt	180
tcattctttt	tttctcatta	tttaagggtc	tttgaaaata	ttttttcttt	ggatgcaata	240
ttctgtacgt	tttttctg	actattaatt	attgcttcac	ttacagtgat	tcctgcaaac	300
tttcaatctt	ctctaagggt	gggctttgtt	tatttatttt	atttgcatct	tcaggtgac	360
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<210> 24

<211> 429

<212> DNA

<213> Homo sapiens

<400> 24

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tcccctggac	gacagcatgc	cctgggaggg	caggaccacg	gccagtggt	cccttcacag	300
gaagcgacac	ctggcacgga	cactgctggt	gagtaggggt	agagggtccc	agcatcaaga	360
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aatgaaaca						429

<210> 25

<211> 492

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(492)

<223> n = a,t,c or g

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cacttcgatt ttttttgata tttgggggta attttgtgtg aggccttagg ttgagggttaa      180
ttttttgtc tgtgaataac cagttgggtc agtgccattt gttgcaaagt ctattcttca      240
ttgaattact ttacaaaaa tccactttgg ggtatttgtg ttgatctctt tctgggtttt      300
cggttctctt ctattgatct gagtgtctat tcttccatag ataccctgtc tcaagtattg      360
tgggtgatcaa atagtaagtt taatatcagg tagcgcgagc tctcttactt tgttcttcta      420
gtttctttgc cttatcatat atattaggat aagntgtcta tatctacaaa aaaatctggg      480
tgggattttg ag                                     492

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<210> 26

<211> 388

<212> DNA

<213> Homo sapiens

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<400> 26
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aaaaacttca tataaactta agacttaagt ttgttgatat ccacaaaatt tgctgggatt      180
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tcatcagact ttcttcatat agatcttata catattgtta gatttgtgcc tgagaatata      360
aatgggtttg tgtttttcac ttcaaatg                                     388

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<210> 27

<211> 380

<212> DNA

<213> Homo sapiens

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<400> 27
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tacatgggtca atatctaaaa attaatgta tattctgtat gctaacgatg aacagttaga      180
aattgaaatg aacaaaattg taccattaca atggcagtaa aaacaaaata gcttttacao      240
atctaacaaa ataccagaat atacagaatc gacatgctga gaattacaaa atactgggtga      300
acaaaatcga agatctaaat aagtgtagaa atgtactgct ttcattggatt ggaagacgga      360
atattatcaa cacgatgact                                     380

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<210> 28

<211> 427

<212> DNA

<213> Homo sapiens

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<400> 28
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gaaagacaca aactatccaa actgactcaa gaagaagtag aaaatctaata tacacttaaa      120

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acaagtagag	agactgaatt	agtaataaat	aaataagtaa	ttccccacaa	agaaaagcca	180
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tcacaaactc	ttccaacaa	taaaatatgg	aagaataactt	cccaattcag	tctatgaaac	300
cagtattacc	ctgaagccaa	aaccagaaaa	agatctcaca	ggaaaactac	agaccactac	360
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ataagaa						427

<210> 29
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 29						
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tgtctctattg	ccattgtctg	aaaaagctat	ccttcctcca	ctcagtggct	tctgcacctt	180
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accttgacat	ogggtagacg	gattcctctc	actttattct	ttttcaaaat	ttagttatta	360
agcctttgce	tttccatgca	catttttagaa	taaatttata	totacaacaa	ttt	413

<210> 30
 <211> 228
 <212> DNA
 <213> Homo sapiens

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accacgcccc	agctaatttt	tgtattttta	gtagagacag	ggttttacta	tggtgcacag	180
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<210> 31
 <211> 392
 <212> DNA
 <213> Homo sapiens

<400> 31						
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tttggttgact	gtgcttttga	tgtcttggtt	ataaattatt	tgccatagacc	agtgtcctga	180
attgtttttc	ctgtgttttc	ttctactagt	tttatagggt	caggctcttac	agttaagtct	240
ttatcttgag	ttgattttta	tataacgtga	gagatagggg	ttcagattca	ttctcttgca	300
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tattcttgac	acctttgtca	aacatcagtt	gg			392

<210> 32
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 32

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cacctcgga	ttgtacacc	aatgtttgca	gcacctgtat	ctgtaatagc	ccaaactaga	300
aacagtccaa	atgcaaaaac	agtgatatgt	ccatagaatg	gaatactaca	caacaataaa	360
aaggagtgg	atactgatat	gtactacaac	atgggtggac	ttcagaaaca	ctattctacg	420
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<210> 33

<211> 1823

<212> DNA

<213> Homo sapiens

<400> 33

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ctccgaagcg	tatgtgccag	gtttgagtg	cgagggtgat	gctggctgct	cttctgaaca	1800
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<210> 34

<211> 421

<212> DNA

<213> Homo sapiens

<400> 34

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tcgggcctgt	catctactac	ttcgagccgg	gcctgcagga	ggcgacaaag	tgggcgatgc	180
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tcggcgggccc	ggaggtctga	gcgcacttgc	aaaggggata	ggcgggcggc	acggggcgcc	300

cttccccagc	cgcggccgcc	cgcccagccc	ggagaccccc	aaggcagagg	gaggccggcc	360
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g						421

<210> 35
 <211> 475
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (1)...(475)
 <223> n = a,t,c or g

<400> 35						
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<210> 36
 <211> 1709
 <212> DNA
 <213> Homo sapiens

<400> 36						
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1709

<210> 37
 <211> 828
 <212> DNA
 <213> Homo sapiens

<400> 37
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<210> 38
 <211> 427
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(427)
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<210> 39
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 <212> DNA
 <213> Homo sapiens

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tcgcctccag gtgactgggg ccccggtcca ccaaggcacc tgcctagggtg gtgcccgagg 720
gagggaccca atgctgtccg ggttgccgggt gaccgacggg gagtggcacc acctgctgat 780
cgagctgaag aatgttaagg aggacagtga gatgaagcac ctggtcacca tgaccttgga 840
ctatgggatg gaccagggtga gctggcacct gcacctcctc tggggataga cccttcctcc 900
ggcccaggga aaaacaggcg cctctgaaga caaggtctcc gtgcgccgtg gattccgagg 960
ctgcatgcag gtgcgtgggg gttgtggggg gcggggggag gcctgcccct cacaggcagc 1020
tccgaggctg 1030

```

```

<210> 40
<211> 453
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1) ... (453)
<223> n = a,t,c or g

```

```

<400> 40
tacggcgnc gcaattcttg gggcgaacca cgcgtgcgct ccatctgaga aaagtaataa 60
atatttaaat acataaaata attattcaca aggaagatct gaataaatgg aaatatatac 120
tatgttcagg gatggaaaga ctcagtactg taatgatacc agttgtcccc cagataatct 180
acaaatttaa tgcatagcaa gctgaccta aaattcacat ggtaagaatg aggagcaaaa 240
ataacaattt tgaggaagaa caagttgagg ggacttgttc ttgtcccctt aagtacttgt 300
taggtaaagt acctgttaga taaagtcttg ccacatatta agacttacta tgaagccaga 360
gtaacaaga gtgtagtact ggtgcaggta acaattatgt agcagaacag aataaagagc 420
cctgaaaaaa atatatacat agatacttct cct 453

```

```

<210> 41
<211> 409
<212> DNA
<213> Homo sapiens

```

```

<400> 41
tcgtccagca tgctgaagga aagaaaagtt ttccaatttc ctctctgctt atttttccaa 60
tatattacat ggctgggtcc accttaccac gtcctgtttg attccagcgt taccaacttt 120
tctattggag ccaaataaga catactgcaa tcagtgtatg actgtctata tgccaagcgt 180
atcccttggt taactgtgta atggctgaaa ctgagaaatt ggggctaagt atcaagtggc 240
ttaaaggatt gtcaaggatc caaaatttga acgattacca aattacctcg cacaggaagg 300
aatttatgca gatgactgtt taccacagag agttacttat cataagtgtt gtagccacga 360
acctgggacc ttaaaagaag aatcctaaga ttcttggagt tcctatcat 409

```

```

<210> 42
<211> 415
<212> DNA
<213> Homo sapiens

```

```

<400> 42
gggtcgaccc acgcgtccgg ttatgacaaa acaccagact tcattttaca agtaccagtt 60
gctgtagaag ggcacataat tcactggatt gaaagcaaag cctcatttgg ggatgaatgt 120

```


agccaccacg	cctacctgca	tgaccagttc	tggagctact	ggaatagcct	caagcacaga	180
acttggcagg	gaattggaac	tggtgccagc	aatctttccc	agctctaaac	tctaaatgca	240
ccttttccag	agttgttact	gttcagaagt	ctggctagaa	ctggatttgt	gttaacctaa	300
aagatttggg	ccaggcttag	tcattctattg	gtatggattt	atccaggagc	tggactgcaa	360
ccgggaaagg	ggcatcctgc	tcaaagcctg	tttccccacg	aacattgtca	cctta	415

<210> 43
 <211> 394
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(394)
 <223> n = a,t,c or g

<400> 43						
ccggaattcc	cnmntcgacg	ggaggcagga	ggatgcagag	ccggggacag	agacagacag	60
agaggagag	acagagagag	attaggcaag	aagggacaga	gatgggttca	ggtggtggag	120
gccgggctgag	gccagcgtga	gatgggggca	gcatgggtct	ctgggggaagg	agtgtgtggg	180
gcggagttag	aagtgggggt	gtggctggga	gtgacctggt	gtccccgggg	ccccgcctgg	240
gctatagcct	cggccatccc	agtccaacag	agaggagcca	tgaactaggg	ccaaggcagg	300
ggtccagagg	cagagggctc	ccctttttct	ggggtacagg	ggctggggac	agggcaggat	360
gcaagagcca	gaccagctc	ctcctcgaca	gcgc			394

<210> 44
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 44						
gcggaaccgc	tccggaatth	ccgggtcgac	gtttcgtcta	gtggagaagg	tgagaggccg	60
cgggagtggc	ggttgccgag	gccgtggtgg	aggtcttagg	tggaggggaa	ggggcttctc	120
tcggggggaga	gtgggtcgcg	gtgggcagct	gacctggcct	tgtagggaatc	gggagggagg	180
gtgcccttta	acaagggttag	gcgcttgatt	gaggggttgt	gaggtcgagc	gcagcatgtg	240
agttgggggt	gatctgtata	tgcaggagg	gtcttcaatg	gggaaagttg	taaagcagga	300
gacagcagat	ggtaaaaatat	agagacgtcc	ttggaaatgca	gcgtggcgat	ttagtaggag	360
gttttaaggc	agagggttat	tacagcgcac	tatgctttac	aagctttgat	ttgggtgaaa	420
gtcgtgggaa	gaagcaatat	tgaggaaggg				450

<210> 45
 <211> 394
 <212> DNA
 <213> Homo sapiens

<400> 45						
cactatctcc	agccccatac	ctctcttcag	ggctccatac	ctgtgcttct	agttgtctgc	60
cagacatgtc	cattttttcat	tgcccactg	gcaacttatt	gtctgattgt	ctatctagtt	120
gtacatccta	gaaatcatag	tcataattta	ttccatcttc	acttcccat	actcatagat	180
aaccaagtcc	cataaattgg	aaattctaag	ttgccaatgg	aaaaacaaat	aacaaagata	240
ctgggtctggg	gttaggagag	tgttcgagc	catcatactc	ctcttggcca	gcagtgctcc	300
acgtgttcag	gctaacgatt	tgcccataca	cggatgtctg	gacgtataaa	ttgtcaaaga	360
cagtgggggg	atatactcct	caggaaagac	atth			394

<210> 46
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 46
 acgactaaga aaaccttgat aagtaataat gtttccagta ggagtttgcc catccttcca 60
 gaactgaaag ccttttcttt ggcttttaat gatccttttag aaatacaaaa atatatgaga 120
 actgtcagta gtgtgtcact catgacattt ctctttatat tgtcacaaaag ttagcactaa 180
 tttttttaat tcccagggtt tttcttttcc atcaattgaa cattacctaa taatgtttac 240
 atttctttac tatgacgacg tttattgcaa ttccattttc ttttcttttt cttggttagag 300
 acagtctctt gctatgttgc caaggctggg ctcaaaactcc tggcctcaag tgatcctccc 360
 acctca 366

<210> 47
 <211> 162
 <212> DNA
 <213> Homo sapiens

<400> 47
 tttttttttt ttctgaaaaa gtctcgctgg gtcaccaggg ctggagtgcg ggggggcaat 60
 ctactgcat cctccgcctc ccgggttcaa gcgattctcc cgccttagcc tcctgagtaa 120
 ctgggattac aggcaaccgc ggctggctaa attttgtaat tg 162

<210> 48
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (410)
 <223> n = a,t,c or g

<400> 48
 actaggccca gcctcatggc ctggaattcc agtctgttat ctggagcaaa tcagcatttc 60
 cgtccagcgt tcctaggctc ccttttatct gccccccaca gcactgactg ttactagcgt 120
 gagccgccac ttctccccgt tcagtgcagg ctggctgtac ggggttgatt ccttagacat 180
 ataaaaatct ggcaaaatca gaaaacagtc attctcactt cacacctgat agaatagcca 240
 ttgtcaaaaa cacaagagac agccactgtt ggcgagggtg ttgagaagag ggagccccag 300
 cacgtgcac cgttggtagg aatgtagggt ggtacagcca tgatggaaaa caatatggaa 360
 attcctaaag aaataaaaact agaactacta tatgactcag cagtcccttcn 410

<210> 49
 <211> 465
 <212> DNA
 <213> Homo sapiens

<400> 49
 gtagggtcga ccacgcgctc cgatatgggc gccggcgagg agcgccgagg ggcaacgcgg 60
 tgtctatcat ggctgagctg cagcagctcc gggggcagga ggaggagggg tccatgggtga 120
 agagtctgga aagagagaac atccggaaga tgcaggtagc ggggctgggg ccgaaccagg 180
 acccccttct cagcgggtgg gtgcggggcc cttccctcag ccaccacgag acgccttgca 240

ctgcagccgc	gtacccgcag	accgggtgtg	ggcgccctg	gggtcgccgg	ggcgccctcg	300
gacaggactt	cggtgcttt	ggcgatcgg	atgaaatacg	tgtgcccttg	ccgtgcgcga	360
ggcgtgtttc	cgcccttcc	agcctggggc	aggagcgtcc	tcggcgccag	gtgggaagcc	420
cctggtggca	ggcgctcgcc	ccaccaactt	tcctctttac	gcggg		465

<210> 50
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 50						
atgtctgcta	acagcattca	ataaaagctc	tgggtcgggg	gtaagagaaa	tgcattcagg	60
cttttagatgt	ctttgttttt	tgttatattg	atcacagcag	ccattgtttg	atgtcctgtg	120
actgagaaac	caggctttaa	actttatgcc	tttgagatg	gagcccaaga	tgagcaaac	180
ggcctttggc	tgtcagagaa	gttccacatc	agatgatgac	tctggctgtg	cattggagga	240
gtacgcctgg	gtcccccccg	gcctgagacc	agagcagatc	cagctctatt	ttgcttgctt	300
accagaggaa	aaagtccctt	acgttaacag	ccccggagag	aagcatcgga	ttaaacagct	360
tttgtaccag	ttaccaccac	atgataatga	ggtacggtat	tgccagtctt	tgagtgaaga	420
g						421

<210> 51
 <211> 2095
 <212> DNA
 <213> Homo sapiens

<400> 51						
tttttttttt	ttgtggcgag	cagtcagtac	tttaattcag	gtcaggctcc	gacacctggg	60
gagacggggt	cctgcccggc	ccacctgag	gtggaacccc	cagctgctcc	tgggcacaga	120
atcatttaca	aaaataaata	tgaaaaaagc	agcaactctt	tagtgatcat	ggaattaatc	180
tgacagcaat	taaatgtgtt	taagcatctg	gcatactctc	tcaattgcac	caaaagaatt	240
tggaagcact	tggtttggtc	tcaaaggcaa	aaggaaagga	cgaggaaggg	gccaggcctc	300
ccgccaggcc	cgcgcccccc	tcacatttct	gagtcgcat	acatcccgtt	gattaagtag	360
tcacacctgg	tgtagtcctt	cttctttag	ctctcatagg	cctgcagggc	aaacaaaacc	420
aagactgtga	tgaagagggt	caccccgagt	aacagcacca	ccagaaggag	agttttgtct	480
accacggcct	gggtgagggg	ctcagtggtg	accaccatgt	actggccttg	ggtgctgggc	540
tggcacagat	ccgtggctgg	catcttagtg	ccccctgagc	tcctgggtgt	tggcccagtg	600
gaatcagtac	ctggtgtggc	ttcagctctc	acctgctccg	gtgctgggga	tgtgctgggc	660
ccagcggccc	tctgggtata	tggcatgggg	cttggctgtg	togtggggga	catggcctcc	720
atctcaggga	ttgggctggt	gtgaggtact	ggcactgggc	tggcagttgg	ctccctggct	780
tgtgccttgg	tggtggtcac	cactgtgggg	gtggggggcg	gctctggggg	tgtgtttgag	840
ggcatgggtg	tggaattatt	tgttgtgtta	accacaggct	ggtccactga	cacctggcta	900
atgggacott	tgctttgggg	acgcataagg	ggtacagggc	ttgccgagg	gtcactgggc	960
atgtgcttgg	aaggacttgg	acgagtgctc	atggggctgc	ttgtgtttgc	tgtggtcgct	1020
acagtctgag	cacgtgtggc	caatgtggcc	agggttgctg	ttcttggcaa	cgcctgtctc	1080
tttggcactt	gtcgaggggc	tgtgctgaga	gatggatgcc	cagtgggcgt	agtggacggg	1140
gtccgcccctg	tggaaagtga	cgtgggccc	gggagtgcga	gtgtcatggg	agtgtctggg	1200
gcgcagtcac	tactggaggc	tgcagtcgtg	ggagcaatgg	aggccacagt	tgtactggag	1260
gctgcagtcg	tgggagcact	ggaggccaca	gtcatactgg	aggccgcagt	cgtaattggg	1320
gcgcagtcog	tactggaggc	cacagccgtg	ggagcaatgg	aggccacacc	atcagctgca	1380
actcctgaag	ttgctgggtt	actcacatct	gtcctgcttg	tgtcctctgt	tgtgacttcc	1440
atagagtgtg	ggtgggctgc	cgaagtcctt	ttggtcaatg	tgacaggaga	agctgctgcc	1500
atgggttacc	cttcagacgt	tttattatca	actgtttcca	cagatgcatt	cctcttgact	1560
aatcccttcc	acattttgtt	agggacaaag	ttgcgtggat	cgttggatgc	cgcattggctt	1620
tcagataagg	acaaggagaa	aatccaaatg	agcacaagag	ctgtccacat	cttgtgggtg	1680
agctgggagc	aaggctgggc	gggtcccagag	gctcccagcc	agccagctcc	tcaggctgct	1740
aatggttccc	tectgcttgg	ccaagggatc	agaggctgct	gctaagggga	tgctcccagc	1800
ctggaccatc	ttctccttgg	gagagctgtg	ggcttgacac	tgtgtcgctg	ggcgaagtct	1860
ggctttgcag	ggggtgaaag	ccaogtggtg	gggcactccc	gggcatgccc	atcctttgtg	1920

gcacatgtga	gacgaaggta	gactctccac	ttagtaaca	gacgcatccg	ggcgagcag	1980
gccccggcg	gcctggtggc	cctcggacag	taggaaggag	cctgaggccc	ggcgcgggga	2040
cgtggccggc	agcgcaacce	aggcagctcc	gggcagcctc	gtgccgaatt	ogaat	2095

<210> 52
 <211> 462
 <212> DNA
 <213> Homo sapiens

<400> 52	
gagagtggcg	aattcctagt tagtttcaca ttaaaaaaac caaccaatgt tttccaccac 60
attaatggaa	tgaattttt taataaacta tcttctagag ccatacagat atagcatttt 120
ataaaattca	gcattccattt atgttataaag ctcttataaa atgggcgtag gagggaaactt 180
aacctgatag	aagatatcta cactgaagcc tgagacttaa tggatgaacag ttgaaaactt 240
tccctctgag	atcaggaatg agatgaggct ggccatattg ccacttgtag tcaatgccat 300
gctatctatt	gtcccagctg ttgtcccagc cggtaaaaaca aggcattgaga aagaaataac 360
atgtccattg	attggacaag aagaaaaata attttcatga tttgtgggtg atatgaatac 420
atgtgtgaaa	aataaaaaag aatctaaaaa attactagaa tt 462

<210> 53
 <211> 630
 <212> DNA
 <213> Homo sapiens

<400> 53	
cctgaagtta	ttcaacagtc agcttatgac tcaaaagctg acatttggtc attgggaatt 60
actgctattg	aactagccaa gggagagcca cctaactccg atatgcatcc aatgagagtt 120
ctgtttctta	ttccccaaaa caatcctcca actcattgtt ggagacgttt actagagtct 180
tttaagggaag	tttagttgat gcttgccctga accaaagatc catcgatttc gtcctacagc 240
aaaagaaactt	ctgaaacaca aattcattgt aaaaaattca aagaagactt cttatctgac 300
tgaactgata	gatcgtttta agagatggaa ggcagaagga cacagtgatg atgaatctga 360
ttccgagggc	tctgattcgg aatctaccag cagggaaaac aatactcatc ctgaatggag 420
ctttaccacc	gtacgaaaga agcctgatcc aaagaaagta cagaatgggg cagagcaaga 480
tcttgtgcaa	accctgagtt gtttgtctat gataatcaca cctgcatttg ctgaacttaa 540
acagcaggac	gagaataaac ctgacaggaa tcaggcgatt gaagaactcg agaaaagtat 600
tgctgtggct	gaagccgccg gccccggcgc 630

<210> 54
 <211> 222
 <212> DNA
 <213> Homo sapiens

<400> 54	
atttcaattg	atgcttgaaa agcatttgat aaaattcaac attcttcatg ataacaactc 60
tcaaaaaact	gggtatagat ggaaaaatc tcaacacaat aaaagccata gacgacagac 120
acacagttag	taccatatta aatgtggaaa aactgaaagc ctttctctga agatctggaa 180
cacgacaaaag	attcccaatt tccgggtccg gagctcgaat tc 222

<210> 55
 <211> 366
 <212> DNA
 <213> Homo sapiens

```

<400> 55
cccacgcgtc cgtggacggc gacgaaggct ccgatgacgt gtactactat tacacacctg      60
ccatcctcag ggagctgcaa gcgctcaaca ccgcagaggc ggcggaacac cgaccggagg      120
aggaccggat gctcagtgag gacccttgta ggctgtctca catgatcaag ggctacatgc      180
cacttcacaa catcccccat acggagggtga tcgatgtcac cggactgaac cagtgcgacc      240
tttaccagca tctcaacaag ggcaccccta tgaagacca gaagcgtgcc gcactctgtac      300
acctggcacg tcctagagca actagagatt ctacgacaga tcaatcaaca gagccatggg      360
cctggg

```

```

<210> 56
<211> 460
<212> DNA
<213> Homo sapiens

```

```

<400> 56
ataaagtgtt ctgacgcttc agactagatc cccaagtaag cccttgctta cggaaattaa      60
tggattggga agtagtaagc agaaattcaa tatctgagga caggttagaa acacaaagtc      120
gtgcatcacg atctccaccg gtaactccta atcaatcaca agagaccctt gtagatggca      180
agcctctagc tttaccaccc aaccagtccc agaaaaacat tcggtaccat atccattatt      240
tacatttaca atactaccta gaccgtcata ttagtgccac acttccaatc ccatcctctt      300
ctggtatacc cactcctatt gccgtaatca ctgacgcctt aactgaacct gtagagctga      360
ttcttgggtc gccttgctct gaggagtctg gtagggcacc aggtaccctt ttcttgcttg      420
ccctctgaag cttacttccg tgtagcttgt cactctagcg      460

```

```

<210> 57
<211> 431
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = a,t,c or g

```

```

<400> 57
cagccgancg ggccgctatg cctttgagac caacggcttc cccatcatgc tgggtgtcac      60
gaccgacaag atcgagggcg acgtcggcat tgccgggcctg tacgacatgc acactctccc      120
tgccatgggc gttcttactg cgaactttag taagatgcac ctcatatata ataccagtca      180
cccattgtgt aagcacacca gtgacctgcc tgaggcggcg tgagaaggac ggcgtcattg      240
tggacgtgct gacgcacacg gcgtccaatc acaacggctt ccccggtggag gagcatgccg      300
atgacaccca tcttgcgccg cttcagggcc cgaccctgag ctctcagccc atggggcctc      360
taaagcaciaa ggcgtttgag gagcgtgcca acctgggcct ggtacagcgg cgcctgaggg      420
tagaggactc n

```

```

<210> 58
<211> 421
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(421)
<223> n = a,t,c or g

```

```

<400> 58
catcttggag cgcagagcat gctatggcct tcaacttctt actgcagagc cggggcagct      60
acaattttct gacatcaccc agcctcaggt acgaagagat gtcttctgtg cccagaggag      120
cagtactcaa gccgcaccag agatggctgc ctgccaggga cagagacett cctggccttt      180
gacgaccccc tgggactcat gctgccttg gtggcgctca tgctggccag cctggcagtg      240
ctggctctca gactgttctg aagcaccgag acacacctgt ggtcggggcc aacaacagag      300
ctctcagctg cagcgcgctc acctccctga cectctgtgc cctctgtccc ttgccttgcc      360
ttggttgttc cacagntgcc acctgccgcc tctaccagac cacagttggt gttgtgttca      420
n

```

```

<210> 59
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (441)
<223> n = a,t,c or g

```

```

<400> 59
gaaaagcctt cagtttcacc acatctctta ttggacacca gagaatgcat actggagaga      60
gacottataa atgcaaggaa tgtggaaaaa catttaaagg tagttcatct ctttaataatc      120
accagcgaat tcacacagga gagaagccct ataagtgtaa tgaatgtggg agggccttca      180
gtcagtgtct atctctcatt cagcaccaca gaattcatac tggggagaaa ccgtatgaat      240
gtactcagtg tgggaaagcc ttcacttcaa tatcgccggt aagtaggcac catogaattc      300
atactggaga gaaacccttt cattgtaacg agtgtggaaa agtattcagc tatcactcag      360
cccttatcat acatcagaga attcactctg gtgagaaacc atatgcatgc aaagatgtgg      420
gaaagccttc accaaagctc n

```

```

<210> 60
<211> 419
<212> DNA
<213> Homo sapiens

```

```

<400> 60
atatatatgg ctggacatgc acgtatatct atagaagtag acccatttgc tggaaacagcc      60
ctgtgtaatt agtcgagacg aagtctgcct ggtttaaaaa gccttttgta cacatatattt      120
taataaagat ctctcccttg tgtctgccta tcctcctgcc aagccgagga gctgcttacg      180
ttcacccctga ctttttcctg taagggtggg ccccagggcc attcctggca cacacacatg      240
ctggactcca agccccaggg cccctccttg ccccagctgg ggacgagggg gacctcctgc      300
tccttgcaat gcaacagagc tgccctggcag accatctgct gacagcgtca tggggggggca      360
aaatccaatc ccaaccaagg ctcttgagaa gggacaagaa gggcttccct tgactgtgg      419

```

```

<210> 61
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (385)
<223> n = a,t,c or g

```

```

<400> 61

```

agaggcacag	tcgggcacac	ctgtgccagc	catttcacat	ggatcatgagg	gacctgctgc	60
aactggggcca	ggacataccc	cagggatgcc	actacctgga	ggaaaatcac	ttgatccaca	120
gggatattgc	cgcccgcaac	tgctgtctga	gctgcgctgc	acccaccgga	gcgggccaga	180
tcggggactt	tgggatggca	cgatatatct	accggaccag	gtattaccag	ttgggggacc	240
gggccttgct	ccaaggaagt	ggatgcccc	agaggcctta	ctggagggca	tcttcacata	300
caatacagat	tcctggactt	ttgggggtgct	gctctgggag	atcttctcac	tgggctacat	360
gccctatcct	gggcgcacca	accaa				385

<210> 62
 <211> 859
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(859)
 <223> n = a,t,c or g

<400> 62						
gtgggtggaat	tcctctggag	caggaggccc	agtggctctt	ctgacccaag	gccccgcctg	60
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agcatcaagg	tggtgtctca	gtcggctctg	agcctgggcc	gcagcctgga	tgccggaccat	180
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aagaagagtt	ttattggcca	aaataaatca	ttctttggtc	ctttggagct	ggtggagaaa	300
ctttgtccag	aagcatcaga	tatagcgact	agtgtcagaa	atcttccaga	attaaagaca	360
gctgtgggaa	gaggccgagc	gtggctttat	cttgactca	tgcaaaagaa	actggcagat	420
tatctgaaaag	tgcttataga	caataaacat	ctcttaagcg	agttctatga	gcctgaggct	480
ttaatgatgg	aggaagaagg	gatggtgatt	gttggctctg	tggtgggact	caatgttctc	540
gatgccaatc	tctggcttga	aaggagaaga	cttggattct	caggttggag	taatagattt	600
ttccctctac	cttaaggatg	tgaggatct	tgatgggtgg	aaggagcatg	aaagaattac	660
tgatgtcctt	gatcaaaaaa	attatgtgga	agaacttaac	cggcacttga	gctgcacagt	720
tggggatctt	caaaccaaga	tagatggctt	ggaaaagact	aactcaagc	ttcaagaang	780
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acaaaatgaa	ttaattcga					859

<210> 63
 <211> 615
 <212> DNA
 <213> Homo sapiens

<400> 63						
ttcaagcttt	gctaaacata	agaggattca	tacagggtgag	aaacccttta	tatgtttaga	60
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agagaaaccc	tacacatgtg	aagaatgtgg	caaagccttt	agacagtcag	caatccttta	180
tgtacatagg	agaattcata	ctggagagaa	accctacaca	tggtggagaat	gtggcaaaaac	240
ctttagacag	tctgcaaatc	tttatgogca	taagaaaatt	catactggag	agaaacccta	300
caegtgtgga	gactgtggca	aaacctttag	acagtctgca	aatctttatg	cacataagaa	360
aattcatact	ggagataaaa	ccatacaagt	gtaagaaatg	tggcaagcc	tttaagtcac	420
actacagcat	tcttaaacat	aagagaactc	ataccagggg	aatgtcttac	gaaggtgacg	480
aatgtcggcg	tctttaaatg	ctcctcaatc	ctttctaatc	ataagataat	tcataatgaa	540
gagaaactct	aaaatgtgaa	aaatgtgaga	aggcttttaa	tcacacctca	atctgttgta	600
gacataaaaa	gaatt					615

<210> 64
 <211> 945
 <212> DNA

<213> Homo sapiens

<400> 64

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tttgtggcct	gctccataca	ttgggatgct	ggatgacgtg	gctagtagca	ttaattctac	180
ctttgtacag	tggacatgga	gactgaagaa	acattgtcac	tttctcatct	tccagcatca	240
actgtaaaaa	taatcttcg	tataaacctt	ggaaatgttc	ccagatgttg	gaaggttccc	300
tctttgagga	gatgtctgaa	atagttcaca	aagaacctgt	gccatcagct	tttgattatt	360
aggatggcat	gaatatgca	tgtagaaaag	aacgcaacag	ttgcattctt	caattgctgt	420
gcgctgttga	gtagtcagtc	ctgttggttag	ccagctgaag	aaagagaagc	tgatcttgca	480
ctggctcctgt	tgtgcacctt	aaattatttg	cttcagaag	tggacccaga	gtgacacaat	540
aaaaacagaa	gtgctgtcca	tagtggattg	acttcagaac	caccaagcca	atctttcata	600
atatggctat	tgccaacttc	tgtcaaaaac	ctaagaatag	gagcaactag	gtcggctgtg	660
ataggcatct	tattacattg	ttgtgggaca	tgatggcgcc	tgagtttgtc	ctgggaaata	720
tctattgact	gggcaatgct	ttctgagcta	gaaatgtggc	taaagcagaa	actagccaga	780
ctcctcacia	gaagagaagg	caaacctgag	tctagtaatt	gtttaatagc	ttcaggagat	840
tgagaagagg	aagcaagggt	agccaaatgt	gattcagtta	atgcgagagg	tgcttggtgca	900
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<210> 65

<211> 324

<212> DNA

<213> Homo sapiens

<400> 65

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ggtcggagca	ttcattacat	attctactgt	gtaatgcctt	aaccgogggc	ctttgaattt	120
gtacacactg	aaatgattgt	ggggctgtgc	aaaacattca	cctatttacc	ttgcaagttt	180
tagaagacag	ggcacttttt	accatgagtg	ttgggtccag	cctgtgggtc	acttatctaa	240
tacacgtgat	ggctctcccc	gcggggagct	gctcaagccc	aacgcctcag	tggccctoca	300
caagctcagc	aatgcactgg	tggg				324

<210> 66

<211> 493

<212> DNA

<213> Homo sapiens

<400> 66

ggcagagagc	ctgctctgta	actcacattg	tgtccttctc	tctcccttcc	cttaaccctt	60
cccatccgcg	ttcaactcct	ggccatacag	agaatgaaca	gccttccctc	gtttggtttg	120
acagaggaaa	gtttttattg	acttttgaag	gttcttccag	gggacccagc	cccctaacca	180
tgggagctca	ggacactctc	cctgttgagc	cagcatttac	agaaacagtc	aatgcctatt	240
tcaaaggagc	agacccaagc	aaatgtatcg	ttaagattac	cggagaaatg	gtgttgatcat	300
ttcctgctgg	catcaccaga	cactttgcca	acaaccgctc	cccagctgct	ctgacttttc	360
gggtgataaa	tttcagcagg	ttagaacacg	tcttgccaaa	cccccaactt	ctctgctgtg	420
ataatacaca	aaatgatgcc	aataccaagg	gaattctggg	taaacatgcc	aaatttgatg	480
actcacctaa	aga					493

<210> 67

<211> 400

<212> DNA

<213> Homo sapiens


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<400> 67
actatagcca tgcagctgac aacattttgc aaaatctctc gcctctaaca gcctttctga      60
aactgacttc cttgggtttc ataataggag tcagcgtggt gggcaacctc ctgatctcca      120
ttttgctagt gaaagataag accttgcata gagcacctta ctacttctctg ttggatcttt      180
gctgttcaga tatcctcaga tctgcaattt gtttccattt tgtgttcaac tctgtcaaaa      240
atggctctac ctggacttat gggactctga cttgcaaaagt gattgccttt ctgggggttt      300
tgtcctgttt ccacactgct ttcattgctct tctgcatcag tgtcaccaga tacttgatat      360
cgcccatcac cgcttctata caaagaggct gacctttaa      400

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<210> 68
<211> 1890
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(1890)
<223> n = a,t,c or g

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```

<400> 68
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acagcctctg gccaatcaga agaagcaact caacaaagca gtcagaaacc tcagccacat      180
tatacaactt accagtcttc ctcttttctg aaatacagca gtgaaagcca tctccttgcc      240
tggagggaga actcatcaga aggggtccttt cagttcccg gcccggagccg ggcctcctc      300
ccgcgaacgc ggcaacaaag gcgaggagcg gcggcggttc ctggacgcgg ggcagttagg      360
ctcgccacc ccagagagcg agcgcagccc cagctgcgag cagccgcacg gatcccagag      420
tcgcccgcgg cgttcccagc ccagcccggg ccgggggtccg ccgggaacag cgacgcctca      480
ggcccggcaa tctctctctg gacctggggc cgagcctcct cgcgccgcc gcccaggcc      540
ccggatgtga cggcacgcgc gcccgcagcg ctgcgccac gggccgcgcg tggagggtcc      600
cgcgccgcgg ccttggctgg agccgaggcc gaggagccac tgcgcacgct cgcgccccgg      660
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ccccgcacac cagttcgctg cgtgtcgagg cgagcacgcg ctccgcccctg gaggctgcgg      780
cgacgggtcc tctccgcgcg tccggtcgcg cctctcgcca agctcggcag tgcgcgtgog      840
cccgccaccg cactccaaat tagaaagggg acgtctagt ggttgcccgg gagggtgggc      900
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gcggtggaga gaactggaat ggccaaatat caaggtgaag ttcaaagtgt gaaactggat      1020
gatgattcag ttatagaagg agtaagcgac caagtacttg tggcagttgt ggtcagtttc      1080
gctttgattg ctaccctggg atatgcactt ttcagaaatg tacatcaaaa cattcaccca      1140
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gctgccactc gacagcagtt ctacactgac atgtactgtc ccactctgct gcaccaagcc      1260
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actccctcag cocacagagc acctctcacc ggctaacata ctctgtggtc acgtgtttgc      1680
tatctgcctc cctaattgtc ttgagaacat tagctccctg agggcagaaa tctccttcac      1740
tgacatatcc caagccccca gaactatgct tgcagcatag nnnnnnnnnn nnnnnnnnnn      1800
nnnnnnnnnn gaaaacaatt tcagggaact ctaagttgaa atacactttc tcagttcaca      1860
atgttatcca ttctgacctt tatcagacac      1890

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<210> 69
<211> 466
<212> DNA
<213> Homo sapiens

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<400> 69

ttttgatact	gcccggtgc	acgaattcgg	cacgagtata	actcagattt	ttgcagttga	60
caatagagaa	gatcttcaga	agtggatgga	agccttctgg	cagcatttct	ttgatcttag	120
ccaatggaag	cactgttgtg	aagaacttat	gaaaattgag	attatgtcac	cacggaaacc	180
acctttgttc	ttgacaaaag	aggcaacctc	agtctaccat	gatatgagca	ttgattcacc	240
tatgaaactt	gaaagttaa	cggatataat	acaaaaaaaa	attgaagaga	caaatgggca	300
gttccttatt	ggtcagcgtg	aagaatcctt	accacctcct	tgggccacac	tctttgatgg	360
taaccatcaa	atggatcatcc	agaaaaaggt	actgtatcct	gcaagtgagc	cattacatga	420
tgaaaaaggg	aaaaagagac	aagctccctt	tcctccttct	gataaa		466

<210> 70

<211> 698

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)... (698)

<223> n = a,t,c or g

<400> 70

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tggccacccc	atgcacatgc	ccctgcccct	ccatgtcaga	tgcgtgcccc	tcggggctgg	180
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tgaccgcgt	ctccaccag	cogtgcgggt	aggcgggtgt	ctcgccggca	aagtagatgc	300
ggccataagg	gaccgtccag	tcatcctttt	cggtttgcca	gagcgccggc	ggctgtacca	360
ogaagccacc	ctggctgtgc	tggtcctccg	cccaacgctt	gacgacggcg	gtgccgtccc	420
agagctggcg	cacgacaggc	cogtgcaatg	ccgccacgtc	gtcgagcgcc	aagcgcaacg	480
cctcttcccg	gctcaagccg	gogaacgctg	cgcgcgcgtc	cgaccacgtg	tacgaggcca	540
gcagcagcgc	gccttcgcgc	ggcggcgggt	agaaaatcat	gcgcgacggg	cgatcgggtgt	600
ttgagtggcc	gccttcaatg	tgctcctcgc	gccagaagg	cctgcgggaag	cttangaaca	660
acctttgtgg	cccgcacgta	gtgcagcctt	cgcagcgc			698

<210> 71

<211> 385

<212> DNA

<213> Homo sapiens

<400> 71

tcagaaacaa	actctgcaga	atgggtat	agattcaagt	atggatatac	tgtatctggg	60
cagcctgcct	ccagaaactc	aggtgagctc	agatgagcct	ccagggcctc	ctgagcaagc	120
tggactttct	cagttccatc	tagagcctga	aactcaaat	ccagaaacca	ctgaagagat	180
ccagtcctct	actccagcaa	gaagctgcag	cgcagcttcc	acagctccct	gaggtggtag	240
aactttcttc	aaccaaagct	ggaggcccca	gctctgcctt	cacagtccct	tgaggggggtc	300
cactcttcaa	cagagcagaa	ggctccagca	cagcagctac	ctgcctttga	agagatccta	360
gccccactat	tgatacatca	tgagg				385

<210> 72

<211> 906

<212> DNA

<213> Homo sapiens

<400> 72

cacgcccaat	atgtggggcc	ctatcggtg	gagaagacgc	tgggcaaagg	acagacagg	60
------------	------------	-----------	------------	------------	-----------	----

ctgggttaaac	tcgggggtcca	ctgcatcacg	ggtcagaagg	tcgccatcaa	gatcgtgaac	120
cgggagaagc	tgtcggagtc	gggtgctgatg	aaggtggagc	gggagatcgc	catcctcgag	180
gctcatcgaa	caccacatg	tctcaagct	ccacggcgtc	tacgagaaca	agaaatattt	240
tcccccgat	gaactgacat	caggtccgtc	gatgctggcg	caggtttcac	cacacgggaa	300
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gcaogtctcg	gggggtgagc	tattcgacta	cctggtaaag	aaggggagac	tgacgccccaa	420
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ccacttcatt	cctccagatt	gccagagcct	cctgagggga	atgatcgaag	tggagcccg	840
aaaaaggctc	agtctggagc	aaattcagaa	acatccttgg	tacctaggcg	ggaactttat	900
ctcctt						906

<210> 73

<211> 802

<212> DNA

<213> Homo sapiens

<400> 73

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gacttctctga	accccactat	catgcggcag	gtgttccttg	gaaaccacaga	caagtgccca	120
gtgcagcagg	ccagcttgaa	ccacttggaa	gcaaaacaga	gaccttgga	ctgagagcag	180
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agtggaaagg	ttccaatagt	gttccaacct	ctgtccacca	gctccgacca	gcagacatca	360
aagtgtgtgg	cgcctcgggt	gactctctga	ctacagcagt	gggagctcga	ccaaacaact	420
ccagtgcact	ccccacatct	tggaggggac	tctcttgag	cattggaggg	gatgggaact	480
tggagactca	caccacactg	cccaacattc	tgaagaagtt	caacccttac	ctccttggct	540
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ctagggacat	gccagcccag	gcctgggacc	tggtagagcg	aatgaaaaac	agccccgaca	660
tcaacctgga	gaaagactgg	aagctgggtca	cactcttcac	tgggggcaac	gacttgtgtc	720
attactgtga	gaatccggag	gcccacttgg	ccacggaata	tggtcagcac	atccaacagg	780
ccctggacat	cctctctgag	ga				802

<210> 74

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(480)

<223> n = a,t,c or g

<400> 74

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tagccaccc	cccattggtc	tgtggggcac	agattctcct	ctgtgctgtg	tggagtcgc	180
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ctgctctctg	agagaccctg	aagagattga	ggtaggaag	cagcctgctg	ctgatgcagc	360
tgtggccaag	ggggagtttc	aggggaacag	attgctccag	tgctgctga	tcattgccgc	420
ccatcctgag	gctgcagacc	cagcccctgt	gcatactacc	gctcatcca	agggtgcaga	480

<210> 75
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 75
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 tgcgtgggtca gtgtccaggt ccagtcctgg ggggtgaccac aacatctgac ctgtgttccc 120
 tgcaggtccc agtgtccagc caccgcaacc ccctgctgga cctggctgct tacgaccagg 180
 agggccgccc gttcgacaac ttcagctctc tgagcatcca gtgggagtcc accaggccag 240
 tgttggccag catcgagcct gagctgccca tgcagctggt gtcccaggac gatgagagtg 300
 gccaaaagaa gctgcacggt ttgcaggcca ttttggttca cgaggcatca ggaaccacag 360
 ccatcactgc cactgccact ggctaccagg agtcccacct cagctctgcc aga 413

<210> 76
 <211> 410
 <212> DNA
 <213> Homo sapiens

<400> 76
 gcgtacgtac aatttttgag tttttggtgt ctgttgaccc ataatttcag cccagccca 60
 agatgatcca attctgttga gtttcatcca ctgtctgcat gctaacctgc tttgtgtatg 120
 gcgtogtgat gtcaaaccag attgcaaaga gatatggata ttctgggtggg gagatgaacc 180
 caacctagtg ggtgcaatac atcatgaact gcatgtttgtg gaagaaggac tctgggaaaa 240
 tggcctttcc tatgaatgta ggaagctgct cttcaaagag atccacaatc tgttagaaaag 300
 gtgcctaata gataaaaaact tcgtattgat tgggaaatgg tttgtccgac cctactataa 360
 ggatgaaaag cccgtcaaca aaagtgaagca tttgtcctgt gctttcacac 410

<210> 77
 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 77
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 aacaagggga actttgtggg gtgtctgtgg ctgtctacag tgacatctgg caggactaac 120
 tgggtcatca gagccacaga ataaggactg ggaagggtggc cacaactgca aggactgggg 180
 ccatgtgggg ggaggactct gagactgacc acttgggctg gtaacttggg ctgtccagtg 240
 tatggggaat ctcaagtgaat tcctgggcct gaagtcagac tctgtctctg acgcagacgt 300
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 ggcctttgca tttgttttct tcctgtacct ttccacttg tctgaagacc cgcagcagg 420
 ttccacgaag gacaccctga agctcttcct cactccagcc acgactcagc aactcctcta 480
 tcaggacogg gtatgtggac acgtcttcca gccoctgagg gaatctgtgt ggocaccagc 540
 tagtgggttt cagacctgat tccctgatca tgactcagaa ccacagtcca gggctctatga 600
 aacccagacc ctggtcaggat atgggaagtg gagacttggg gagagtaggt aattctctc 660
 tgctctttat ccttcagaag gaggcctcaa aacctccttg aatatttatc aaaacttatt 720
 gaatcatact attaagatct atgcctttta ctgaatgcaa atgatccccc aaa 773

<210> 78
 <211> 1293
 <212> DNA
 <213> Homo sapiens

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<400> 78
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gtcaccacgg agcagcccg agcccgagc ccccatcct ccccgccagg cctggaggag 120
cctctggatg gagctgatcc tcatgtccca caccagacc tggcgccctat tgccttcttc 180
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ctgctcctgg acacactgcc catgtggggg aatgtcctgc tgcctgctt ctttgtcttc 660
ttcatctttg gcatcatagg tgtgcagctc tggcggggcc tgcctgctaa ccgctgcttc 720
ctggaggaga acttcacccat acaaggggat gtggccttgc caccatact accagccgga 780
ggaggatgat gagatgccct tcatctgctc cctgtcgggc gacaatggga taatgggctg 840
ccatgagatc ccccgctca aggagcaggc cgtgagtg tgctgtcca aggacgaagt 900
ctacgacttt gggcgaggc gccaggacct caatgccagc ggctctgtg tcaactggaa 960
ccgttactac aatgtgtgcc gcacgggcag cgcaacccc cacaagggtg ccatcaactt 1020
tgacaacatc ggttatgctt ggattgtcat ctccagggtg atcactctgg aaggctgggt 1080
ggagatcatg tactacgtga tggatgtcct ctcttctac aacttcatct acttcatcct 1140
gcttatcata gtaagtgtca gggagcctgg gctcctaggt ggcagcttca gcacagcaca 1200
gtccccaaaa tgtcaagggt attcatcccc aggagtcgct gctgaatccc tgctgctgcg 1260
aggttggggt ctctggcttc ctggtgggtg gag 1293

```

```

<210> 79
<211> 446
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(446)
<223> n = a,t,c or g

```

```

<400> 79
cctaataact tcttcaagga catgttcctt gacctgcgg gggggcctct gggaccatc 60
aaggcgagga acgactacgg tgccatcttc aacttctga gtgccacca cctgggaggc 120
ctcttccacc cctggcccct ggtagaagag cgcaagctga agcccaaggc ctctcagcag 180
tgcccatctt gccacaaagt catcatgggg gccgggaagc tgccgcggca catgaggacc 240
cataccgggg agaagccata catgtgcacc atctgcgagg tccgcttcac caggcaggac 300
aagctgaaaa tccacatgag gaagcacaca ggggagcggc cctacctgtg catccactgc 360
aacgcaagt tcgtgcacaa ctacgacctc aagaaccaca tgcgccttcc accacgggag 420
tgccggccca ccagtgcgag ttctgc 446

```

```

<210> 80
<211> 468
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(468)
<223> n = a,t,c or g

```

```

<400> 80
gaggtgggtc ctctcctttg ggggtgagatg aacgagcttt cccagcagct ttctcagcaa 60
ggaggtcggg gcgcctctca gtgtccctca cctccggccc ccacgcttcc aaaccaact 120
cctctctgcc agctccagct ccagcgtgtg aacacgggac tgcccacccc accatgccac 180

```

ccccgagccg	gcgcgcgagg	gccatgcctc	cgaggacatg	cagcctgtcc	gtgcctgtcg	240
agagcctgat	ggttctaact	caggaccgag	ctcagcaggg	acagcgggtg	tgccccctgc	300
cctcgcccag	gcgccctgca	cagcgcctgc	tctgaagatc	tgtgggggtt	ccctcgagcc	360
cgactggctg	aagtggggac	cagagagcgg	ggggnnngtg	agaggtctct	gtgcttgtgc	420
tgcttgntan	tttnnttcn	ccgcntggnc	taatgactcg	acacgccc		468

<210> 81
 <211> 583
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1) ... (583)
 <223> n = a,t,c or g

<400> 81						
tttcgtcgca	gcccgaagaaa	agaaagcttg	agtctggggg	cgccggcgaa	ggaggggagg	60
gaactgaaga	gcaagatggc	gcggagcggg	aggcggccct	ggagcgaccc	cggaggacta	120
agcgggaacg	ggaccagctg	tactacgagt	gtactcggga	cgtttcgggtc	cacgaggaga	180
tgatcgcgga	ccgcgtccgc	accgatgcct	accgccctgg	gtatccttcg	gaactgggca	240
gcactgcgaa	ggcaagacgg	tactggacgt	ggcgcggggc	accggcattc	tgagcatctt	300
ctgtgcccag	gccggggccc	ggcgcggtga	cgcggtagag	gccagcgcca	tctggcaaca	360
ggcccgggag	gtggtgcggt	tcaacgggct	ggaggaccga	gtgcacgtcc	tgccgggacc	420
agtggagact	gtagagttgc	cggaacagggt	ggatgccatc	gtgagcgagt	ggatgggcta	480
cggactcctg	cacgagtcca	tgctgagctc	cgtcctgcac	gcgcgaacca	aagtggtgaa	540
ggatggcggg	tttttcttgc	cggnetccag	cgaacttttc	atg		583

<210> 82
 <211> 716
 <212> DNA
 <213> Homo sapiens

<400> 82						
ggatttcgtt	gatgctgtct	ggaaccttcc	cctggagtcc	accaagtcc	cagcagaacc	60
aagtaaatca	gtgccctcct	tggaggggacc	cacgggcttc	cagccaagga	ctcccaagcc	120
agggtccggt	tcagaatcag	ggaaggagag	gagaacaacg	tccaaagaaa	tttctgtcat	180
ccagcacacc	agctcctttg	agaaatctga	ttctctcgag	cagccgagtg	gcttggaagg	240
ggaagacaaa	cctctggccc	agttcccatc	acccccacct	gccccacacg	gacgctctgc	300
tactcctctg	cagcctaagt	tggtccgcca	gcccacattt	caggttcctg	agatcctagt	360
aactgaggag	cctgaccggc	cggacacaga	gccagagccg	ccccctaagg	aacctgagaa	420
gactgaggag	ttccaatggc	cccaggggcag	ccagacactt	gcccagttcc	cagttgagaa	480
gttgccaccc	aaaaaaaaaga	ggttgggcct	ggcaaaagatg	gccaatcat	caggggagtc	540
cagtttcgag	tcctctgtgc	ctttgtttcg	cagcccgagc	caggaaagca	atgtttcttt	600
gagtgggtcc	agccgctcag	ccttgtttga	gagggatgac	catgggaaag	ccgaggcccc	660
cagtccctca	tttgacatgg	gccccaaacc	cctgggcacc	cacatgttga	ctgtcc	716

<210> 83
 <211> 1082
 <212> DNA
 <213> Homo sapiens

<400> 83						
tttcgtcagc	ctggctggca	gcagccttgg	actccgcccg	tggagccctg	ggcctgttga	60
cccaccagct	taggagcacc	caccaagctc	tgggtcaacg	tggaggtacc	aggccaccat	120

```

getcagtctc aagctgcccc aacttcttca agtccaccag gtcccccggtg tgttctggga 180
agatgggcatc atgtctggct accgcccgc caccagctcg gctttggact gtgtcctcag 240
ctccttccag atgaccaacg agacgggtcaa catctggact cacttcctgc ccacctggta 300
cttctctgtgg cggctcctgg cgtctggcgg cggccccggc ttccgtgcgg agccgtacca 360
ctggcgcgtg ctggtcttcc tgetgcccgc ctgcctctac cccttcgctg cgtgctgcgc 420
gcacaccttc agtccatgt cgcctcgcat gcgccacatc tgctacttcc tcgactacgg 480
cgcgtcagc ctctacagtc tggtttcctg gagctggaaa gccctgggct cagtaaggtc 540
ctcgcacag gagccttcgc ctatccattc ctgttcgaca acctccact cttttatcgg 600
ctcgggctgt gctggggcag gggccacggc tgtgggcagg aggccctgag caccagccat 660
ggctaccatc tcttctgcgc gctgctcact ggcttctctc tcgcctccca cctgctgaa 720
aggctggcac caggacgctt tgattacatc ggccacagcc accagttatt ccacatctgt 780
gcagtgcctg gcacccactt ccagctggag gcagtgcctg ctgatatggg atcacgcaga 840
gcctggctgg ccacacagga acctgcctg ggctggcagg gcacagtggc cacactggtc 900
ttggctgcag ctgggaacct actcattatt gctgcttca cagccacct gcttcggggc 960
cccagtacat gcctctgct gcagggtggc ccactggagg ggggtaccca ggccaaacaa 1020
cagtaaggcc ccatccctga ccctgtcctg gagggggcag aggccacgcc tcagtgtcga 1080
ct 1082

```

```

<210> 84
<211> 480
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(480)
<223> n = a,t,c or g

```

```

<400> 84
cgcgggtgag ccgcatggag ccccgggcgg cggacggctg cttcctgggc gacgtgggtt 60
tctgggtgga gggacccct gtgcacgagg cagcccagcg gggtagagc ctgcagctgc 120
aacagctgat cgagagcggc gcctgcgtga accaggtcac cgtggactcc atcacgcccc 180
tgcacgcagc cagtctgcag ggcacggcgc ggtgtgtgca gctgctgctg gcggctgggg 240
cccagtgga tgctcgcaac atcgacggca gcaccccgct ctgcgaatgc ctgcgcctcg 300
ggcagcatcg agtgtgtgaa gctcttgcgt tcctacgggg ccaagggtcaa ccctccctg 360
tacacagcgt ccccccgtga cgaggcctgc atnagcggga gtccgaatg tgttgaggct 420
tcttatttga cgtcggggnc aatcttgaag cgcacgaatt tcattttggg gaacctctt 480

```

```

<210> 85
<211> 435
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(435)
<223> n = a,t,c or g

```

```

<400> 85
nagccccct tgaaccctcn gttgacacac tgaanatctt acgccagctt ggcacgaggc 60
tgagcccgaa aaggctctgag gaggtctctg cacctccttt tcccttgggg gggacaggag 120
cagcccttac ccgagccagt ctccccgagc aaatcctgct gccagaagc tgctggaag 180
ccagaaagag ccagccagat gaaaagtgc tgtctgcttt gcacaactcc aggacctgga 240
attaagagcc acgccggagc cagcacagac tgggtgtccc agaggtgcat cccggaagac 300
gaggcagcag ccttgagtg gctgaatgca aacttacatc ggcatacttc agaacaggac 360
gatgcacctg cccctcgctt cgggggacaa cacgaacgaa ctcttgcta caccaattct 420
gcgctgacaa gcctc 435

```

<210> 86
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 86
 ttctcccccag ccacacatgt gggaaccag ggaggctgcc caatggcatc cagcagggtt 60
 caaccttcaa cctcggtgac aaggctcgt acagctgcaa ccttggcttc ttcctggagg 120
 gccacgccgt gctcacctgc cagctggct ctgagaacag cgccacgtgg gacttcccc 180
 tgccttcctg cagagctgat gatgcctgtg gtgggaccct gcggggccag agtggcatca 240
 tctccagccc ccacttcccc tcggagtacc aaaaacaatg ccgactgcac atggaccatc 300
 ctggctgagc tgggggacac catgcctg gtgtttattg acttcagct ggaggatggt 360
 tacgacttcc tggaaagtac tgggacagaa ggctcctccc tctggtaa 408

<210> 87
 <211> 964
 <212> DNA
 <213> Homo sapiens

<400> 87
 ccggtcgacg atttcgtgga cgctggcagc tgggttctcc cgtttccctt gggcaggagc 60
 agggctcgggt tcaaagcctc cggaacgcgt tgtggccctt tctccggctc gcagccgacc 120
 ggaagaccgg cctcctccct cggcgggccc tggggccgtg tccgcgggc aactccagcc 180
 gaggcctggg cttctgcctg cagggtgtctg cggcgaggcc cctagggtac agcccgattt 240
 ggccccatgg tgggtttcgg ggccaaccgg cgggctggcc gcttgcctc tctcgtgctg 300
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 cagctcctgc ttcaggagga ggtggccgag ctgcagggcc aggtccagcg caccgaagtg 420
 gcccgggggc ggctggaaaa gcgcaattct gacctctttg ctgttgttgg acacgcacaa 480
 gaaacagatc gaccagaagg aggccgacta cggccgcctc agcagccggc tgcaggccag 540
 agagggcctc gggaagagat gcgaggatga caaggttaaa ctacagaaca acatatcgt 600
 tcagatggca gacatacatc atttaaagga gcaacttgct gagcttcgtc aggaatttct 660
 tcgacaagaa gaccagcttc aggactatag gaagaacaat acttaccttg tgaagaggtt 720
 agaatatgaa agttttcagt gtggacagca gatgaaggaa ttgagagcac agcatgaaga 780
 aaatattaaa aagtttagcag accagttttt agagggaacaa aagcaagaga cccaaaagat 840
 tcaatcaaat gatggaaagg aattggatat aaacaatcaa gtagtaccta aaaatatcc 900
 aaaagtagct gagaatgttg cagataagaa tgaagaaccc tcaagcaatc atattccaca 960
 tggg 964

<210> 88
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 88
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 ccgagcgtcc acaaagcagt ggaaatcgag caggagcggg tgaagtcagc gggggcctgg 120
 atcatccacc cctacagcga cttccggttt tactgggacc tgatcatgct gctgctgatg 180
 gtggggaaac tcatcgtcct gcctgtgggc atcaccttct tcaaggagga gaactcccc 240
 gccttgatc gtcttcaacg tattgtctga tactttcttc ctactggatc tgggtgctcaa 300
 cttccgaacg ggcacgtggt tggaggagggt tgctgagatc ctgctggcac cgcgggccat 360
 ccgacgcgc tacttgcgca cctgggtcct ggttgacctc atctctteta tccctgtgga 420
 ttacatcttc ctagtgggtg agctggagcc acggttgagc gctgaggtct acaaaacggc 480
 acgggccccta cgcacgttcc gcttcaccaa gatcctaagg ctgctgaggc taaa 534

<210> 89
 <211> 743
 <212> DNA
 <213> Homo sapiens

<400> 89
 atggggtctcg acgaggtctt catgatcaac ctgaggcggc ggcaaggaccg gcgggagcgc 60
 atgctgcggg cgctgcaggc acaggagatc gaggccggc tggaggaggc cgtggacggc 120
 aaagttaggga tgctcacccg tagcaacgct gccccggga gacacttggc aatgctggag 180
 acattgggtgg ttgtcgcacc cagggtttgta gatgcggaca acctgatcct caaccctgac 240
 acactgagcc tgctcatcgc tgagaacaag acggtggtcg ccccatgct ggattcccg 300
 gctgcgtact ccaacttctg gtgtggaatg acttcccagg gctactacaa gcgcacacct 360
 gcctacatcc ctatccgcaa gogagaccgc cggggtgct ttgcagtcc catggtgcac 420
 tcgaccttcc tgatcgacct goggaaaggcg gcgtccaggc acctgggct tctaccacc 480
 tcacctgac tacacctggc cctttgacga catcatcgtc ttgctctct cctgcaagca 540
 gggcagaggt tcagatgtat gtgtgcaaca aggaggagta cggattcttg ccagtgccat 600
 tgcgcgcccc cagcaccctc caggatgagg ccgagagctt catgcatgtg cagctggagg 660
 tcatggtgcc ttcattctca agctcagctc agagcatggc ggtggtgtct gctgatcata 720
 ttggttagt catcagctat tta 743

<210> 90
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 90
 gaataaaacc agcttcatat tctatctcaa aaacatagtg gttgcagacc tcataatgac 60
 gctgacattt ccatttcgaa tagtccatga tgcaggattt ggaccttggg acttcaagtt 120
 tattctctgc agatacactt cagttttgtt ttatgcaaac atggatactt ccatcgtggg 180
 ccttgggctg ataacaatga cgcctattga aggtggtcag gcatttgggg actcttggat 240
 gaccggcata ccttcacgag ggtttatctg ttgggggttg gggccaggct tgtttggtt 300
 ggcaaaactta tccttgcaaa gggcgccac ggaggcattt cctggctgg 349

<210> 91
 <211> 2598
 <212> DNA
 <213> Homo sapiens

<400> 91
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 cgcggtgggt ggctgcccag gcctacaacc tgacctctgc cctcacgccc atcctcacgc 120
 gctcccggt gctcaacgag gagccctga cgtggcggg ctttcagcag ggccccggcc 180
 aacctcagtg agtggtgca gctcatdtt ctggtggaact ccaatccctt tcccttggc 240
 tatacagca actacacct ctccaccaag gtggcctcga tggcgttcca gacacaggcc 300
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 ccaggccttc gtcggtgctg tggtcacct ggacagcagc aacctgagg cgtgctgca 480
 tctgcagctc aactatacgc tgcgtgacgg ccgctacctg tctgaggaa cccagcccta 540
 cctggcagtc tacctgcact cggagccccg gcccaatgag cacaactgct cggctagcag 600
 gaggatccgc ccagagtccc tccagggtgc cgaccacgg cctacacct tcttcatttc 660
 cccggggacc agagaccag tggggagtta cgtctgaac ctctccagcc acttccgctg 720
 gtcggcgctg gaggtgtccg tgggcttgta cagctccctg tgccagtact tcagcagga 780
 ggacgtgggt tggcggacag aggggctgct gccctggag gagacctgc cccgccaggc 840
 cgtctgctc acccgccacc tcaccgcctt cggcaccagc ctcttcgtgc ccccaagcca 900
 tatccgctt gtgtttctc agccaacagc ggatgtaaac tacatcgtca tgctgacatg 960
 tgctgtgtgc ctggtgacct acatggtcat ggccgcatc ctgcacaagc tggaccagtt 1020

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ggatgccagc cggggccgcg ccatccctt ctgtgggcag cggggccgct tcaagtacga 1080
gatcctcgtc aagacaggct ggggcccggg ctcagggtacc acggcccacg tgggcatcat 1140
gctgtatggg gtggacagcc ggagcggcca cgggcacctg gacggcgaca gagccttcca 1200
ccgcaacagt ctggacatct tccagatcgc cacccegcac agcctgggta gcatgtggaa 1260
gatccgagtg tggcacgaca acaaagggtc cagccctgcc tggttcctgc agcacatcat 1320
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cactccagaa gaaaatctca gtacatctat agcaagtga gaggccgagt tagtccctta 2160
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gaggccgagg tgggcccgatc tgagtccagg agtttgagac cagcctgggc aacatagcaa 2280
gaccccatct atataaaaca ttaaaaagg ccaggcacgg tggctcacgc ctgtaatccc 2340
aacactttgg gaggccgagg cgggcagatc agttgaggtc aggagttcga gaccagcctg 2400
gccaacacaa tgaaacccca tctctactac aaatacaaaa acttagctgg gcatggtggc 2460
gggcgcctgt agtcccagct actcgagagg ctgaggcagg agaattggcat gaaccagga 2520
ggcggagctt gcagtgaacc gagattgcgc cactgcactc catcctgggc aacggagcaa 2580
gactccgtct ccaaaaaa

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<210> 92
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (660)
<223> n = a,t,c or g

```

```

<400> 92
tttcgtcttt gatgaggaaa atattctcaa tgaactcaat gatcctctga gagaggagat 60
agtcaacttc aactgtcgga aactgggtggc tacaatgoc tttatttgcta atgcggatcc 120
taattttgtg actgccatgc tgagcaagtt gagatttgag gtgtttcaac ctggagatta 180
tatcatacga gaaggagccg tgggtaaaaa aatgtatttc attcaacacg gtgttgctgg 240
tgtcattaca aaatccagta aagaaatgaa gctgacagat ggctcttact ttggagagat 300
ttgcctgctg accaaaggac gtcgtactgc cagtgttcga gctgatacat attgtcgtct 360
ttactcactt tccgtggaca atttcaacga ggtcctggag gaatatccaa tgatgaggag 420
agcctttgag acagttgcca ttgaaccgact agatcgaata ggaaagaaaa attcaattct 480
tctgcaaaag ttccagaagg atctgaacac tgggtgtttc aacaatcagg agaacgaaat 540
cctcaagcag attgtgaaac atggacaggg agatgggtgca ggcaatcgct cccatcaatt 600
atccttcaaa tgacaaccct ggaatttcca cattcgtctt acttaocgan ccccgaccct 660

```

```

<210> 93
<211> 1141
<212> DNA
<213> Homo sapiens

```

```

<400> 93
gcatgatgtc attgatttgg agtttctaag tcagtatatg tgogttggta atcttgaggt 60

```

aattttgaca	gatattgtca	gaatggcecca	cacagagatt	gcaacccaag	tgaggaaattc	120
tcagggttcca	acgatcccc	agagtcagtt	ctgggtttcc	gtggtgatgc	cagctctaaa	180
oggtaccccc	ttccccaggt	ggcccatccc	ctgcacccct	gcaccccaaa	cgagagccga	240
cgagcacggg	ggaggcggag	ctgaaggagg	agcggtctgc	aggccggaag	gcgagctgca	300
gcaccgoggg	gagtgggagt	cgagggtctg	ccccctcca	gccccatggt	cagcagcgcc	360
cacaacccca	acaaggcaga	gatcccagag	cggcggaagg	acagcacgag	caccccaac	420
aacctccctc	ctagcatgat	gacccgcagg	aacacctacg	tttgcacaga	acgcccgggg	480
gctgagcgcc	cgctactgtt	gccaaatggg	aaagaaaaca	gctcaggcac	cccaagggtg	540
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gggggtgggg	gtggtggggg	tgtgcagaat	ggggccctcg	cctctccac	actggcccat	720
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<210> 94
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 <212> DNA
 <213> Homo sapiens

<400> 94						
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<210> 95
 <211> 550
 <212> DNA
 <213> Homo sapiens

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<210> 96
 <211> 1456
 <212> DNA
 <213> Homo sapiens

<400> 96

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<210> 97

<211> 2277

<212> DNA

<213> Homo sapiens

<400> 97

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<210> 98
 <211> 455
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(455)
 <223> n = a,t,c or g

<400> 98						
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<210> 99
 <211> 1660
 <212> DNA
 <213> Homo sapiens

<400> 99						
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<211> 916
<212> DNA
<213> Homo sapiens
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<210> 101
<211> 445
<212> DNA
<213> Homo sapiens
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```
<210> 102
<211> 545
<212> DNA
<213> Homo sapiens
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<220>
<221> misc_feature
<222> (1) ... (545)
<223> n = a, t, c or g
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 cttacacatg aaatctccaa agatccagtt ttcgccactg gcatagtagt gaatcaggaa 480
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 gctgn 545

<210> 103
 <211> 410
 <212> DNA
 <213> Homo sapiens

<400> 103
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<210> 104
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 104
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 ccctcgaccc cgctgtgggg gccttgactg cctggggcca gccatccaca tcgccaactg 240
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 catoggcttc caggtccgcc agcgaagtgg cagcaaccct gctcccgcgc acggggggccg 360
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 gccatcttc tg 432

<210> 105
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 105
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396

<210> 106
<211> 432
<212> DNA
<213> Homo sapiens

<400> 106
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<210> 107
<211> 720
<212> DNA
<213> Homo sapiens

<400> 107
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<210> 108
<211> 629
<212> DNA
<213> Homo sapiens

<400> 108
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<210> 109
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 109
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<210> 110
 <211> 350
 <212> DNA
 <213> Homo sapiens

<400> 110
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<210> 111
 <211> 344
 <212> DNA
 <213> Homo sapiens

<400> 111
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<210> 112
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 112
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 aggacaacct ggtggagatc ccgcaggagc tcgcaaagga cctgttcaag ggcgtgttca 180
 ggggcacgtg cacggacatg gtgaaggatc tcatgaacgt catcctcctc atgttcaacc 240
 tcgtgctcaa gttcctcctc caggatcatg ggcaggcctg ggggccccct gggggcccg 300
 ggggtgcata tcacctcatg tttgaactca tgcagtgtt ctagtactac ttctagtact 360
 acttccaatt tt 372

<210> 113
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 113
 ggcacgagga tattatgaca cactacgaca gactggtgga cgaataggcc ctaaagtctg 60
 ggaaacaaag gtatgagaag atgatcagtg gtatgtacct gggtgaaatc gtccgcaaca 120
 tcttaaatcga ctttaccgaag aagggaattcc tcttacgagg gcagatttct gagatgctga 180
 agaccogtgg cattttttta acctttcttc tttctaactt cttgattgta tgtgtattac 240
 tgttttatgt ttcattttat ctttttcaat cttgtattaa ttttgttctc tagactattt 300
 ttgtttctta ttataattta tgatctattt ctttattttt cttattttatg ttttgtagta 360
 gtcttctctt ccaatcg 377

<210> 114
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 114
 aagcaacaag ccgtccctga gccacattcc tctacgacga ctccacagga acaggagcag 60
 aattggtatg gacaggactt gcttaatttg caacagagga caaaagtcca ttgcccagga 120
 cacaaaacgg gtccctgcggg agcaaaggat acaccagagc cggtaaaaaa agaatttact 180
 gtacctgccca ccagtcaagg ccataatct cctttttctg aggagcccc attgccacct 240
 tcaaattgagg aagtgccacc tactctccca ccttaggaac cccagtctga ggaccataa 300
 aaaaatgcct agttaagca aatgcatgct gctacaacac actgtcagca gcaccagcaa 360
 catcaagtgc gctgccagta tcatggaata atgcag 396

<210> 115
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 115
 cattacagta attattctcc ccctgtttcc acaggggtgag aaaaaagaaa cctggattta 60
 cctctgggtt gagaatttct agcgttgatt tottataatg attcatgttc tccacgccta 120
 aattggacac tgtgaggaag ccaaactcga tccgagagtc tttttctaatt ggccagtact 180
 ggccacactt tctcctgcgg ccttcctcaa agctgtagac tcacagagcc cggcgcttct 240
 gtgttactcc ccaatggcaa ctccaaacca tagatggata gctccctgct catctttcca 300
 catccctgct attcagtata gtccgtggac caatcacacc agcatogtat ggcagagcgt 360
 tagaaacatg aatctgcatg tcaacgagat cccacgtga g 401

<210> 116
 <211> 667
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (667)
 <223> n = a, t, c or g

<400> 116
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 agggaaagaaa acattttcca aggatagtaa gtattctacg aattcctagc cagcttttgt 120
 cttcttgaaa attatcacca taaggaaaga attaaattac actggcattt ataagggatt 180
 aggcacacca ggtaccctat gcttcaatcc tgtcctttca tcttccttcc atttctctgt 240
 cttgggacat ggtaatttgg aggtgagacc accctttctt gtccctgaca aagaatcctg 300
 tcatctgcag aatctctatt ctccagctg gctcctagca gggtagggag agacacagaa 360
 agagagagtc accgttccac ttcagatgct gcaagttgct gtagaggagc tgccccgcgc 420
 tcccagccgc ccgggtgaac tcctgcaaac tcatgctgca gaggtgctcg ccgttgatgt 480
 cgaactcttg gaaagggata caattggcat ccagctgggt ggtgtccagg aagtgtctga 540
 gccactccca cacttggtac tttgtccagt actgaagatg aatntcatgc gactggcctg 600
 caagaaaccc actggaaaca ttgcacgtgg agtagctgtc tgttcaggct gggcgctgtg 660
 gagggag 667

<210> 117
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 117
 ggcacgagtg gaggtccaaa acgtgttctc gtgactgagc ggtttccttg gcagaatcca 60
 ttacctgtaa atagaggcca ggctcagcgg gtcttgggtc cttcaaatto tttccagcgc 120
 gttccttttg aagcacaaaa gcttgtctcc agtcacaagc cgggtcagaa tcagaagcat 180
 aagcaattgc aggcaaccag tgtacctcat cctgtctgca tgccactgaa taacacccaa 240
 aagagcaagc agcccctgcc atcggcacct gaaaataatc ctgaggagga actggcttca 300
 gatccgaaca atgaagaatc attatagagg ccgtgggctt tggaagactt tgaaattggg 360
 cgccctctgg gtaaaggaaa g 381

<210> 118
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 118
 ttacctactt atggctatga gggaaccctc ccttttatga aaagaatgat ggcggcctct 60
 ttgagctgat tttgaggggc aaggacgagt ttaactctcc ttactgggac gacatgtctg 120
 actctgccaa acatttcatc cggcccttga cggggaggga cccctagaaa ccattccctt 180
 gtgaccagcc cttgcagcac ccattggattg agggacatac ctgtctagat aataatatcc 240
 accaggccgc gagcgagcca atcaacaata actttgccga gagcaagagg aatctagcat 300
 tccttgccac ggggtgtgtg cggcacatga ggaaactgtt tatgggcgcc aacctagagg 360
 ggctggggcc caggtgagc catgg 385

<210> 119
 <211> 398
 <212> DNA
 <213> Homo sapiens

<400> 119
 ggcacgacga gcaaacacca ctagcttgcc cggagttaa taaggaggacc ttttgaccac 60
 gatctgaaac ccaatgctgc cagcagagat cagttaaata ttattgtgag ttatccacca 120
 accaagcaac ttacatatga agaacaagat cttggttggg agtttagata ttatcttaac 180
 aatcaagaaa aagccttgac aaaattcttg aaatgggtta attgggatct acctcaagag 240
 gccaaacagg ccttgggaact tctgggaaaa tggaagccga tggatgtaaa ggactccttg 300
 gagctgttat cctctcatta caccaaccca actgtgaggg gttatgctgt tgcccggttg 360

cgacaggccg atgatgagga tttgttgatg tacctatt

398

<210> 120
 <211> 1156
 <212> DNA
 <213> Homo sapiens

<400> 120

tcatgggcca	gtctcctgca	gtgtagggct	actttgtcct	ggcaggaatg	aactctgctg	60
gcctttcatt	tgggtggagga	gcccggaaagt	accttgccga	atggatggta	catggttatc	120
cctcagaaaa	cgtttgggaa	ttggacctga	aacgttttgg	agccctccag	agcagccgca	180
cctttctgcg	ccaccgggtc	atggaaagtca	tgcctttgat	gtatgatctg	aagggtcccc	240
actgggactt	ccagaccggt	aggcagttac	gcacctctcc	tctctacgac	cggtctggatg	300
cacagggagc	caggtggatg	gagaaacatg	gatttgagag	gcaaagtac	tttgttcccc	360
ccgacaagga	cctcctggca	ttggagcaga	gcaagacttt	ctataagcca	gattggtttg	420
acatcgtgga	gtctgaagtc	aagtgcctgta	aggaagctgt	gtgtgtcatt	gacatgtcct	480
ctttcacaga	gtttgagata	acatccactg	gggatcaggc	attagaagtt	ctacagtacc	540
tcttctccaa	tgacctggat	gtgcctgtgg	gccacattgt	gcatactggc	atgctcaacg	600
aggggtggagg	gtatgaaaat	gactgcagca	tagcacgact	gaacaagcgc	agtttcttca	660
tgatctctcc	aaccgaccag	caggtccact	gttgggcctg	gcttaagaaa	cacatgccga	720
aagacagcaa	cctgctcctg	gaggacgtca	cctggaagta	cacagccctc	aatctgattg	780
gccctcgagc	tgtggatgtg	ctgtctgagt	tgtcctatgc	ccctatgact	ccagaccact	840
tcccaagcct	cttttgcaag	gagatgagcg	tgggctatgc	aaatgggatc	cggtgtgatga	900
gcatgacgca	cacaggagag	ccaggattca	tgtctctacat	ccccatagag	tacagatggg	960
gcttcaccat	gttgtccacg	cttgtctcca	actcctgacc	tcaagtggtc	cacacacctc	1020
agcctcccaa	agtgtctggga	ttacaggcat	gagccactgt	gcctggcccc	agggcgacca	1080
cggaacggat	cagcgaggcc	aagtacacta	ccaccatctg	gtcattgggtc	ttcagggtaaa	1140
aggccttgac	gaactc					1156

<210> 121
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 121

gtgcacagtt	tttgctggtt	ggatgggac	acattttgtg	actcattgtc	ttgtagacga	60
atctcacaga	actagggcgg	accacatgtg	accagaactg	gccaaattcc	cccagcgtct	120
tgaaccacgg	ctgtttttac	atgcagtgtc	tatcaaagga	ctgtaccatc	ggctatgtgt	180
cccagagaaat	gctggctgca	cacacccata	ccgttgaaga	acatacaggg	acacatctac	240
agtacgtatc	atggcctgac	cacagtgtgc	ccgatgactc	ctccgacttt	gtggaatttg	300
aaaact						306

<210> 122
 <211> 425
 <212> DNA
 <213> Homo sapiens

<400> 122

aagggcagga	aggagaaggg	gccaagatga	agtgaaccct	tccttgttca	cagtaactct	60
gtggcttcag	actctaaaca	gagctttcca	tttggcttat	cttccaataa	aaagatttta	120
ctagggtctgt	tttcccttgt	atggacagaa	gtacttgagg	agcccaagga	ctttctctgt	180
gaaaccgagg	acttcaagac	tttgcactgt	acttgggatc	ctgggacgga	cactgccttg	240
gggtggtcta	aacaaccttc	ccaaagctac	actttatttg	aatcgtaagt	tggctctggt	300
tacattattg	acaacttctt	ccttgcttga	ggagcttggt	acaacatggc	aaaaatctac	360
acttagatgt	tgcaggaaat	ttgaacaaat	atttcagaac	cacctgccaa	ggtcaagagg	420

aaacc

425

<210> 123
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 123
 agctgctgcg ggagctccag gtctagtctt tactgctctg tgtattctgc tcttagaggc 60
 ccagcctctg tgactccgtt atctgcaggt attgggagat gcacagctaa gatgccagga 120
 ccacctggaa gcctagaaat ggcagcagcg ggatttgcc tggggatgga gcaaagtgc 180
 cccctgctgt agagcaagct gagaggggccc atgttgaaat gatagaaaaa cttaccttcc 240
 taaacctgca tacttcagaa aaggacaagg ggggaaacac tgccttgac ctcgctgcga 300
 agcatgggtca cagtctgca gtgcaggtgc tgctagccca gtggcaagac ataaatgaga 360
 tgaatgagaa gcagcaaac cctctgcatg tagctgctga tcgaggaa 408

<210> 124
 <211> 901
 <212> DNA
 <213> Homo sapiens

<400> 124
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 cagaccacaa gtttacgcct atcagaccta cacagaaaat cgcattcttg gagaggaaata 120
 gtcagcatca ccttgattga agggagagac ctcaaggcca tggattccaa cgggttgagc 180
 gatccctacg tgaagttccg gcttgggcat cagaagtaca agagcaagat tatgccaaaa 240
 acgttgaatc ctcagtggag ggaacaattt gatcttcacc tttatgaaga aagaggagga 300
 gtcattgata tcaactgcag ggacaaagat gctgggaaaa gggatgattt cattggcagg 360
 tgccagggtcg acctgtcagc cctcagtagg gaacagacgc acaagctgga gttgcagctg 420
 gaagaggggtg agggacacct ggtgctgctg gtcactctga cagcatcagc cacagtcagc 480
 atctctgacc tgtctgtcaa ctccctggag gaccagaagg aacgagagga gatattaaag 540
 agatatagcc cattgaggat atttcacaac ctgaaagatg tgggatttct ccaggtgaaa 600
 gtcacagag cggaagggtt aatggctgcc gacgtcactg gaaaaagtga cccattttgt 660
 gtggtagaac tgaacaacga tagactgcta acacatactg tctacaaaaa tctcaatcct 720
 gagtggaaata aagtcttcac gttgtaagta ggcatttctt tgggctctga atccaaaatt 780
 gtgttaaatt tgattatttt tgagggtttt aaaaaaaatg tgggtgttat tcttaactga 840
 ttcacaactc aatgcatctg gcctgccttt gctaacaaca atgaattttc ctctacctt 900
 c 901

<210> 125
 <211> 509
 <212> DNA
 <213> Homo sapiens

<400> 125
 acttgaaacg cctgctggaa ttcgccatga gcctcatatg gaccagtaac cattaggggg 60
 ggcccgaccc caattcacgc tatgctgagc cttagaagaa ctcactggcg atgacctgag 120
 ctcatgctga ctgtgaaaac tatgttgccct gtggaggctt ggacaacatc tgctctatat 180
 ataacttaaa gaccagagag ggaaatgtga gagtaagccg agagttgcca ggtcacacag 240
 ggtacttgtc ctgctgtcgt tttttagatg acagccaaat tgttacaagt tcaggagata 300
 caacttgctg tttatgggac atcgaaactg cccagcagac caccacattc actgggcatt 360
 ctggagatgt gatgagctct tctttgagtc ctgacatgag gacttttgtt tctggtgctt 420
 gtgatgcctc ttccaaatta tgggatattc gagatggaat gtgtagacag tctttcacgg 480
 gacatgtctc agatatcaat gctgtcagtc 509

<210> 126
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 126
 aaaaatcaga gaagagctgt gtttcctctc ttgctcaett tgggaacctc tgccaacggg 60
 actatgatgc gatgggtgaag ctggtggaaa cactggagat gctgcctacg tgtgatttgg 120
 ccgatcagca taacattaaa ttccactatg cgtttgcact gaataggtaa gaacgataat 180
 gtacgtacag gttttgaaac atgccaccca ttgaattgtg cttccttctt tcattcaaca 240
 tcgggtatga gccaggtcac gtgctaaatg ccaaggttat gaagatggac aagggtccagt 300
 ctttgtcctc agggactttg tatttggcat acacattcta gctgtgagat tgaacacatc 360
 aatccatcct aatagcttag

<210> 127
 <211> 497
 <212> DNA
 <213> Homo sapiens

<400> 127
 acggagtctc cactgctggt ccgaccatat ttaccttaca tcaccaagtc tgaactccac 60
 gccatcatga ccgccgggtt ctctaccatt gctggaagcg tgetaggtgc atacatttct 120
 tttgggggtc catcctccca cttgttaaca gcgtcagtta tgcagcacc tgcgtcattg 180
 gctgctgcta aactcttttg gcctgagaca gaaaaacctt aaataaccct caagaatgcc 240
 atgaaaatgg aaagtgtgga ttcagggaat cttctataag ctgcaacaca gggagcatcc 300
 tcctccatct ccctggtggc caacatcgct gtgaatctga ttgccttctt ggccctgctg 360
 tcttttatga attcagccct tgcctgggtt ggaaacatgt ttgactaccc acagctgagt 420
 tttgagctaa tctgctccta catcttcatg cccttttctt tcatgatggg agtggaatgg 480
 cccgacagct ttatggg

<210> 128
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(488)
 <223> n = a,t,c or g

<400> 128
 nggaaannng ggaggcccgga gtccnnnaat tganancctg cntgtttttg cagaactacn 60
 ggnnnggaan nnnngggncg acccacgcgt ncnnggatgn ncaaaagaca ttgaattgga 120
 tccttgctta gttccaagcg cctacaaagg ctagggaagg accagtaacc atgcgataaa 180
 ggaatagctc agcatagggt cagaaatgac actagccgct gacaacaaaa gaatactttt 240
 ccattttaac gcaaaagcaa aacaaaacac atgaaacctg gagcatgttg tatgaatagt 300
 aaggcacagg aatcagtttt taaaaatgta ctctgtaacc ccctgcact ttcagaaatg 360
 ccagacgtga aagctgaaga tgaagtggat ttttagagcaa gttcaatttc tgaagaagtg 420
 gctgtaggga gcatagctgc tacactgaag atgaagcaag gcccaatgac ccaggcgata 480
 aaccgagt

<210> 129
 <211> 395

<212> DNA

<213> Homo sapiens

<400> 129

ccgacgcgtg	gggccctacg	ctactggatc	ttcggcaggt	tcttatgcaa	catctgggcg	60
gcagtggatg	tgcggtgctg	caccgcgacc	atcatggggc	tctgcatcat	ctccatcgac	120
cgctacgttg	gcgtgagcta	cccgtgctgc	tacccaacca	ttgttaccca	aaggagggggt	180
ctcatggctc	tgctctgctg	atgggcactc	tccctgggtca	tatacatatg	acccctgtta	240
ggctggagge	atccggcccc	cgaggacgaa	accatctgcc	agatcaacga	ggagccgggc	300
tacgtgctct	tctcaacgcc	gggctccttc	tacctgcctc	tggccatcat	gctgggtcatg	360
aactgacgcg	tctacagggt	ggccaagacg	gagaa			395

<210> 130

<211> 714

<212> DNA

<213> Homo sapiens

<400> 130

cgacccacgc	gtccgtacga	aaattgtaaa	taggaagacg	acaatctatg	aaattcagga	60
taaaacagga	agtatggctg	tagtaggaaa	aggagaatgc	cacaatatcc	cctgtgaaaa	120
aggagataag	cttcgactct	tctgctttcg	actgagaaag	agggaaaaata	tgtcaaaact	180
gatgtcagaa	atgcatagtt	tcatccagat	acagaaaaat	acaaaccaga	gaagccatga	240
ctccaggagc	atggcactac	cccaggaaca	gagtcagcat	ccaaaacctt	cagaggccag	300
cacaacccta	cctgaaagcc	atctcaagac	tectcagatg	ccaccaacaa	ccccatccag	360
cagttccttc	accaagggtca	ccaaggacaa	ggatatcaaa	taactactgt	tcaatcttta	420
ctcaagtgtg	gaaattttgc	ctgaagtctc	ccacctaaaa	acctgatgcc	attggtaatg	480
atgtttatga	agataagatc	aaagcacaga	aaataatata	tgtatatata	tgtatatata	540
tctggttgaa	atactatata	tatatatata	tatataccag	ctattaattc	taggaaatgg	600
agtattaagg	gtgcatttta	tttcattagt	tttactttta	tgcattttct	tcatatcata	660
ttttgcattc	agaattttca	taatttgaaa	aaaaataaac	tttttttttc	ttaa	714

<210> 131

<211> 605

<212> DNA

<213> Homo sapiens

<400> 131

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ttatcaagtg	cttgctagcc	atggatgcca	actaacttot	tcaattgaag	gccggaggat	120
catatcgggt	tccaggagcc	tcttgagcag	gtcctggcaa	tcggccgaga	tgctcagatg	180
agtggggaag	gacaccccc	tctgctgctg	ccacagcatc	ttggggatgt	ctgtgtcgtc	240
aaaaggtagg	ctggcacaga	gcatgacata	caggaccaca	cccatgctcc	agacatcacc	300
ttttttgcta	tcgtggggaa	tgccctgcag	caacctgggg	gcagcatagg	ctgtactgcc	360
gcagaaggtc	tggtctcagct	cccgtgtgtga	cttgggcaac	accttggcaa	agccaaagtc	420
agtcagcttc	aggttgaagc	cctgcaacaa	ggcgttctca	catttgagggt	cccgtggggc	480
cacaccacag	ccatggcagt	agcggatggc	ctcaaccatc	tgacggaaga	gggccttggc	540
ccggctttca	ggcagtggcc	ccccattcag	cacgcagtca	aagacatccc	ctccctcagc	600
gagct						605

<210> 132

<211> 348

<212> DNA

<213> Homo sapiens

```

<400> 132
tgtatttcca gcacttactt tgggtgcttg cactagtag atgctcagta aatatttgta      60
gaccagatgg acgggtgggtt gtattctaag tcaaatgagg gaaaatacat attcataaat    120
ctcaaaaaca aataatagga gacttttaac tagtagcaaa gagtttgcta tattgcgggt    180
gtttgttttt tctgttacag ctggccaaga atgtaggaaa caatagtttt aatgatatta    240
tggaagcaaa tttaaccagc ccctcaccaa aaccaccccc ttcaagtgat atgtaagtat    300
ttctgatata ttgaactttt ttaaaccatt ctataattgt ttttctaa                 348

```

```

<210> 133
<211> 406
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1) ... (406)
<223> n = a,t,c or g

```

```

<400> 133
agcgaataca tattaaactg cttattcaaa agttgtctga tgtcccttaa gagggtcaga      60
acaatcagct atagaagoto acagaaatct gtgagaaaga aaagaaagaa ttcaagaaga    120
aaatggatga ccagagggcg gagaagatta ccgaagctta atccaaagac aaaagtcgga    180
tggaagagga gaagacagag atgatccggg catatattca ggaagtgggg cggatatatca    240
agagggttga agaagcgcaa agtaaacggc tagaaaaact ccgagagaaa cacaaggaaa    300
tacgtcagcc gatcctggat gaaaagccca aggggggaagg gtcctcctca ttcttgcggg    360
aaacttgcca tgaagatacc tcttggttcc ccaactttac tccccc                     406

```

```

<210> 134
<211> 1276
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1) ... (1276)
<223> n = a,t,c or g

```

```

<400> 134
caagaagtgt ccacagcagt aatggataaa gactagtttt aaatcctcaa agccctaaga      60
ggggcccccctt ggttgcccctt tgtgaatgcc agccccctta agagagtggg gtttgattaa    120
caaaaaaact gtggcccca gttggaaccct tgaccttttc ctcagataat ctgtgtatgt    180
acacagctaa cacagctctt tagattccct gttaagtgcac tcattcacat tcccttcttg    240
gatataaagt cattgctgtc tttttatttt tgaatatagta caagacaaag atttttaact    300
taacatgaaa aattcactct tttattttgg aaaaaaagtt aacttttcat actaacaac     360
agaacaagat ttaaggtaaa tttotttaaac attatocaga aaaataacaa gatttatagt    420
atctacttct ggtactaata tacacaaaag gccaaaacca tgcctattct gcagggtgtag    480
cttcgggtgct ctctgttca ggggcaggct cactgcccgc ttcttttctt tctttgcttc    540
ttttagattt tttgtgtttg tgtctcctgt gactatctcc ttcttcactt tcatggcgac    600
gtctactatt acttcagaga gacttatgtc tggtttcttc tttctccctg tgcgtctttt    660
ctctatgtcg ttcttctttt tctcgacttg ctctgtgacg ctcataacct ctttctgcat    720
attccctgta tctgtatcgt tcttcacgcg tgttgaaaac acttggtgta ggactgtgat    780
cacgctccct ctctctctct ctgggtgcgtt atctttctct gtcccgatca cggnnnnnnnn    840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn tctggcataa tagtcccact    900
gcttgctggg gtccacaaga ctaggccacg aaggagcaga accaggaaga tggggaaagg    960
caacattgcc atatggaaat gcacgtgcag aacgactatc ataaccagag gaatgtccac   1020
tttctattgt tggatataaga gatggaggtg gagcgctcgg tggaggagga aaaccgggtg   1080
gtggaatcag aggtggagca gtgctgacag tgggagnnnn nnnnnnnnnn nnnnnnnnnn   1140
nnnnnnnnnt gggaggagct cctgcaggga aaaaaggagg tggtttgcta aaattgttgt     1200

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<210> 135
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 135						
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gtcctccaga	gttgtgaatc	tgccctgact	cactatcgtc	ttgttgccaa	tcattgttgc	180
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gaaaatccag	gaatgaacag	tggaatgcta	caagaagatt	tgattcaata	ttaccagttc	300
ctagctgaaa	aaggtgatgt	acaagcacag	gttggctctg	gacaactgca	cctgcacgga	360
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<210> 136
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 136						
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caggccctcg	aggggctgat	cccagccaca	ggccaggcag	aggagctagc	agccaaagat	180
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gaagcgggtg	atgaggaccc	agaggaggaa	gaggacaaag	agtgcactct	ggagacagaa	360
gcgatgcagg	acaggaaatc	ggaaggggac	ggggacatgg	aaggagaagg	aaacacacaa	420
aagaatgagg	gcatgggagg	aggaagggtt	gtggctgtgg	aagtcttaca	cggaggtggg	480
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<210> 137
 <211> 3131
 <212> DNA
 <213> Homo sapiens

<400> 137						
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aactttctact	tgtccaaaca	actcgatgag	gcttctggcg	ccaacgacga	gattgtacaa	180
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agccagaagc	aaacgatgga	ggctctgaag	accacgtgca	ccatgctgga	ggaacaggtc	300
atggatttgg	aggccctaaa	cgatgagctg	ctagaaaaag	agcggcagtg	ggaggcctgg	360
aggagcgtcc	tgggtgatga	gaaatcccag	tttgagtgtc	gggttcgaga	gctgcagaga	420
atgctggaca	ccgagaaaca	gagcagggcg	agagccgac	agcggatcac	cgagtctcgc	480
caggtggtgg	agctggcagt	gaaggagcac	aaggctgaga	ttctcgctct	gcagcaggct	540
ctcaaagagc	agaagctgaa	ggccgagagc	ctctctgaca	agctcaatga	cctggagaag	600
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gagctcaaac	agaggcttct	ggaagagcaa	gccaaattac	agcagcagat	ggacctgcag	720
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caagccaaaa	tggaccaacc	tgctaaaaag	aaaaaggttc	ctctgcagta	caatgagctg	960

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ccacacccat	ccacgccagc	caccgcgagg	cagcagatcg	ccatgtctgc	catcgtgcgg	1140
tcgccagagc	accagcccag	tgccatgagc	ctgctggccc	cgccatccag	ccgcagaaag	1200
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tacttgctag	ctcccagctt	cctgcacaaa	cagcgtggg	tcaccgcctt	agaatcagtt	1860
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tcctgtctga	aactggaagg	tgatgaccgt	ctagacatga	actgcacgct	gcccttcagt	1980
gaccaggtgg	tggtggtggg	caccgaggaa	gggctctacg	ccctgaatgt	cttgaaaaac	2040
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ctgtgtttcc	acgaatttgg	agtgttcgtg	gattcttacg	gaagacgtag	ccgcacagac	2640
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gcccagagcgt	acctggacat	cccgaaccgc	cgctacctgg	gccctgccat	ttcctcagga	2820
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aataccacct	t					3131

<210> 138
 <211> 526
 <212> DNA
 <213> Homo sapiens

<400> 138	
aggtcgctcct	cagggcccag caccggagc tgggtcccca ccgaatccg gccctggcct 60
atgggctgct	ctgggctgct ctttggtttg ggtgcctctg tgctgtctcg gcggggcggc 120
agggaggctg	tgagcaagga gtggaaagtc tggcctccgg aggcgcgcgc ctcatgctgg 180
acctccacca	ggtggggccat gtaattcttg tccatgatgt tctgctccag agtctggggg 240
tcgtgggcca	ctgcctggtc caggaactgg aggagtgtgc tcatgctgga cacggggatg 300
ccaaacgact	gcaogaacag cagcagctgc tgcggctcca ggtcctgcag ggcggcgtcc 360
accaggcgga	gcacctcaga acggatcatg cgcagcttca gccagtcagg aagcagcagc 420
gcctcctccg	atgtgtccac caggaaggcg gtgggcagtg gcttctcctc cggaaaccag 480
atgtccagca	gcgcctggaa ctgcgtgtcg tcggctcgag gcggct 526

<210> 139
 <211> 376
 <212> DNA
 <213> Homo sapiens

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<400> 139
ttcttccctc aatgtcaaat tgtacatcat gtttcagatt acagagtaga actgaaagtt      60
gaattaggca ggcagggcac ttgctaggta gaaatgagtt tatagagacc aaagccttgg      120
ggtgtgcttg gttttcgctt tgttattatt tagtgctata ttttgagtct tctcaciaag      180
tggtttttgt ttttattgtc tgatgtttct ctactcctcc aggtgcccag atgactatca      240
tgagccaagc ttgtgcagaa aggtgtaaca taatgagact ggtggaccgt cgggtgggcag      300
ggattgccaa aggagtgggc acccagaaga ttattggaag ggtacatcta ggtgagcaaa      360
aggcactggg gcttgg

```

```

<210> 140
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (404)
<223> n = a,t,c or g

```

```

<400> 140
tcgagaggac caacaagtgc atcaagagc tcattatgga cgggaagaac ctcacgctg      60
cgacgaaaag tctgtcagtg gccacagcga agtttgcctc ttactcaga gactttaagt      120
ttgagtttat oggtgatgct gtgacagatg atgaacgatg catagatgct tccttacgtg      180
aattttcaaa ttttttgaag aatctggagg aacagagaga aattatgggt agttgagagg      240
ggtgtaaatt aataagtcag ctttcaaggg ggaaaaaaat ctggatttgg aagcttgctc      300
tggtagaagt tgtgaagcat ttatccctgg gtacagtagt gcattgtaat ggaaagatga      360
ggtttccgga gccctgattt ctagttcctt gagggtgctg accn

```

```

<210> 141
<211> 362
<212> DNA
<213> Homo sapiens

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```

<400> 141
ctcatcacca acaaagtttt tgtggcccga gagctgtcat gcctggatgt gcatctggac      60
agcacagggg gcaccgctgt ggttgacgat caagacaagc tggagctgga gctggtgctg      120
aaggggtcct atgaggacac acagacatcc ttcttgggca cagcctctgc cttccgcttc      180
cactacatgg cagccctata gacagagctg agcgggccc tgaggagctc caaaagcaat      240
ggctggaatg gggacaactc aactgggtac ctactgtgct ccctgaggcc cttgaccatt      300
gtgaaggagg tgactatgga tgttcctgct ccaaatgtaa ggggcctcaa ctggatggga      360
aa

```

```

<210> 142
<211> 406
<212> DNA
<213> Homo sapiens

```

```

<400> 142
aacaacccca gcaacccttc ccgtggatcc tagcccatga gtcctcgaac tacaatgggg      60
cggaggaggc agcgaagaag ggaacacaag agctcgttgt cgctagcctc cagcacgggtg      120
gggccggggc ggcagattgt gcacacggag accacggagg tegtgtctctg tggagacccc      180
ctcagcgggt ttggcctcca gctccagggc ggcattcttc ccaccagagc cctgtcctcc      240
ccaccctctg tgtgcttcat cgagcctgac agcccgctg agaggtgtgg gctgctgcag      300
gtggggggac gtgtcctgtc catcaatggc attgccaccg aggacgggac tatggaggaa      360

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gccaaaccagc tcctgcggga cgccgcgctg gccacaagg tcgtgg

406

<210> 143
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 143
 cagatgctta ggaacggggg agaccagaac acagtcctg attaccactt tgctgataga 60
 attcgggagc ttctgtgacc tacagaggat cagaagaatt gtatacctta ggatacatc 120
 ctcaggccaa gtgctttagg taacattgta gaagaagtga ctcacccctg tagcccaggt 180
 ccttgccctg ccaatgagct ctgtgaagta aaccgaaaag gatgtacatc tggagatccc 240
 tgtcttccat acttttgtgt gcaaggatgc aaactgggac aagcttctga ttccattgcc 300
 cgtcaaggga cactaatcca ggtgccatca tctgcagggg aagttgagtg ctataaaatc 360
 tgttcatgtg gacaaagtgg actcttagaa aactgcatgg aaatgcactg tatggacctt 420
 cccaccgaca catccgccct tgtgaga 447

<210> 144
 <211> 404
 <212> DNA
 <213> Homo sapiens

<400> 144
 ccgggtcgac gatttcgtcc gaggtgagc caagcaggca ctgattcttg cagttagggtg 60
 ttccctgact ccttcccgtc agcgccagca gagccgctgc cctacttccg gcaggagcca 120
 caggagcctt acattgtgaa gaacaagcct gtggagctcc gctgccgcgc cttccccgcc 180
 acacagatct acttcaagtg caacggcgag tgggtcagcc agaacgacca cgtcacacag 240
 gaaggcctgg atgaggccac cggcctgcgg gtgcgcgagg tgcacatcga ggtgtcgcgg 300
 cagcaggtgg aggagctctt tgggctggag gattactggt gccagtgcgt ggcctggagc 360
 tccgcgggca ccaccaagag tcgccgagcc tacgtgcgca tcgc 404

<210> 145
 <211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (450)
 <223> n = a, t, c or g

<400> 145
 gctatatgac tgagcggagg aattccngt tgaagagaaa catgcagaca catggcgctc 60
 tgnctgttta tctgatttct tttttcatgc tgccaaagng ctgtgcanag aatgaaactg 120
 tggagatgcc atatctcttt ctgtgggaga tcactttgga aaaggggaatg gtctaacttg 180
 ggccgaaaaa gtccagtggt aaggagtgta aactcacctt gcattatgcc ccattgttca 240
 acatccggaa gacacttgta tccacagcag agaagttgga gttgtctgtt cccgatatac 300
 agatgtccga cttgtgaatg gcaaatccca gtgtgacggg caagtggaga tcaacgtgct 360
 tggacactgg ggctcactgt gtgacaccca ctgggaccca gaagatgccc gtgttctatg 420
 cagacagctc aactgtggga ctgctctctn 450

<210> 146
 <211> 650

<212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(650)
 <223> n = a,t,c or g

<400> 146
 ggaagaatta atacagatca aaaaaatatt tgaacattca aatcttttta ctaccagaga 60
 gacttcattt aaacagaaaag agtaggggaaac attccatatt caggaaacact ttagcctcta 120
 tgagcagtaa atgtaggttg ccattttgat aaacttctct ggcaactccat tttccccact 180
 aacgtacaga agcttcatga agtcatagac tatgttgtct tgttcagcca tagcccccto 240
 cagcatctgg caggctgcca ggcaacataa caggctacttg gcaaataactt gaatgggtga 300
 ggcaactctag gcaggccacc agcccaactta cgtctcatca aacagggggtt ccaaggtctt 360
 ccgcttcact gaagtcttct tacgacatgc ccacttcctt tctggcaaca agtagacacg 420
 gacgtaggga tcagctccac tggctgggtac atgggtgttag gttctcgcag ccattgatta 480
 gcacgctgag gcagcgcgca gacacacata gcgcaactgtg agctgaatct caccagctg 540
 ccgtcgcctg aggtcccccac cttcattgttg angcgatata tgccagtcaa gcaagagagg 600
 ccangagttg agnaagacat gctnaggagcc agcctctggn ggccagnгаа 650

<210> 147
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 147
 gaacgtctgg tcctaaccag tgagcactgt ttagtactga ccctcttctg gccatcatgg 60
 acctaaccaca cactgctgct ttcccgtcag catgtgcggc ggctacctaa gctgacctat 120
 gctgagcatg atcatctagc ctccatcatg aataagctct tgaccaacta tgacaacctt 180
 tttgagacgt ccgttaccta ctccatgggc tagcatgggg ctcccacagg atcagaggct 240
 gggggccaaact ggaaccattg atagctgcac gctcattact accctccgct cctgcgctct 300
 gacactgtcc ggaattcat ggttggatca caaatgcttg ctccggctca gagggacctc 360
 acccttgagc ag 372

<210> 148
 <211> 568
 <212> DNA
 <213> Homo sapiens

<400> 148
 ctgattacga attccatgtc cgtacctgta catcgtggag actcgaaata ccctgccggtt 60
 acaccgctta cgccacttgc gtgcccaccg cgacaatcaa cggtagcgca aaagagattc 120
 cgctcaacag tgccctgtttc agtccggttt tgacactttt caccgggttg gtatcttgct 180
 gtacggtagc cgtctcatcg ctacgcttga gggtaagcgc ttgttgcatc aacgcttctg 240
 catggcgaat cggctcggca acaggcactg aaagcgcggg aatgccatta aaacgctcac 300
 tctccttgat ggcgacttca gccgcaaaaa tacaggcggg tgcaactattg agttgatccg 360
 ccgttaaacy cccttcaatg ccgttagcgc cttgtttttc aacgtaacaa tttacgccga 420
 gtttgcgctc ggctttttcc agatattccg cagccatata ggtgtgagca ataccgcgcg 480
 gacaggccgt tacgcagacg atagttggcg cgttggaaaa agaggcagaa ggttgcgctg 540
 ctcccttgct atccagcgcc gagagcaa 568

<210> 149
 <211> 609
 <212> DNA

<213> Homo sapiens

<400> 149

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tccccgtgtc	catcatgatt	tccgtgtaacg	cctgcacggg	gacggaagca	ccacgcactt	120
ctttccagct	gtgatatcgt	aattcatcgg	caaccggacg	taacacttcg	cggtccgctt	180
tttgtgcagc	atcaaaattt	tccgtgcccc	gattacgacg	ggcaaaatag	cgttccagcc	240
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ccagttcagt	actggctccg	cctatatcca	ccaccaggcg	ctgatcggca	ccaccagtgg	360
tgtgagcaac	gccctgataa	atcagacgtg	cttcctcttc	accgctgac	acctgtaccg	420
gacaaccgag	aatttcctgc	gctttggcaa	taaaatcacc	cgcattgacg	gcaaggcgta	480
acgtcgccgt	agcgacaacg	cgaatttgcg	agggaggaat	atcttgcaga	cgttcagcaa	540
acaggcgcaa	acattgccaa	ccgcgctcca	ttgcttcatt	ggagagggca	ttttcgctat	600
tcaggccag						609

<210> 150

<211> 750

<212> DNA

<213> Homo sapiens

<400> 150

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tgtcttagat	gagcaaacct	agcaggctcc	tcactcttatg	cctccaccat	tcttggtaga	120
tgtagatgga	aatcctcatc	caaccaagta	tcagagatta	gtaccaggcc	gagaaaatcc	180
tgcagatgaa	catttgatcc	cacagctggg	ctatgtggca	acaagtgatg	gagagggtat	240
tgaacaaatt	ataagcctgc	aaaccaatga	taatgatgaa	cgcagcccag	aatcgagtat	300
tcttgatgga	atgataagac	agttgcagca	gcagcaagat	cagagaatgg	gagcagatca	360
ggatactatt	ccaagaggac	tttcaaattg	tgaagaaaca	ccccggagag	gttttagaag	420
gctgagctta	gacattcagt	cccctccaaa	tattggtctg	cgtcgtagtg	gacaagttag	480
aggtgttcgt	cagatgcac	aaaacgctcc	acgcagtcag	attgctacag	aacgtgacct	540
gcaggcttgg	aaacgaagag	tggttgtacc	agaggtacca	ctaggcatat	ttaggaagct	600
ggaagacttc	cgattagaga	aaggtgaaga	ggaaagaaat	ctttatataa	taggaagaaa	660
aagaaagact	cttcagctct	cacataagtc	ggattcagtg	ggtttgggtat	cacagtctag	720
accaaggaca	tgtaggcgta	aatatccgaa				750

<210> 151

<211> 810

<212> DNA

<213> Homo sapiens

<400> 151

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tgatttttaa	agatcagcaa	acttaaagat	acagcaatag	aaactttcca	aaatggagta	120
cagaaggaaa	aaaagactag	ggaaaaacaa	tacaaatata	aaccacaatg	caaaataaat	180
acaaaacagt	acaaaaacaa	tacaaaacaa	taccaaaaaa	caaaaaggcc	atggaaatgc	240
aaattaaaaa	acagtttcag	gacacttgca	aagtacagac	caaacagtat	aaagcactca	300
agaatcacca	gttggaggtt	actccaaaga	atgagcacia	aacaatctta	aagacactga	360
aagatgagca	gacaagaaaa	cttgccattt	tggcagagca	gtatgaacag	agtataaatg	420
aaatgatggc	ctctcaagcg	ttacggctag	atgaggctca	agaagcagaa	tgccaggcct	480
tgagggtaca	gctccagcag	gaaatggagc	tgctcaacgc	ctaccagagc	aaaatcaaga	540
tgcaaacaga	ggcacaacat	gaacgtgagc	tccagaagct	agagcagaga	gtgtctctgc	600
gcagagcaca	ccttgagcag	aagattgaag	aggagctggc	tgcccttcag	aaggaacgca	660
gcgagagaa	aaagaacctt	ttggaaaggc	aagagcgaga	gattgaaact	tttgacatgg	720
agagcctcag	aatgggattt	gggaatttgg	ttacattaga	ttttcctaag	gaggactaca	780
gatgagatta	aattttttgc	catttacaaa				810

<210> 152
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 152
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 cctcaccaac ctgtctgggc ggagtgacaa actccggcag aagatcttta aggagagggc 120
 cttgccagac atcgagaact acatgtttga gaatcatgat cagctgcggc aggcggccac 180
 cgagtgcatt tgcaacatgg tgctccacaa ggaggtacag gaaagggtct tggctgacgg 240
 gaatgaccgg ctgaagctgg tgggtctgct ctgcggggag gatgatgata aggtgcagaa 300
 tgcggctgca ggggctctgg ccatgctgac agcagcacac aagaaactgt gcctcaagat 360
 gactcaagtg acaaccc 377

<210> 153
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 153
 gcgtaaccaga gcttgoggct ggagtaacct cagatccac cggtcagcgg cgcctacacg 60
 actgcctgcg tcctcaccag cgccgcccgt cagttggaat tgatcacacc ttttcagttg 120
 tacttcattc ctgaattaat ctttaaaccac tttcaaatat ggagattaat caccaacttc 180
 ttattttttg tgccatttgg atttaatttc ttactataca tgatttttct atatacttaa 240
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 gcttggtttt ttactattct catc 324

<210> 154
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 154
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 agacaatggc tgcatagatg acatccggac ccgatacgac acggaggtgg atgaggggtc 120
 cttgaatcct ggcaagcaga gatacgagaa aatgaccagt gggatgtact tgggggagat 180
 tgtgcggcag atcctgatcg acctgaccaa gcagggtctc ctctccagag ggcagatttc 240
 agagcgtctc cggaccaggg gcatcttcga aaccaagttc ctgtcccaga tcgaaagcga 300
 tcggctggcc cttctccagg tcaggaggat tctgcagcag ctgggcctgg acag 354

<210> 155
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 155
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 gttccagaat gattttgaaa aagcttgta agcaaaatct gaagctctcg ttcttcggga 120
 aaagagtacc cttgaaagaa ttcacaagca ccaagagatt gaacaaaaag aaatttatgc 180
 tcaaaggcaa cttttactaa aagatatgga tttgctaaga ggaagagaag cagagctgaa 240
 gcaaagagtt gaagcttttg aatcgtatca acttgaactg aaggatgact acatcattag 300
 aacctatcga ctgattgaag acgataggat caatatataa atatctggtc attggcaaga 360
 gagcccatag ctattactca aataaggagg acctctatca ttctggacat cgg 413

<210> 156
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 156
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 agtcctgctg ctgattgcct cctagaaaat gaattggatg aagacatgca tcagaaaatt 120
 gcaagggaga tgaacctctc tgaactgct tttatccgaa aactgcaccc gacagacaac 180
 tttgcacaaa gatcctgctt tggactgata tggtttacac caacgaccga tttacaaatc 240
 ttgacatcat ccatactacc ttcaatactc taaccttatt tactacatat ccctaataca 300
 tcattctacc tttctacata accaactcct tactctttat ctctattaat attccacata 360
 cctcatcata aatcttcctt ctatactcct tatacactcc tacacattcc t 411

<210> 157
 <211> 652
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(652)
 <223> n = a,t,c or g

<400> 157
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 gtggcaagt ctaaaatcacat accctctatg tacattctaa tcttggtcat tctctacagg 120
 tacaacaata tacacattca ctaccccaac tcaccatttc ctggcagcta aaatgacagg 180
 atcttctcta caacttatcc ccaccccat cagtcatacc caccttctgg aagtcagatc 240
 cttcagggtga ttgcctactg gccacaaggg caccatcat ttccgtggcc tctgtgggtt 300
 ctatccctgc ctttctgggg gcagaaatgt ctgotgcagt tectcctttt ggaaatctga 360
 agacttttgg aattgccctt gtgtgtgctt cttattgtgc atatgagtga agaaatcaaa 420
 catggtccca cagatggtgt tgcagtcttt gcaccagtga ttgccagcat cataatactc 480
 ataagcagca gtgggctgat ccaactgctt agtggctgac tgggggcttt cggcaggctt 540
 ggggctctta gtacgaaact tctcattgtt tacttttgat tcctagaggg gnaaaatctg 600
 tacttacaag gaattcaagg caatctagac ttgtcttctg ttagaaatag ta 652

<210> 158
 <211> 423
 <212> DNA
 <213> Homo sapiens

<400> 158
 actacgcata ggctgaacgt gactgcggaa ccgccatgca ettccatgcc tatttactgg 60
 atgcctgatg tgccgcacag gtgcacgact gctaatacat gccagtgga cctgactgac 120
 tactgtgctc agaacggctt ctactgctg gtgtacggat tcctgcccta cggctccctg 180
 gaggaccgtc tccactgcca gaccagggcc tgccacctc tctcctggcc tcagcgactg 240
 gacattcttc tgggtacagc cggggcaatt cagtttctac atcaggacag cccagcctc 300
 atccatggag acatcaagag ttccaacgtg cttctggatg agaggtgac acccaagctg 360
 ggagactttg gcctggcccg gttcagccgc tttgccgggt ccagcccat ccagagcagc 420
 atg 423

<210> 159
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 159
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 tgcctgtcga ggagaaggcc gatgtgctgg cccggggacc cctgaaccag acggcgctgc 180
 acctggctgc cggccacggg cactcgagg tggaggagga gttggtcagc gccgatgtca 240
 ttgacctgtt cgacgagcag gggctcagcg cgctgcacct ggccgcccag ggccggcacg 300
 cacagacggg ggagactctg ctgaggcatg gtgcccacat caacctgcag agcctcaagt 360
 tccagggcgg ccatggcccc gccgccacgc tcctgcgggtg aagcaagacc tagctggctg 420

<210> 160
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 160
 aaagtttctg aaagaccttg agaaacagta caacaagag gaacctcact taagtgaat 60
 aggatcttgc tttcttcaaa atcaagaggg ctttgccatc tattccgagt actgcaacaa 120
 ccaccgggc gcctgcctgg agctcgccaa cctcatgaag cagggcaagt acagacattt 180
 ctttgaagcc tgcgcctgc tgcagcagat gattgacatc gccatcgacg ggttcctgct 240
 cacaccagt cagaagatct gcaaatacc gctgcagctg gccgagctgc tcaagtatac 300
 cacacaggaa cacgtgatt acagcaacat aaaggcagca tatgaggcca tgaagaatgt 360
 ggcctgtctg atcaacgagc gcaagcgcaa gctggagagc atcgacaaga tagctcg 417

<210> 161
 <211> 770
 <212> DNA
 <213> Homo sapiens

<400> 161
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 gctgtttctc ccattcttta cagctcaccg gatgtaaaag aactctggct agagaccctc 120
 caaggacaga ggcacagcca cacgggagtg aaatccaccc ctggacagtc agccgcaata 180
 ctgatgaagc tgagaagcag ccacaatgct tcaaaaacac taaacgccaa taatatggag 240
 aactaatcg aatgtcaatc agaggggtgat atcaaggaac atcccctgtt ggcacatgt 300
 gagagtgaag acagtatttg ccagctcatt gaagttaaga agagaaaagaa ggtgctgtcc 360
 tggccctttc tcatgagaag gctctccctt gcatcagatt tttctggggc tttggagaca 420
 gacttgaaag catcgctatt tgatcagccc ttgtcaatta tctgoggtga cagtgcaca 480
 ctcccagac ccatccagga cattctcact attctatgcc ttaaaggccc ttcaacggaa 540
 gggatattca ggagagcagc caacgagaaa gcccgtaagg agctgaagga ggagctcaac 600
 tctggggatg cgggtggatct ggagaggctc cccgtgcacc tcctcgctgt ggtctttaag 660
 gacttctca gaagtatccc ccggaagcta ctttcaagcg acctctttga ggagtggatg 720
 ggtgctctgg agatgcagga cagaggaggac agaatcgagg ccctgaaaca 770

<210> 162
 <211> 1165
 <212> DNA
 <213> Homo sapiens

<400> 162

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ttcgattctg	tgaacttgaa	aaatgatttg	ggaaggagtg	ggtaaatgag	gctaagtagg	120
aggcttttgt	ggattagatg	ataactggag	tggtttgggc	ataaaacttc	atagtgc aaa	180
atttcctagt	aaagcccttc	cttctttcct	ttttcccttc	tttttctttt	cggtctctcc	240
ctttctttat	gggcttttcc	taaacaacttt	cttcttttct	tatgacctgg	atctcagttt	300
cactatgcac	ttccctaacc	tattttctct	aatttcagtt	aaggtaaaaa	gtccacaggt	360
atcagaactg	gaacctgaag	ttaggttaaa	atgcggtgac	aaaagaagca	gacttcatta	420
tgttcttaag	agttcaggct	cttaagattt	attacccctt	tcttttgtcc	tctcctggag	480
aatagaatga	gccaaatca	gtccttactt	gagcaaatca	ctccagcatc	ctcagcatga	540
tcacagttat	gctttcccca	tccttgatgt	ttgcagttcc	agagagctga	ctcatttccg	600
ttgcatataa	gatcatcaaa	ccagattggg	ccagagcctt	ctccaaaatt	agatgaacca	660
gagaaactga	cagcacttcc	acattcaagt	tgtctacaaa	tgacagatgc	atgatctatg	720
ttgaagttat	catcacacac	tgttccccac	cgctccttga	atttgatctc	tattcttcca	780
gaacacatat	tccttccacg	cgtcagcctc	atttccaaat	tggatccatc	tggagcagag	840
aaaagaccag	agttcagaag	ttacattcat	ttagaagtga	ttttagaaaa	gaagtttcc	900
ctggacactt	gggattttat	gttgtcctta	aaatggtgcc	tgattttgga	cattgcccag	960
ctccacacag	tagagaattt	taatatgtta	aaatctagga	agcaattagg	atttttatct	1020
atatctactt	acaaaggaaa	atgtttacag	gttaaaagtt	ttaaactttc	tgttttgttt	1080
ccacctatta	ctaggacaga	tgtaaatact	cttttttcta	cagaaataga	taaattcgac	1140
tcaagttatt	taaatttgac	tcagg				1165

<210> 163
 <211> 419
 <212> DNA
 <213> Homo sapiens

tttttttttt	ttcaaatttt	aattaaaatc	tttattgaat	aaaaatgttt	cagactaggt	60
aagactaaga	aagcagaatg	ttttacatct	ctaaaaaata	ttaaagctaa	atctctataa	120
atgcagtaca	aagaaaagcc	tacagcttaa	gacacctctc	cctcccatcc	atacaatttg	180
gaatatcaac	tgtgtacaac	aaatgtactc	aagtttataa	tgtccccaaa	ttcagaattt	240
tctcctgttc	caatgacaac	accctttgct	ttgccacatc	tgaccagtgt	tccataaaag	300
gcaatgttac	ttctcgatgc	aagatctcca	ttagttgcag	ctggctgagg	agctgtcacc	360
ttagaacaag	gcgttgtctc	acctgtcaag	ctggactcat	caatggaaag	atccacagc	419

<210> 164
 <211> 597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(597)
 <223> n = a,t,c or g

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tctagcgag	gctagatatg	acattaacaa	ctcaattgtt	ggcaacaagg	ccccacgagg	120
cacaaaggca	cggaacttta	ggacactgct	gccattgggc	tttgagagcc	agccttgcc	180
aatcaaccaa	ggagatctct	tgtttcaggc	tgatttgggt	ggaagtgtga	tggccccagc	240
ccgcatgttt	acatgtctca	aaagaggatg	gccacacaa	taatctctcc	tttgtctttt	300
cccaggcaca	tcactgttag	tatgcaagcc	tatatgcatt	gaaactcagc	tctatgttat	360
tgtggcccag	ctgtttgggtg	gctctcacat	ctataagcga	gacagttttg	caaataaatt	420
cataaaaaatc	caggntattg	aaattctcaa	aatccgaaaa	cccaatgaca	ttgaaacatt	480
caagattgaa	aacaactggg	actttgttgt	tgctgacagt	tcaaaagctg	gttttactac	540
catttacaaa	tgggaacggg	aaacgggttt	ctactcccat	caatccttta	cacgggt	597

<210> 165
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 165
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 cgagctgttc cttaccatca tcgatggccc agccaaactac aacgtggacc tgcccttcat 120
 gtacagcatc acctatgctg cctttgccat catcgccaca ctgctcatgc tcaacctcct 180
 cattgccatg atggggcgaca ctcaactggcg agtggcccat gagcgggatg agctgtggag 240
 ggcccagatt gtggccacca cggatgatgct ggagcgggaag ctgcctcgct gcctgtggcc 300
 tcgctcggg atctgcggac gggagtatgg cctgggagac cgctggatcc tgcgggtgga 360
 agacaggcaa gatctcaacc ggcagcggat ccaacgctac gca 403

<210> 166
 <211> 1130
 <212> DNA
 <213> Homo sapiens

<400> 166
 gtgctgtcag aggggaaggtc tagggctgaa ggctgttgtt cagattcttt tgtccacgg 60
 caggaacggc ctgccagggg agcccgcgag ctcccagggc cttctgtctg cttcctctac 120
 ccagatatt cacttggctc tccaaattga ctacgctcca gataacattg actgggtaga 180
 aatgctattt aataaaaata tgggtgactga acgcttacag aatgtcatgg ttcttgagca 240
 gtgtttcagt gattcttctt ctctttatag attcctcacc tattcctacc tcttggcctt 300
 caatgtgtgg cttctgcttg cacccgtagc cctgtgctat gactggcagg tcggcagtat 360
 tcctctggta gagaccatat gggacatgag gaacttagcc accatcttct tggcggttgt 420
 gatggcctta ttgagcctgc actgcttagc agcctttaag agactggagc acaaggagg 480
 tttagtggg ttgttgttcc tgggtgtccc gttcattcca gccagcaacc tcttcttcag 540
 ggtgggtttt gtgggtggcg agagagtcct ttacatgcct agcatgggct actgcatcct 600
 ttttgtgcat ggaactgagca agctctgcac ttggctgaat cgatgtgggg ccaccaccct 660
 gattgtgtcc actgtgttgc tgcctgttgc tttctcttgg aaaactgtga aacagaatga 720
 aatttggctg tcaagagagt ccctattcag gtctggagtt caaactctgc ccacaaatgc 780
 caaggttcac tacaactatg ccaatttcct gaaggaccaa ggtcggaaca aggaagcgat 840
 ctaccactac agaacagctc tcaataataa taaagcttgg gattatctat gctggagatt 900
 cagaaaaaca ctgacagatc tgccatagac ctccagagct ctccgactgt tcggttaccc 960
 tggagaagg tcttaacatt ctaccttgtg tgatgggagt agaaagtcca gagaccaccc 1020
 aacaagtcag cccttcctac acaaaaactc ccaagaaatg cctcagctaa taagccccga 1080
 aagagaaata gtgattctcc ctgaataaag tcaagataat aatgtgtaaa 1130

<210> 167
 <211> 695
 <212> DNA
 <213> Homo sapiens

<400> 167
 cgtcgacttt tttttccttg ggaagcagga gtttattttt atccttttgt aagtattaac 60
 tcggtaatac caacaaacac ggagcaatct caatgctgtt tatccggagg acagtctgcg 120
 gggtegtgac gattcttttc ttcttgaagt ttttcctttt cctgaatctc ataatgatc 180
 ttggccatga ttctgtcttt tcaatgactg tggtttctac tcgaacaaga tcttttccga 240
 ggagtggctt gccaaagcagc gtgaagtgtg ctgccccaac cagcaggacc ttctccagtc 300
 gaattctctc tccacacgca aggtctagtt catttccaat taagatcagg tcttcagagg 360
 tcaccttcca ctggcggctg gcaaagtgc ccacggcaaa gagcctgcca tactgccccg 420
 tgacgatcat ctcatcacc ttcttcacga cctctgcatg gtgtctggtc tctcaactg 480
 ggtctggcag aacaacttct ggccaagggt gtgaactcag ggatgtttta ggaacatatc 540
 ctggtagata tgaagtgtc tgtgaattga accttcgaga agcagaccaa agggaggctg 600

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ctccggggccc cgaaggtctc aggatgctgt ggctgcacgc ggacgccagc cgcctaagg 660
tgaccgtcag ggaagatgct gccgatgccg ccgcc 695

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<210> 168
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = a,t,c or g

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<400> 168
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gcctctaaag gggcaggctc aggcacctca acgactacaa ggggcagctc ggggtgtcat 120
gccactacag gctcagggtga aggctaaggc ctctaaacct ctacaaatgc agattaaggc 180
acctccacga ctacggaggc cagccagggt gctcatgccca ctacaggcac aggttagggc 240
acctaggctt ctgcagggtac agtcccagggt atccaaaaag cagcaggccc agaccagac 300
atcagaacca caagatttgg accagggtacc agagggaattt cagggtcaag atcagggtact 360
ccgacn 366

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<210> 169
<211> 1053
<212> DNA
<213> Homo sapiens

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<400> 169
cagaacttgg aagacagaga agttttgaat ggtgtacaga cagaactact aacttcgcca 60
agaactaagg acacattgag tgatatgaca agaacagtggt agatttctgg ggaaggaggc 120
ccattgggaa tacatgtagt gcccttcttt tcctctctga gtggaaggat tctaggactc 180
ttcatccgag gcattgaaga caacagcagg tccaagcggg agggactatt tcacgaaaat 240
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aaccgtgaac agtatgaaaa gtcagtcatt ggctctctta acatttttgg taataatgat 420
ggcgttttga aaaccaaagt gccgcctcct gtccatggaa aatcgggact aaagacagca 480
aatctcacag gaaccgatag tcctgaaaca gatgcacag cttccctgca acaaaacag 540
agtccccgag taccagggtc gggaggaaaa ccctcctctc cctcactctc gcctctcatg 600
ggatttggca gcaataaaaa tgcaaaagaa attaagattg acctaaagaa aggcctgaa 660
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gtaaaaaaca ttttaccaaa gggagcagca ataaaagatg gccgcctaca atcaggggac 780
agaattttgg aggtaaatgg gagagatgtc accggacgaa cccagggaaga gcttgtggcc 840
atgctcagga gcaccaagca gggggagaca gcacgcgtgg tcattgcccg ccaagaagga 900
cattttctgc cccgagagtt ggtaatgttc agatctcagt ctactgaat ttttaatgcc 960
gagcttaata cactcaatga actcattata gctgagaaac gagttctaaa tcacaggctt 1020
cattcataac caaatttgaa tcacactcag ggt 1053

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<210> 170
<211> 363
<212> DNA
<213> Homo sapiens

```

```

<400> 170
ggctttctgg gaggaagggt ttgtaacgtc atccccaagc tgctctttgc tttcaccag 60
ggaactctca ctggacgatt ccacagcato ttcttcacac atgagagggc tgaggccagg 120

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gagaacaggc	gcagcctggg	aatctgtgtg	caaagcctgc	agcagttgtt	cgagcttctc	180
gttttaggact	gaacattttac	tggccacggc	atcagctaca	acggcatttt	ccaaggtttt	240
gtcatacgtc	ttttctactt	tggcaacgaa	gtcctttaca	gtttcacata	gcgtcttggc	300
agaagatatg	accactgcat	gttcatcaga	attgaggatt	tttgtaagat	gcgttgcaac	360
tgg						363

<210> 171
 <211> 675
 <212> DNA
 <213> Homo sapiens

<400> 171						
cagggtcgag	gcctgtaatt	ctccccagcc	atccatcgta	catctctcca	acaaacccag	60
atatgtgggc	tcttagactt	actccgatca	tgtaaattgc	atcaagagaa	gctccttctg	120
ccaacatctg	gtcaataaat	tccttcaaga	ccatggctgg	ggagaattac	aggcctcgac	180
cctgcaggcc	ctttattcaa	cgggaaacct	caccaagaca	gattagatcc	cagtgatgcg	240
cagtttgttg	atgtcatcca	ttccgacact	gatgcactgg	gctacaagga	gccattagga	300
aacatagact	tctacccaaa	tggaggattg	gatcaacctg	gctgccccaa	aacaatattg	360
ggaggatttc	agtattttaa	atgtgaccac	cagaggtctg	tatacctgta	cctgtcttcc	420
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gctgataatt	ggaaagacca	tctaaggggg	aaagatcctc	caatgacgaa	ggcattcttt	600
gacacagctg	aggagagccc	attctgcatg	tateattact	ttgtggatat	tataacatgg	660
aacaagaatg	taaga					675

<210> 172
 <211> 361
 <212> DNA
 <213> Homo sapiens

<400> 172						
agttaattca	acacaaatct	gcagtcgagt	atgctcaaag	tcacctcagc	ttggtgagca	60
tgtgcaagga	gtctcacaag	tggttcagagc	ccaagatgga	atggaagggtg	aaaattagga	120
gcgacgggac	acgggtacatc	acaaagagac	ccgtgcgaga	ccgaatcctg	aagggaacgtg	180
ccttaaagat	caaggaagag	cggagtggct	tgaccacaga	cgatgacacc	atgagcgaga	240
tgaaaatggg	gcgctactgg	agcaaagagg	agagaaagca	gcacctgggt	agggggcaaag	300
agcagcgccg	tcgccgtgag	ttcatgatgc	gaatcagggt	aaagtgtctc	aaggagagcc	360
c						361

<210> 173
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 173						
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gaacacatgg	cagctgcagg	tgctcttgca	ttgctgcaag	cttatgcttt	cttgcagtat	120
ctgagagacc	gattaacaaa	acaagagtte	cagacccttt	tctttttggg	tgtatcacta	180
gctgcagggtg	ctgtgttcct	tagtgtcatc	tatttgactt	atacagggtta	cattgcacca	240
tggagtggca	ggtttttattc	attgtgggat	actgggtatg	caaaaaataca	cattccaatt	300
attgcatcag	tgtctgagca	tcaacctacg	acttgggtgt	ctttcttctt	tgatctacat	360
attcttggat	gtaccttccc	agcaggc				387

<210> 174
 <211> 443
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(443)
 <223> n = a,t,c or g

<400> 174
 aggcnnnnnn nntttgctcg tcgtcactag tccgtgctgg ggaattcctg cggactactg 60
 cagtggagct tgactcttaa tgggtcccaa agcaaaaaag tctggcagta agaaaaagaa 120
 agtcaccaaa gctgaacgat tgaagctgct acaagaggag gaggagagac gactgaaaga 180
 ggaagaggaa gcccgtttga aatatgagaa agaagaaatg gaaaggcttg aaatacagcg 240
 aattgagaaa gaaaaatggc atcgacttga agcaaaagat ctagaaagga gaaatgaaga 300
 acttgaagaa ctttatttat tagagaggtg ttttcttgaa gcagagaaat tgaaacagga 360
 aactaaattg ctttctcagt ggaagcacta cattcaatgt gatgggagtc ctgatccttc 420
 agtagcccaa gaaatgaaca cgt 443

<210> 175
 <211> 486
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(486)
 <223> n = a,t,c or g

<400> 175
 agtcccgccc ncccgncaat gagttcatag gcaagnnncg nggaatttat gctcaagagt 60
 taaggctgag gttggaggcg ggtagtttgt ggtgctgtot aaccagggca ggggcagaga 120
 tctcaggaag ttgcctgagc agccctaact tgggtccagc cacaggaatt ctggccaatg 180
 gagatgcagc ccatagtcac agacatgggt acagtgcact ggggtggcca gagcagcaca 240
 gtgggtggc tctgtgccct cttcagggtc acacatgtag gtgttggggc cacagggcat 300
 ggggtgggtg gtgggagaag agtcctgtgt gggctccctc tgccctctcc agcaccaatg 360
 ccgatcatgt ctttgcccga gggggagagt aggaaggaaa gggaggtgca gagactgcag 420
 tttccatacc tggagcctgg gcatgagctg cccgccacca ccctgcttgc cttcctggct 480
 gctgtg 486

<210> 176
 <211> 587
 <212> DNA
 <213> Homo sapiens

<400> 176
 aagagggctc tgtgaatttc aagtttggg tcttttttgc caaagatggg cagctcactg 60
 atgatgagat gttcagcaat gaaattggaa gcgagccttt tcaaaaattt ttaaattcttc 120
 tgggtgacac aatcactcta aagggtgga cgggctaccg tggcggtctg gataccaaaa 180
 atgataccac agggatacat tcagtttata ctgtgtacca agggcatgag atcatgtttc 240
 atgtttccac catgttgcca tattccaaag agaacaaaca gcaggtggaa aggaaacgcc 300
 acattggaaa cgatatcgtc accatttgtt tccaagaagg agaggaatct tctcctgcct 360
 ttaagccttc catgatccgc tcccacttta cacatatttt tgcccttagt agatacaatc 420
 aacaaaatga caattacagg ctgaaaatat tttcagaaga gagcgtacca ctctttggcc 480
 ctcccttgcc aactccacca gtgtttacag accaccagga attcaggagc tttttgctag 540
 tgaaattaat taatggtgaa aaagccactt tggaaacccc ctgtatt 587

<210> 177
 <211> 427
 <212> DNA
 <213> Homo sapiens

<400> 177
 ggcacgagca ggaagcaatg aggcctcccca agaacacacc tgaggaaaag gacagggtgag 60
 cctggagggc cggccgcacc gtgggcctct gtgtctgggg agttgggtggc caggatcccg 120
 agtacctggg tgctgtgacg gggcgtggtt ggcctgggcg tgctgggtgt ttgggaatga 180
 ctccccatcg cccgcttctg cagcctgttc agccctgttg ggggtgcagtg tgtccactgc 240
 ctgcctgtgt gtgcgcgtgt gctcaggctc tcctcttctt cctttcaggc gcacggcggc 300
 cctacaggag ggtctgaggc gggcagtcct tgtgcgcgtg acgctggcgg agacgggtggc 360
 ctgcgtgtgg ccggcgctgc aggaactggc ccgggtgtgg aacctggcct gccggtcaga 420
 cctccag 427

<210> 178
 <211> 409
 <212> DNA
 <213> Homo sapiens

<400> 178
 ggctttgcag agcactctgg gggcggtgtg gctagggctt ctctcaact ctctctggaa 60
 ggttgagaa agcaaggacc aagtgtttca gccttcaca gcggcatctt cagagggagc 120
 tgtggtggaa atcttctgta atcactctgt gtccaatgct tacaacttct tctggtacct 180
 tcacttcccg ggatgtgcac caagactcct tgttaaaggc tcaaagcctt ctcagcaggg 240
 acgatacaac atgacctatg aacggttctc ttcacgcgtg ctcatcctcc aggtgcggga 300
 ggcagatgct gctgtttact actgtgctgt ggagggtgct aacacgcaga agctcatctt 360
 tgggactggg accagattac aagtctttcc aaatatccag aacctgac 409

<210> 179
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 179
 cccacgcgtt cgtccacgcg tccgccctct ctgttcgtcc acgcgtccgc aaaaggaggc 60
 gagaaggaag agggagatga tggccactat cttatgagaa cggaaatcaca tactggccta 120
 aaaaaggggg gaaatgctaa cctggtatct atgcttaaaa gaaacacgga gccaaagaag 180
 ggctcatacc attttgacct ggagcgactg cgtgctgccc acatactgtt tgagagggaa 240
 caggagcacc ttgcgcgggg aggcataatc atgcccctgc cccacacctt gcctctaccc 300
 gcctgttttg gttaaccaag cccaaggata ataatgtcat atattataag atctaagcct 360
 tccgctctca acccggtgat ggtccccgtg cacaagtcct atoctagg 408

<210> 180
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 180
 aaaccagcat aaagagagca attgaaacca cagatgttac aaggagcttt ggatgggata 60
 gcagtagggc ttggcagcag catgatgtac aagaactatg cagagtcatt tttgatgctt 120

tggaacagaa	atggaagcaa	acagaacagg	ctgatcttat	aaatgagcta	tatcaaggca	180
agctgaagga	ctacgtgaga	agtctggaat	gtgggttatga	gggctggcga	atcgacacat	240
atcttgatat	tccattggtc	atccgacctt	atgggtccag	ccaagcattt	gctagtgtgg	300
tgtgtacctt	tcacctgact	gcttgtgtat	ccttacacag	aatacataat	agcacagtgg	360
tataatctct	tgtaaggga	gtatcatcct	agatacacct			400

<210> 181
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 181	
ctatggcctg	ggggcacatt ttgggagact ctttatccag gggggcatta atgaaaatga 60
tttttatgac	ggagcgtggt gcgcgggaag aaatgacctc cagcagtgga ttgaagtgga 120
tgctcggcgc	ctgaccagat tcaactggtgt catcactcaa gggaggaact ccctctggct 180
gagtgcactgg	gtgacatcct ataagggtcat ggtgagcaat gacagccaca cgtgggtcac 240
tggtaagaat	ggatctggag acatgatatt tgagggaaac agtgagaagg agatccctgt 300
tctcaatgag	ctacccgtcc ccatggtggc ccgctacatc cgcataaacc ctgagtcctg 360
gtttgataat	gggagcatct gcattg 386

<210> 182
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 182	
agaacaaaa	cagatgtgta catcctgaat ttggctgtag cagatttact cttctatttc 60
actctgcctt	tttgggctgt taatgcagtt catgggtggg ttttagggaa aataatgtgc 120
aaaataactt	cagccttgta cacactaaac tttgtctctg gaatgcagtt tctggcttgt 180
atcagcatag	acagatatgt ggcagtaact aaagtcccca gccaatcagg agtgggaaaa 240
ccatgctgga	tcatctgttt ctgtgtctgg atggctgcca tcttgctgag cataccccag 300
ctgggttttt	atacagtaaa tgacaatgct aggtgcattc ccattttccc cegtaccta 360
ggaacatcaa	tgaaagcatt gattcaaatg ctagagatct gcattggatt ttagtagccc 420
tttcttatta	tgggggtgtg ctactttatc acagcaagga cactcatgaa gatgccaaac 480
attaaaatat	ctc 493

<210> 183
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 183	
cacgccaaag	ttggcacgag gctttcaaag tgaggaaaga aattcttact gttatctgtt 60
gtcttctggc	atthtgtatt ggcctgatat ttgtgcaacg ctctggaaat tactttgtta 120
caatgtttga	tgattattct gctacactgc ctctgctaatt ttagtgcatt ttggagaata 180
ttgctgtatg	ctttgtttat ggcataagata agtttatgga agacctaaaa gatatgctgg 240
gctttgctoc	cagcagatat tactactata tgtggaaata tatttctcct ctaatgctat 300
tatcattgct	aatagctagt gttgtgaata tgggattaag tctccttggc tataacgcat 360
ggattgaaga	taaggcatct gaagaatttc tgagctatcc aacatgggga ctggccgttt 420
gtgcctctct	ggatgtcttt gcaatactcc cgtccctgt agctttcatt ggtcgtcgtc 480
tctcccttat	agatgatgga gctggccctt tttgctccgc ggccataact accactgggt 540
gccggacgcc	atacctttta aatcataggg ctgtagaacc cacgcccttc cc 592

<210> 184
 <211> 632
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (632)
 <223> n = a,t,c or g

<400> 184
 ggcacgagct aacagtggct gcagctgacc gtgggcagcc accccaaagc tcagtcgtgc 60
 cagtcactgt cactgtacta gatgtcaatg acaaccacc tgtctttacc cgagcatcct 120
 accgtgtgac agtacctgag gacacacctg ttggagctga gctgctgcat gtagaggcct 180
 ctgacgtcga ccctggccct catggcctcg tgcgtttcac tgtcagctca ggcgacccat 240
 cagggctctt tgagctggat gagagctcag gcacottgct actggcccat gccctggact 300
 gtgagacca ggctcgacat cagctttag tagaggctgc tgaccctgct ggtgcacact 360
 ttgctttggc accagtgaac attgaggtcc aggatgtgaa tgatcatggc ccagccttcc 420
 cactgaactt actcagcacc agcgtggccg agaatcagcc tccaggcact ctctgacca 480
 ctctgcatgc aatcgacggg gatgctgggg cttttgggag gcttcgttac cacctgtngg 540
 aggctgggcc aggacctgag ggccgtgaag catttgcact ggacagctca acaggggag 600
 tgggtcaact tttagactcg cggaatgntt ga 632

<210> 185
 <211> 671
 <212> DNA
 <213> Homo sapiens

<400> 185
 cctagataaa ttactggacc gcatggaaaa ctacaacatt ttcaatgaat atattttaaa 60
 gcaagttgca gcaacatata tcaagcttgg gtggccgaaa aataatttta atggatctct 120
 tgttcaagca tcctaccaac atgaagaact acgtagagaa gttataatgc tggcctgcag 180
 ttttggcaac aagcactgtc accaacaggc atcaacactt atttcagatt ggatttccag 240
 caacaggaac agaataccac taaatgttag agacatcgta tactgtacag gagtgtcact 300
 actggatgag gatgtctggg aattcatatg gatgaaattc cattccacca cagcagtttc 360
 tgagaagaaa atattattgg aagccttaac ttgcagtgat gacaggaatt tattaacag 420
 gcttctaaat ctgtcactga attctgaggg ggtgctggat caagatgcaa ttgatgtcat 480
 aatccatgta gctcgaaatc cacatggtcg agacottgcc tggaagtttt tcagggataa 540
 atggaagata ttaaatacca ggattaggca gaaaacatta gaatttgact ttgcggagcc 600
 actcatttta gcttttccca taatacttta tacagccata gataatectc ctctggtccg 660
 tgaacatgag g 671

<210> 186
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 186
 gggcccaatg tgtgataaac actcagcttt tgcggaaaaa ttccatgctg gtttcatoga 60
 ctacattgtc catccattgt gggagacatg ggcccathtt gactgctctg atgctcaaga 120
 cattctttat acctagaag ataacaggaa ctgggttgac agcatgatac ctcaaagtcc 180
 ctaccacca ctggacgaac agaacaggga ctggcagggg ctgttggaga accttcatgt 240
 tgaactgact cttgatgagg aagattctga aggacccgaa aaggagggag agggacaaac 300
 ctatttcacc agctcaaaga cgctttgtgg gattgtacca caaaacactg attccctggg 360
 agagactggc atacacattt gcgcacatga caagtccccc 400

<210> 187
 <211> 486
 <212> DNA
 <213> Homo sapiens

<400> 187
 caatattgta gatgattttt tatgaggcta aacttatttc attttgcttg taccaaaatg 60
 aaaacaactt tcttatgtta catgatgcca ggctatatcc taggtaagggt catgggtggg 120
 gaatgttact ttaactggca ctttattcag tgctacaagt ttattaagag gtgtttcagg 180
 cattccaaca aaaatttaaa atataacttt gtggagttgc tattgattta attgcttttag 240
 agttgcttca gattcatttc ttgaaaattc ttcccttctg attatgattt tacctctgag 300
 gaatgccact caagaattta taattaggcc aggtgcagtg gcttacacct gtaatccaag 360
 cactttggga ggctgggtg ggtagtcac gaggtcggga gttcgggacc agcctggaca 420
 acatggogga acccatctt aaaaatacaa aaattagcca ggcttgctgg tgggtcgacg 480
 cagccg 486

<210> 188
 <211> 721
 <212> DNA
 <213> Homo sapiens

<400> 188
 ctgcccacct gggtggcgcg tggttacgc aacggtcact gggctcctgg gccgctcccg 60
 ggccagcgag ggctgcgaaa gaagttgtag catgcatacc acagaatcaa aaaatgaaca 120
 ttgaggagat gaaaacttcc aaacatctac aactcctcag ttttgttcta ggtgctgtct 180
 ctctgctgtg tgttgctccct tacatgatgg tgctgcaaga aaatggatat ggtgttgagg 240
 aaggcattcc aaccttatta atggctgcta gcagtatgga tgacattctg gctatccactg 300
 gattcaatac atgcttgagc atagtccttt cctcgggctg tgctagggtcc tctggctcta 360
 gaaacagcaa gagtctccgc accccacttg gaaccatag ogaaggatgt gatgacagta 420
 gcatttttag ccatctcgat cacagctcca aatggagctc tacttatggg cattctgggg 480
 cctaaaatgc ttacacacca ttatgatcca agcaaaataa aactgcaatt gtcaacatta 540
 gaacatcatt aaaaaattta cctgtcatca tctgcctgct tcttttaatg aattatttca 600
 catgacagaa gaatttttaa gtagaaatat gtagggcctg tacagaaaat ccaggattta 660
 gtaaacatgt gatttcagta cagggtcttt cttgaacttt ttactccaaa aaaaaaaaaa 720
 a 721

<210> 189
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 189
 ggaattcctg agttccaacc agatcaccca actgccaac accaccttcc ggcccatgcc 60
 caacctgcgc agcgtggacc tctogtaca caagctgcag gcgctcgcc cggacctctt 120
 ccacgggctg cggaggtcca ccacgctgca tatgcgggcc aacgccatcc agtttgtgcc 180
 cgtgcgcac tcacaggact gccgcagcct caagtctctc gacatcgat acaatcagct 240
 caagagtctg gcgcgcaact ctttcgcgg cttgtttaag ctacccgagc tgcaacctga 300
 gcacaacgac ttggtcaagg tgaacttcgc ccacttccc cgcctcatct cctgcactc 360
 gctctgcctg cggaggaaca aggtggccat tgtggtcagc tcgctggact gg 412

<210> 190
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = a,t,c or g

<400> 190
 tggttgagg aggtagatca ccctttctgc gggggacgat ttcgtcggtg gtaggctgct 60
 accatgaggt tgaatcagaa cacccttgctg cttgagagtt ttgggnncn ccgaccctac 120
 acctcggagc atgccccac gtaccaccag tggatgaaag cagatgagct tctgcgttgg 180
 acaacctccg agccgctgac cctggagcac gagtatgcc tgcagcgac ctggctggaa 240
 gatgcatacg agtgtacctt cattgtgctg gatgccgaga agcggcacgc ccagccaggc 300
 gccaccgaag agagctgcat ggtgggagat gtgaacctct tcctcacaga tctagaagac 360
 cttaccttgg gggagatcga ggtcttgatt gcagaacccc 400

<210> 191
 <211> 469
 <212> DNA
 <213> Homo sapiens

<400> 191
 tgtttgacc gcgctgcagg aattcggcac gagcggaatg ttatttatat caatgaaact 60
 cacacaagac accgcggatg gcttgcaaga cgcctttctt acgttctttt tattcaagag 120
 cgagatgtgc ataagggcat gtttgccacc aatgtgactg aaaatgtgct gaacagcagt 180
 agagtacaag aggcaattgc agaagtggct gctgaattaa accctgatgg ttctgcccag 240
 cagcaatcaa aagccgttaa caaagtga aaagaaagcta aaaggattct tcaagaaatg 300
 gttgccactg tctcaccggc aatgatcaga ctgactgggt ggggtgctgct aaaactgttc 360
 aacagcttct tttggaacat tcaaattcac aaaggtcaac ttgagatggg taaagctgca 420
 actgagacga atttgccgct tctgtttcta ccagttcata gatcccata 469

<210> 192
 <211> 475
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(475)
 <223> n = a,t,c or g

<400> 192
 aaggccgggg naatgagact gagagcctag caagnccggg ggaattcgcc tcctgctgac 60
 tggcacacag ctctatgggc gattcggctc tgccatcgca cccctgggag acctcgaccg 120
 ggatggctac aatgggtgagg gaagagagga gccctacttg ctgcagaggg gttaacagcc 180
 actcaaaaag catggagtgg gcctgagggc agccagaacc aggatgggtt ttaagcatat 240
 aagtatgtgg cttatacaca tgggggtgctg agtggagagc agatgggaga gttgaagact 300
 aattaggaag tgtttgcctt aatccaagca agagacaatg accacctgga tgtggatttt 360
 ggcatgtggag ttatagatgg gagtgacttc acagatatat aggactcgga ttattatgac 420
 ttggtgggag actggatgtg gggccagggg agaggatgga gttgggtgcc tgtgt 475

<210> 193
 <211> 400
 <212> DNA
 <213> Homo sapiens

```

<400> 193
agaatacttt ccaaactcca tatggaggtc acttttctcc acaatggatc tcggggatat 60
tggaattttat acatacagaa tattacaagc tctttcatat acgcattcaa aggggaattat 120
gcatagagat gtcaaaccat taaacattct ttgcaattcg cctagaaca aagttatcct 180
tgctgactgg ggcctggccg aattttatca cccaatgaga aagtattctg tccacgtcgc 240
gacaagatat tacaaatctc ccgaaattct tcttgattac gaatattacg attactcgtc 300
cgatatatgg gctgttgggg ttatactcct cgagctttta actctcaaac tccacgtttt 360
cgaaggcgga gacaacgagc aataaattga ctccattggg 400

```

```

<210> 194
<211> 409
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(409)
<223> n = a,t,c or g

```

```

<400> 194
tnnnnnccag ccctgagccc tgagacgctc gctttctggt tggcaatgga aagtcttagc 60
aggagttcca cgttcagctt ttctttggag aattctgatg gtgaaggaaa ggagtgggta 120
agatgccaac gtcagaagga agaccaggac aagaaaggag tgactgggtg acatcctata 180
aggatcatggg gagcaatgac agccacacgt gggctactgt taagaatgga tctggagaca 240
tgatatattga gggaaacagt gagaaggaga tccctgttct caatgagcta ccggtcccca 300
tgggggcccg ctacatccgc ataaaccctc agtcctgggt tgataatggg agcatctgca 360
tgagaatgga gatcctgggc tgcccactgc cagatcctaa taattatta 409

```

```

<210> 195
<211> 675
<212> DNA
<213> Homo sapiens

```

```

<400> 195
atgggggttg cctctgactg gaccaagagg attgagtacc agcctggctc cgggagcatg 60
ccctgttcc ccagcatcca cctggagacg tgcgatggag ccgtgtcttc cctocagatc 120
gtcacagagc tgcagactaa ttacattggg aagggttggt accgggagac ctactctgag 180
aaatcccttc aaaagtattg tggagcctcc tctggcatca ttgacctctt gccatccct 240
agcgtgcca ccaactggac tgcaggactg ctggtggaca gcagtgagat gatcttcaag 300
tttgacggca ggcagggtgc caaaatcccc gatgggattg tgccaagaa cctgaccgat 360
cagttcacca tcaccatgtg gatgaaacac ggcccagcc ctggtgtgag agccgagaag 420
gaaaccatcc tctgtactc agacaaaacc gaaatgaacc ggcatacta tgccctgtat 480
gtgcacaact gccgcctcgt ctttctcttg cggaaggact tcgaccaggc tgacaccttt 540
cgcccgcgagg agttccactg gaagctggat cagcaggtc tggccaaggt ggatggacag 600
ccaggtaaat ctattaccag gcagctccag gagatgcctg tgacaatcca gggcatctca 660
ctaaagccat cataa 675

```

```

<210> 196
<211> 396
<212> DNA
<213> Homo sapiens

```

```

<400> 196
tttcgtggga cgcctgtcag cgggctcacc aaccgggaca ccctggctgt catccgccac 60

```

```

ttccgcgagc ccattccgtct caagactgtg aaaccaggca aagtcattaa taaagatttg 120
cggcattacc taagtcttca gtttcaaaaa ggatcaattg accacaaact gcagcaagtg 180
atcagagata atctctactt gagaaccatt ccatgcacta caagggtccc cagggatgga 240
gaagtaccag gagtggatta taatttcatt tccgttgaac agttcaaagc actggaagag 300
agtggagcat tgttagaaag tgggacatat gatggaaact tctatggaac tcccaagcct 360
ccagcagaac ccagcccttt tcagccagat ccagtg 396

```

```

<210> 197
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(594)
<223> n = a,t,c or g

```

```

<400> 197
attcggcaca gggccgagga ctgctccggc cgcaccatgc nccagctggc cattgagatc 60
gggggtgcgag cctctgctctt cggagtcttc gtttttacag agtttttggg tccgttccag 120
agagtcatcc agccagaaga gatctggctc tataaaaatc ctttggggca atcagataac 180
atacctaccc gcctcatgtt tgcaatttct ttctcacac ccttggtgtg tatttgtgtg 240
gtgaaaaatta tccggcggaac agacaagact gaaattaagg aagccttctt agcgggtgtcc 300
ttggctcttg ctttgaatgg agtctgcaca aacactatta aattaatagt gggaagacct 360
cgccccgatt tcttttacgg ctgctttcca gatggagtga tgaactcgga aatgcattgc 420
acaggtgacc ccgatctggt gtccgagggc cgcaaaagct tccccagcat ccattcctcc 480
tttgctttt cgggccttgg cttcacgacg ttctacttgg cgggcaagct gcaactgttc 540
accgagagtg ggcggggaaa gagctggcgg ctctgtgctg ccattcctgcc cttg 594

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<210> 198
<211> 404
<212> DNA
<213> Homo sapiens

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```

<400> 198
aaacttgtag cactgtggta gtaatccctc gcatgttggg ggactttcta tcagagagca 60
agaccatttc tcttcctgag tgtgccacac agatgttttt cttcttgggc tttgcatcca 120
acaactgttt catcatggcc gctatgtcct acgaccgcta cacggccatc cacaaccac 180
tgcagtacca cacccttatg acaagaaaga tctgcttgca gatgatgatg gcttcttgga 240
tggttggggt cctgttttct ctgtgcatca tcgtcactgt attcaacttg tctctttgag 300
acttgaacac tatccagcac tatttctgtg atatctcacc agtgggtctcc cttgcttgta 360
attacacttt ctatcatgaa atggctattt ttgtgctctc tgcc 404

```

```

<210> 199
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = a,t,c or g

```

```

<400> 199
cttaccacga tgttctttat tcatgccctc tcagccattg aatccacat cctgctggcc 60

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atggcctttg	acogttatgt	ggccatctgc	caccactgc	gccatgctgc	agtgtcctaac	120
aatacagtaa	cagcccagat	tggcatctgt	gctgtggtcc	gggatccct	cttttttttc	180
ccactgcctc	tgtgatcaa	gcggctggcc	ttctgccact	ccaatgtcct	ctcgactcc	240
tattgtgtcc	accaggatgt	aatgaagttg	gcctatgcag	acactttgcc	caatgtggtg	300
tatggtctta	ctgccattct	gctggtcatg	ggcgnggaca	gaatgttcat	ctccttgctc	360
tatcttctga	taatacg					377

<210> 200
 <211> 409
 <212> DNA
 <213> Homo sapiens

<400> 200						
cccacggctg	gggcctcagc	aacgaaaaat	gtcttttttt	ttcaagactg	agctaggaga	60
aaagctgggt	actaaattct	tatttgagac	tgattttctca	gatgatccaa	tgcttccttc	120
acctgaccaa	ctcaaaaaga	aagccccctt	tacaaacaag	aagctaaaag	cccatcagac	180
gccagtggat	atcttaaagc	aaaaggctca	tcagtttagca	tctatgcaag	tgccaggctta	240
taatgggtggg	aatgccaaac	cccgacctgc	caataatgag	gaagagggaag	atgaggaggga	300
ogaatatgat	tatgactatg	aatccctttc	tgatgacaac	attctggaag	acagacctga	360
aaataaatca	tgtcatgacc	agcttcagtt	tgaatataaa	gaagaaatg		409

<210> 201
 <211> 512
 <212> DNA
 <213> Homo sapiens

<400> 201						
cgatttcgtg	ggaagctcag	attgoggaaa	tcattcagtg	ggtcagtgac	gagaaagatg	60
ccgggggtta	ccttcaagct	cttgcttcca	agatgaccga	agagctcgag	gctttgagga	120
gttctagtct	gggggtcaaga	acactggacc	cgctgtggaa	gggtgcgccg	agccagaagc	180
tggacatgtc	cgcgcggtcg	gagctgcagt	cgcccttgga	ggcgagatc	cgggccaagc	240
agcttgtcca	ggaggagctc	aggaaggtca	aggacgcca	cctcaccttg	gaaagcaaac	300
taaaggattc	cgaagccaaa	aacagagaat	tattagaaga	aatggaaatt	ttgaagaaaa	360
agatggaaga	aaaattcaga	gcagatactg	gtaaattaat	gttggtcgat	tctgcattat	420
ttgaatataa	gtatttttca	aatgaatgtt	tttattttct	tttcgactta	atagttactt	480
tagaagcacc	tacagaattc	caaattcagt	at			512

<210> 202
 <211> 1003
 <212> DNA
 <213> Homo sapiens

<400> 202						
ccttctctct	actcatctga	cgagctgtcc	ccaggcgagc	ccttgacttc	gcgcacctgg	60
gcccctctgg	gcgccccga	gcggcccgag	catcttctga	accgggttct	ggagcggctt	120
cctggagggg	ctaccaggga	cagcgccgcc	tcagatatcc	tgctggatga	cattgtcctt	180
accgattctc	tcttctctcc	gacggagaaa	tttctgcagg	agctacacca	gtactttgtt	240
cgggcaggag	gcatggaggg	ccctgaaggg	ctgggcggga	agcaagcctg	tctagccatg	300
cttctccatt	tcttggacac	ctaccagggg	ctgcttcaag	aggaagaggg	ggccggccac	360
atcatcaagg	atctatacct	gctaattatg	aaggacgagt	ccctttacca	gggcctccga	420
gaggacactc	tgaggctgca	ccagctgggtg	gagaoggttg	aactaaagat	tccagaggag	480
aaccagccac	ccagcaagca	ggtgaagcca	ctcttcggcc	acttccggcg	gatagactcc	540
tgtctgcaga	ccgggtgggc	cttcgggggc	tctgatgaga	tcttctgccc	tgtatacatg	600
cctgaccact	cttatgtgac	catacgagc	cgcctttcag	catctgtgca	ggacattctg	660
ggctctgtga	oggagaaact	tcaatattca	gaggagcccg	cggggcgtga	ggattccctc	720

atcctggtag	ctgtgtcctc	ctctggagag	aaggctcctc	tccagccac	tgaggactgt	780
gttttcaccg	cactgggcat	caacagccac	ctgtttgcct	gtactcggga	cagctatgag	840
gctctggtgc	ccctcccgga	ggagatccag	gtctccctcg	gagacacaga	gatccaccga	900
gtggagcctg	aggacgttgc	caaccaccta	actgccttcc	actgggagct	gttccgatgt	960
gtgcatgagc	tggagttcgt	ggactacgtg	ttccacgggg	agc		1003

<210> 203
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 203						
gaacaaccta	aactgtgctg	agccactggt	tgaacaaaat	aactcactta	atgttaattt	60
caacacacaa	aagaaaacag	tctggcttat	tcacggatac	agaccagtag	gtcccatccc	120
attatggctt	cagaacttcg	taaggatttt	gctgaatgaa	gaagatatga	atgtaattgt	180
agtagactgg	agcgggggtg	ctacaacttt	tatttataat	agagcagtta	aaaacaccag	240
aaaagttgct	gtgagtttga	gtgtgcacat	taaaaatcct	ttgaagcatg	gtgcatctct	300
tgacaatttt	catttcatag	gtgggagcct	aggggctcat	atcagtggat	ttgttggaaa	360
gatatttcat	ggtcaacttg	gaagaataac	aggtcttgac	cct		403

<210> 204
 <211> 476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (476)
 <223> n = a,t,c or g

<400> 204						
ggcgggtgcn	nccctcgaga	tcatatgcag	tgctcaggaa	ttcggaggct	gttgtgcctc	60
gggttttggg	agggaaagaa	atgcgctgat	aggacacagg	aaggcagaag	gtccttgggc	120
ggagccgggg	cggcagctga	gaggtgggog	ggcgcatccc	cattccatcg	gatcctctgt	180
tccattgtct	gtctgtctcc	tggacccatc	ctggcctcgt	ctttgccttc	cgctcgagcc	240
tggccttggg	cctgcccttc	ccggggacac	tgggtctgat	ccccttccct	cctccctcaa	300
tgctctcatg	ccctgtctga	tctctccctt	tcccctgccc	caccgtccca	tctgtcccca	360
cgttgccctc	ccccccaggc	cgggagcagg	ctgggagcca	tgcggnggtg	tgcgaggag	420
atggatgcca	ccccgatgcc	tcctgcaccc	tcattgccct	cggagcgagt	gactgn	476

<210> 205
 <211> 745
 <212> DNA
 <213> Homo sapiens

<400> 205						
tttttttttt	agtattccaa	acagcagggg	gtcactgtct	ttactttagg	attcataaag	60
cctgttaatg	aatgggtgtg	ctgggggcac	tgctcatgtt	ttcagcatgc	tgcttgggcg	120
acgaggaggc	ccttcctagg	gtctgacctg	gtctcccttc	ccagggtggg	gcaggtgcca	180
tgctccagtc	tctccattga	ctggggcaca	gccttcccca	agccgctgct	gacaccctat	240
gaggtaacac	caagctctgg	gagagagtgg	gctttggacg	tggttctcaa	aggtagggtc	300
tggagtggag	tgggggtggg	gggcagcact	tcgttatgtt	cgttagattcc	ggagtctgtc	360
tcgattttct	cagcggagtc	acttccctagc	tgtgtagcct	taggcaaggc	cctgaaccac	420
acagttccct	tctgtggcag	gggacagtgt	gcccttcaca	ggccgtcgtg	aggactgaat	480
tcagtaatcc	aggggcagaa	aaacactggc	agatgttatt	gtccctccct	cccctccctt	540

```

agggcgccgt ggcctctgagg gacatttctt ggcagcagcc ctacccgatg gacttctacg      600
ctggcagctc cttggggccc tggacgggtga accacggcca ggaccgccgt cccacgccc      660
cgggcccggc cgcgcggggg aaggtgcagg aggggtccgc gcgtccccct tcggccgtgg      720
cttgcgagga ctgcagctgc aggga                                     745

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```

<210> 206
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = a,t,c or g

```

```

<400> 206
cgtgcgnccc aatgacnccc aaagagctta cgcangcgcn nccggncggg aanncccggg      60
gcgaggcacg cgttagaaga gggcctcctg caccctggtc tcannnnncc catcctcatg      120
agatctcagc ccagactcaa gggaggatca ccctcagggc cacaggaggc tacttccaaa      180
gaggcctgtg agaggaagcc taatgcctgg gcacacccat caccctgcc ctgtgtcctc      240
aacaactaat gacacaccag accaaatctg ggtctctgtg ggcagtctta ggatgggaac      300
aggaggggatg ggagctaatt cctcaacctc ccccaggtgc tgggacttga gctccgggaa      360
caaaaagtgg atcatccagg tgcccatcct ggcctccatt gtggagagca ggggtgggct      420
gctggccaca ggggtgggtg ggatgtgcgc ctgcgtcccc cggaaccagc ccctgacagg      480
gacctag                                     487

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```

<210> 207
<211> 439
<212> DNA
<213> Homo sapiens

```

```

<400> 207
acattttgtt tgcttttcca ttaatccact ggttttagttt ccagaacgca atgtcagacc      60
tgagggtgaca gaaaaggga aacgtgagag agtgtcttct tccctgaaga gagtggggcc      120
tgagggttga cagtggcgct gcctgagtga cctagccgct gggctgggccc ctggacagct      180
gatcccgagt tcctgcaatt gtcgccaccc ttccgtagtc cacaggcctg atggcggcgg      240
cggctgagcc gatgggcccg gcacagggtc ccatgaactc agaagtaatt gtggacccta      300
tacagacaca agcagcaagt ccaacacaat cacagcaaca gactctcctg cagaccttc      360
caggaagaca gagccacaca caccatcatg gtctctggaca aggaaaacac tctttcctaa      420
tctggttgtc atgccatga                                     439

```

```

<210> 208
<211> 494
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = a,t,c or g

```

```

<400> 208
atgtgtgnac ctgggactga cgtacgtgcg acnggccggg aannnccggg ncgacgattt      60
cgtgtgcagg gcacaggccn nnnatttcac gccttcactg aggccatgac gcatttcccc      120
gectccccgg tctgggcccg catgttcttc ttgatgctta tcaacctggg cctgggcagc      180

```


atgateggga	ccatggcagg	catcaccacg	cccatcatcg	acacettcaa	ggtgccaag	240
gagatgttca	cagggggctg	ctgtgtcttt	gcattcctcg	tggggctggt	gttcgtccag	300
cgctccgga	actactttgt	caccatgttc	gatgactact	cggccaccct	gccactcact	360
ctcatcgta	tccttgagaa	catcgctgtg	gcctggattt	atggaaccaa	aaagttcatg	420
caggagctga	cggagatgct	gggcttcgcg	ccctaccgct	tctatttcta	catgtggaag	480
ttcgtgtctc	cact					494

<210> 209
 <211> 877
 <212> DNA
 <213> Homo sapiens

<400> 209						
ttgaaaagga	gcgcctttta	gatgaatggt	tcactctgga	cgagggtccc	aaggggaagc	60
tacacttgag	actggagtg	ctcacgttaa	tgccaaatgc	gtcaaacctc	gacaaggtgc	120
taacagacat	caaagctgac	aaagaccaag	ccaacgatgg	tctttcctct	gcattgctga	180
tottgtactt	ggatttcagca	aggaaccttc	cgattcgata	caaaaaccaat	gaacctgtgt	240
gggaggaaaa	cttcaactt	ttcatteaca	atcccaagcg	ccaggacctt	gaagttgagg	300
tcagagacga	gcagcaccag	tgtccctg	ggaacctgaa	gggtccctc	agccagctgc	360
tcaccagtga	ggacatgact	gtgagccagc	gcttcacgct	cggtaaactc	ggtccaaaca	420
gcaccatcaa	gatgaagatt	gccctgcggg	tgtccatct	cgaaaagcga	gaaaggcctc	480
cagaccacca	acactcagct	caagtcaaac	gtccctctgt	gtccaaagag	gggaggaaaa	540
catccatcaa	atctcatatg	tctgggtctc	caggccctgg	tggcagcaac	acagctccat	600
ccacaccagt	cattgggggc	agtataagc	ctggtatgga	agaaaaggcc	cagccccctg	660
aggccggccc	tcaggggctg	cacgacctgg	gcagaagctc	ctccagcctc	ctggcctccc	720
caggccacat	ctcagtcagg	gagccgaccc	ccagcatcgc	ctcggacatc	tcgctgcccc	780
tcgccaccca	ggagctgcgg	caaaggctga	ggcagctgga	aaacgggacg	accctgggac	840
agtctccact	ggggcagatc	cagctgacca	tcccgcga			877

<210> 210
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(456)
 <223> n = a,t,c or g

<400> 210						
ngggantttg	aaccctgaga	ccattgnaca	nnnnccggga	ttcgcagcct	ctgatcttga	60
gccttttacc	cccacagacc	agcctatttc	cctgaggct	attactcaac	ccagttgcat	120
caagaggcag	agagccgctg	ggaacctgg	ttccctcgca	gctaccattg	accataagcc	180
ttgctctgca	cccttggaac	ctaaaaatcca	ggcctcaagg	aaccaaagat	ggggagcagt	240
gagagcagca	gaatccctta	cagacattgc	tgagcctgcc	tctccccagg	ttcatgagac	300
accaattgat	gcctcccaga	ctcaaaagg	ggaaccagcg	agcaaatcta	ggttcacccc	360
gggaactccag	gctaaggctc	ctcacagtcg	tgagagggtc	ttatctacca	tgatgcaac	420
accacatcat	gcacagcccc	aacgagggga	aggctc			456

<210> 211
 <211> 764
 <212> DNA
 <213> Homo sapiens

<400> 211

```

cgcagggtatt ctcagaaact gatccagcac accgcctgtc agctgctgag aacttaccct 60
gctgccacccc gcatcgactc ttccaaccog aacccccctca tgttctggct ccatgggata 120
cagcttgttg cactcaacta ccagactgat gatctccctt tacattttaa tgctgcaatg 180
tttgaggcaa atggtgggtg tgggtatgta ttgaaacctc cagttctgtg ggacaagaac 240
tgccccatgt atcagaagtt ttctccacta gaaagagatc tggacagcat ggatcctgca 300
gtctattctt taactattgt ctctggtcag aatgtgtgcc ccagtaatag catgggaagc 360
cogtgcattg aagtcgacgt cctgggcatg cctctggaca gctgccattt ccgcacaaag 420
cccatccatc gaaacacctc gaaccccatg tggaaacgagc agtttctgtt ccacgttcac 480
ttcgaagatc ttgtatttct tcgttttgca gttgtggaaa acaatagttc agcggtaact 540
gctcagagaa tcattccact gaaagcttta aaacgaggat atcgacatct tcagctcgga 600
aaccttcaca atgaagtctt ggagatttct agtttattca ttaacagcag aaggatggaa 660
gaaaattcct ctggcaatac catgtcagcc tcttcgatgt ttaatacaga agaaagaaaa 720
tgtttgca ctacagagt cagggtgcat ggcgtccag ggc 764

```

<210> 212
 <211> 411
 <212> DNA
 <213> Homo sapiens

```

<400> 212
ggcataaggg gcaccacggg gcacctgggg tgtcctatta atgacgaccc ctccctgaca 60
ctgaccgtct catgggtgat ggaggacaag ccgatctata ttggaaacgg gacgaagaag 120
gaggacgact ccctgacct ctttgcggtg gcaaagcggg accacgtcag tgacacgtgt 180
ggagcctgca ccgatctaga ccataacctg gacaagggtc acctcaccgt gctaggtgag 240
caggccactc caactaacgg gttgggtgcc ctgcccaaag gacgggcaaa ccggaccggg 300
gacctggagc tgacctacct ggccgagagg atcgtgcggc tgacctggat ccccggggat 360
gctaacaacc gtcccatcac agactacgac tgccagattg aagaacacca a 411

```

<210> 213
 <211> 1294
 <212> DNA
 <213> Homo sapiens

```

<400> 213
atgagctcta ttggatgcct gtgggtgtct agaagcagtc agatagatgg gctcacggca 60
gagaagtctg gcccggagaa gcctcatggc acgtggctaa tgccagagtt gcacccaaag 120
gagcagatct tagaactgct ggtactggag cagttcctga gcattctgcc tgaggagctg 180
cagatctggg ttccagcaaca taatccagaa agcggcgagg aatctgtgac cctgttggag 240
gatttagaga gggagtgtga tgacccaggg cagcaggtcc cagctagtcc acagggacca 300
gcagtgccat ggaaggattt aacatgtctc agagcatccc aagagtcaac agacatccac 360
ctccagccct taaagacaca gctgaaatcc tggaaacccat gcctttccc taaaagtgtat 420
tgtgagaaca gtgaaacagc aacaaaagag ggcattctcag aagaaaaatc acagggactc 480
cctcaggaa cttcatttct aggaattagt gagcatgaaa gcaatttagt gtggaagcaa 540
ggaagtgtca caggggagaa actaagatct ccttcccagg ggggcagttt tagtcaagtg 600
atcttcacaa acaaatctct aggaagaga gacctttatg atgaggctga aagatgcttg 660
attctaacta cagactctat aatgtgtcag aaagttcctc cagaagagag accttataga 720
tgtgatgtat gtgggcacag cttcaagcag cattcctctc taacacaaca tcagagaatc 780
catactggag aaaagcccta taaatgtaac cagtgtggga aggccttttag tttgaggtcc 840
tatcttatta ttcacagag aattcatagt ggtgagaaag catatgaatg tagtgaatgt 900
gggaaagctt tcaatcagag ctccagccctc attagacatc ggaaaatcca tactggtgag 960
aaagcttgta aatgtaatga gtgtggcaaa gcattcagtc aaagtccata totcattata 1020
catcaaagaa ttcacactgg tgagaaacct tatgagtgtg atgaatgtgg gaaaaccttt 1080
agccagagct caaaactcat tagacatcag cgaattcaca caggagagag accctatgaa 1140
tgtaatgaat gtggaaaagc tttcaggcag agctcagagc tgattactca tcagagaata 1200
catagtggag agaaacccta tgaatgtagt gaatgtggaa aagctttcag tttgagctca 1260
aaccttatca gacatcagag aattcatagt gggg 1294

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<210> 214
 <211> 801
 <212> DNA
 <213> Homo sapiens

<400> 214
 ggaattcccg ggtcgacgat ttctgccagc cgtaacatat ttttagagga tgatttggcc 60
 tggcaaaagt tgattcatcc agattcctca aatactcctc tttcaacaag acttgatatc 120
 gtgcaagagg atgctgggaa atctcctgct cgaatatagat cagccagcat tactaacctg 180
 tcaactggata gatctgggtc tcctatggta ccttcatatg agacatctgt cagtccccag 240
 gctaaccgaa catatgttag gacagagacc actgaggatg aacgcaaaat tcttctggac 300
 agtgtgcagt taaaagacct gtggaaaaaa atctgccatc acagcagtggt aatggagttt 360
 caggatcacc gctactgggt gagaacgcat cccaactgca ttgtaggaaa ggaattagtc 420
 aactgggctaa tccgaaatgg gcatattgcc acaagggcac aagctatagc aattggacaa 480
 gcaatgggtg atggacgttg gctggattgt gttagtcatc acgaccagct tttcagagat 540
 gagtatgcgc tgtatagacc actgcaggta cttttcagtg tttactgcca attagaatgt 600
 agcaagctta ttttatagtc tttcttcac cgtgggaata aaaagtagtt tattagaaga 660
 tgatttttct aacatttttt cctgctgttt gaggaaagtt aaaacttttt ttacttggta 720
 ggcagcagtg atgaaaaagc tgccattaga atcaaacatt ttattgttta ctttaaattt 780
 gatcagacaa taataaaaaa a 801

<210> 215
 <211> 2932
 <212> DNA
 <213> Homo sapiens

<400> 215
 atggcccggtg tgttcgttca tctcaggacg gcatggccga cgtgttcgtt catctcagga 60
 cggcatggcc cagggtgttcg ttcattctcag gacagcatgg cccaggacgg cacggccgac 120
 gtgtttgttc atctcaggac agcatggccg acgtgtttgt tcatctcagg acggcatggc 180
 cgaactgttc actcatctca ggacagcagc gccaggtga gtctgtttct tatgaagatg 240
 acgacattcc agccccagca agcctgctgc atgtgaacgc cgcagcaccg gcaactcaca 300
 atccaactgc acctgttcta tgcactgcac cgaataacac agctcagaaa gagaaagtcc 360
 ccagtggaaat gagacagaga cctgcgggtg ttgcgcatct ctcacgcaca cccgacctta 420
 cgtgtgctgt ttctaccacac tcgactgttc ctggtgttcg catctcctcg tgcacaccgg 480
 accttaactg tgcgtgtttc atccactcga ctgttcccag tgtttgcac tccctcgtgc 540
 caccgatctc tacgtgtgct gtttctaccc actcgaactgt tcccgggtgt cgcactctct 600
 cgtgcacacc ogatcttaag tgtgctgttt ctaccactc gactgttccc ggtgttcgca 660
 tctctcagc cacaccgat cttacgtgtg ctgtttctat ccacgcgact gttcccgggtg 720
 ttgcgcatct ctcgtgcaca cccgatctta cgtgtgctgt ttctatccac gcgactgttc 780
 ccggtgttcg catctcctcg tgcacaccgg atcttacgtg tgcgtgtttc accactcga 840
 ctgttcccgg tgttcgcac tctcagcga caccgatctc tacgtgtgct gtttctatcc 900
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cacgcacacc	cgatccttacg	tgtgctgttt	ctacccactc	gactgttccc	ggtgttcaca	1980
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ccggtgttca	catctcctca	cgcacaccg	atcctacgtg	tgctgtttct	atccacgcga	2820
ctgttcccag	tggtcacatc	tcctcgtgca	cacccgatct	tacgtgtgct	gtttctatcc	2880
actcaactgt	tccaggcctc	ctgactagt	tttctcagac	ctccacgggc	ca	2932

<210> 216
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 216						
tttcgtacga	aatcgtacag	gaagggctcc	tacaggtgta	tcgtcagcga	gtggatcgcc	60
gagcagggca	actggcagga	aatccaagaa	aaggccgtgg	aagttgccac	cgtgggtgatc	120
cagccgacag	ttctgcgagc	agctgtgccc	aagaatgtgt	ctgtggctga	aggaaaggaa	180
ctggacctga	cctgtaacat	cacaacagac	cgagccgatg	acgtccggcc	cgaggtagcg	240
tggtccttca	gcaggatgcc	tgacagcacc	ctacctggct	cccgcgtgtt	ggcgcggtt	300
gaccgtagt	tcctgggtgca	cagctcgctt	catgttgctt	tgagtcatgt	ggatgcacgc	360
tcctaccatt	tactgggttcg	ggatgttagc	aaagaaaact	ctggctacta	ttac	414

<210> 217
 <211> 463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (463)
 <223> n = a, t, c, or g

<400> 217						
atgccggacc	ctatgtgagg	ggcctcagag	atttgaagaa	tatgagtatt	taggggtataa	60
ggctgggtctg	tatgaagcta	ttgcagatca	ctacatgcag	gtgcttggtt	gtcagcatga	120
atgtgtgagg	gaacttgcca	cccgccctgg	ccgcctctct	cccatcgaga	atcttcttcc	180
tctgcactat	gattacctac	agtttgctta	ctatcgagtt	ggtgagtatg	tgaaagccct	240
ggagtgtgcc	aaagcctatc	ttctatgcc	tccagatgat	gaggatgtcc	tagacaatgt	300
ggattactat	gagagtctgc	tggtatgatg	cattgaccgg	gcattccattg	aggccagaga	360
ggatttaaca	atgtttgtga	aacgtcataa	gctggagtct	gagctgataa	aatcagctgc	420
agaaggtctg	gggntttcat	acactgaacc	gaattattgg	atc		463

<210> 218
 <211> 383
 <212> DNA
 <213> Homo sapiens

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<400> 218
gcatcctgcc cggccttttgc tgggggttggg agggggcagg caggaagcga gggcctgcgg      60
ggtctctgcg tttccggggg aaacagccgg ccctgccctg ggagggtcac agcccgcccg      120
ctgctgaagg cggctctgag ctttttctgc gccacatccc tctcccgccc ctgagttccc      180
tgagtgtggc ttctacggcc tttacgacaa gatcctgctt ttcaaactg accccacgtc      240
ggccaacctc ctgcagctgg tgcgctcgtc cggagacatc caggaggcgg acctgggtga      300
ggtggtgctg tcggcctcgg ccacctttga ggacttacag atccggcgcg acgcccctcac      360
ggtgcactcc tatcggggcgc ctg                                     383

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<210> 219
<211> 428
<212> DNA
<213> Homo sapiens

```

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<400> 219
tttcgtcgcg gttggtcctg ctagctgggg cagcggcgct ggcgagcggc tcccagggcg      60
accgtgagcc ggtgtaccgc gactgcgtac tgcagtgcga agagcagaac tgctctgggg      120
gcgctctgaa tcaactccgc tcccggccagc caatctacat gagtctagca ggctggacct      180
gtcgggaaga ctgtaagtat gagtgtatgt gggtcacagt tgggctctac ctccaggaag      240
gtcacaaagt gcctcagttc catggcaagt ggcccttctc ccggttctctg ttctttcaag      300
agccggcctc ggccgtggcc tcgtttctca atggcctggc cagcctgggtg atgctctgcc      360
gctaccgcac ctctgtgcca gcctcctccc ccattgtacca cactgtgtg gccttcgcct      420
gggtgtcc                                     428

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<210> 220
<211> 1297
<212> DNA
<213> Homo sapiens

```

```

<400> 220
atggacgggtg aggcagtcgc cttctgcaca gataaccagt gtgtctccct gcacccccaa      60
gagggtggact ctgtggcaat ggctcctgca gcccccaaga taccgagget cgttcaggct      120
accccgccat ttatggctgt gaccttggtc ttctctcttg tgactctctt tgtagtggat      180
catcaccact ttggcaggga ggcagaaatg cgagagctta tccagacatt taaaggccac      240
atggagaatt ccagtgcctg ggtagtagaa atccagatgt tgaagtgcag agtggacaat      300
gtcaattcgc agctccaggt gctcgggtgat catctgggaa acaccaatgc tgacatccag      360
atggtaaaag gagttctaaa ggatgccact acattgagtt tgcagacaca gatgttaagg      420
agttccctgg agggaaccaa tgcctgagatc cagaggctca aggaagacct tgaaaaggca      480
gatgctttaa ctttcagac gctgaatttc ttaaaaaagca gtttagaaaa caccagcatt      540
gagctccacg tgctaagcag aggccttagaa aatgcaaaact ctgaaattca gatgttgaa      600
gccagtttgg aaacggcaaa taccagggt cagttagcca atagcagttt aaagaacgct      660
aatgctgaga tctatgtttt gagaggccat ctagatagtg tcaatgactt gaggaccag      720
aaccaggttt taagaaatag tttggaagga gccaatgctg agatccaggg actaaaggaa      780
aatttgaga acacaaatgc tttaaactcc cagaccaggg cctttataaa aagcagtttt      840
gacaacacta gtgctgagat ccagttctta agaggtcatt tggaaagagc tgggtgatga      900
attcacgtgt taaaaaggga tttgaaaatg gtcacagccc agacccaaaa agcaaatggc      960
cgtctggacc agacagatac tcagattcag gtattcaagt cagagatgga aaatgtgaat      1020
accttaaatg ccagatttca ggtcttaaat ggtcatatga aaaatgccag cagagagata      1080
cagaccctaa aacaagggaat gaagaatgct tcagccttaa cttccagac ccagatgtta      1140
gacagcaate tgcagaaggc cagtgcggag atccagaggt taagagggga tctagagaac      1200
accaaagctc taacctgga aatccagcag gacagagtc gcctgaagac cctccatgtg      1260
gtcattactt cacaggaaca gctacaaaga acccaaa                                     1297

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```

<210> 221

```

<211> 500
 <212> DNA
 <213> Homo sapiens

<400> 221
 cacgcgtccg gctcaacaac gacggcctct cgccccctcat gatggctgcc aagacgggca 60
 agattgggat ctttcagcac atcatccggc gggagggtgac ggatgaggac acacgggcacc 120
 tgtcccgcaa gttcaaggac tgggcctatg ggccagtgtg ttctctcgctt tatgacctct 180
 cctccctgga cacgtgtggg gaagaggcct ccgtgctgga gatcctgggtg tacaacagca 240
 agattgagaa ccgccacgag atgctggctg tggagcccat caatgaactg ctgcgggaca 300
 agtggcgcaa gttcggggcc gtctcttctt acatcaacgt ggtctcctac ctgtgtgcca 360
 tggtcattct caotctcacc gcctactacc agccgctgga gggcacaccg ccgtaccctt 420
 accgcaccac ggtggactac ctgaggctgg ctggcgaggt cattacgctc ttactgtggg 480
 tcctgttctt cttcaccaac 500

<210> 222
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 222
 aagacgcaca ctgtcagagg aaactggcca tgcaggaatt catggagatc aatgagcggc 60
 taacagaatt gcacacccaa aaacagaaac ttgctcgcca tgtccgagat aaggaagaag 120
 aggtggacct ggtgatgcaa aaagtgtgaaa gcttaaggca agaactgcgc agaacagaaa 180
 gagccaaaaa agagctggaa gttcatcacg aagctctagc tgctgaagca tctaaagaca 240
 ggaagctacg tgaacagagt gagcactatt ctaagcaact ggaaaatgaa ttggaggggac 300
 tgaagcaaaa acaaattagt tactcaccag gagtatgcag catagaacat cagcaagaga 360
 taaccaaaact aaagactgat ttggaaaaga aaagt 395

<210> 223
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 223
 aaatgatcct gcaattatta gcaacttttc tgcagcagtg gtgcatacga tagtaaatga 60
 aacttttagag tcaatgacat cattggaagt tacaaaaatg gttgatgaac gtacagatta 120
 ttttaactaaa tctttaaagg agaaaacccc tccattttcc cactgtgac aggcagtgtc 180
 gcaatgcagt gaagctagta gcaataagga catgttttgc gaccggttat ctaaatctat 240
 tattaaacat tccatagata agagcaaata agtgcaccca aatatagata aaaatgcagt 300
 atacaaggaa agcttgccctg tttctggaga agaatacacg ttgacaccag aaaagtctcc 360
 caaatttcct gactctcaga atcagttaac tcactgtcga ctttcagctg cg 412

<210> 224
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 224
 gttttcactg cgggggatggc ccaggctgca atgtggaaat aagagctgtg catttcaatg 60
 gcttcatgac cccatttgag tctgtctgcc aaaaaccaag tgagtgtcag aataaaccac 120
 caaatggagc tggccattcc aaaaaagta atcagcaaga aaattattgc acatcctgtg 180
 ttcttaagtc cttcttgatg gagaacaggt tctgtgcct cttcaaaatc acaggatatc 240
 ctttccgggc ctacagtacg cctgacaata taagcaatgc tataaatatt atagcacata 300

ctgagaaata	tgatggggcg	ctcagggtag	gaaaacctac	aagaatcgat	caggaaggtc	360
agtactgtga	aggcagtgga	gatgaaacac	aggctggccc	c		401

<210> 225
 <211> 724
 <212> DNA
 <213> Homo sapiens

<400> 225						
ggtggtaggg	tccggctgaa	tggtccactg	agatggccgt	cagtctgtac	ctgacccgag	60
tctttgtgaa	ccagggctca	tccggcaatgg	gtggaacggc	agagtccatc	aggggatgag	120
atttgatgaa	tgacagagtt	tcatccggga	aatcgatgga	ggttttataa	gcttcggcaa	180
ggccgtgttt	tgacaacag	ccaggccttg	gctttggcac	tttgtcttcg	ggaactgctg	240
tccaaacaga	atctggagtt	ttctgttctt	taaaccgtcc	tttgaatact	ttttcaatgt	300
catccatgct	aaatgcacag	acagcagaac	cagggatgct	attgagctgc	gtggtaaaca	360
ccccgaccac	agtggggatg	ccattgattt	gtattatgtc	tgtaatagac	tcgagaacat	420
caaagttagaa	aaacgaatct	ccagggacag	aacagttcag	ccgagccttt	agaaatgaag	480
tccagtgttt	ctccaggacc	cgctgggaac	cacccatgtc	gtttttacat	atgggggcca	540
cgcggaata	cacagccccc	ttttctttct	ccttctcttc	ctgcttcttc	ttcttcttcc	600
cagcttcttt	ttctctttct	tctcccaatc	cctctctctc	ctcttctttt	tcatcttcat	660
ctccatcttt	ctctccctct	ccttcttctt	caaccttctc	tctccgttcc	ttccttgctg	720
acat						724

<210> 226
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 226						
ggctgaaaat	ccgatccatg	atgtgatcaa	caatagcgtc	ggctggcatc	attttttcgc	60
ggataacgcc	ccgttgcgcg	tgaataccca	tgccgatttc	catttcctcg	gcaccgattt	120
caaaattgtg	gcgtcgcgtc	tgaggcaaaag	aacagggctc	caacgcgaca	cccatcgat	180
aggtgcgcgc	attggccttg	cgtgttaccc	cctcgacgcg	ctcaagcgac	atgccccgat	240
cacaggctgc	acctgccacc	ttgaaaatga	agaagttacc	cgcgacacgc	cgacggccat	300
cgcgatcctc	tatgggggaa	gaggatatgt	cgtctgtcgt	cagaaagggtg	cgcgtcggaa	360
tagcaacttc	ttgcgccatt	tgggcagcca	tctogaagtt	catgaogtct	ccgacataat	420
taccgtacac	gaagagcaog	ccttctc				447

<210> 227
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 227						
ttgtgctttc	tgacctttgc	ctcttttatt	atagagatga	gaaagaagag	ggtatcctgg	60
gaagcatact	gttacctagt	tttcagatag	ctttgcttac	ctctgaagat	cacattaatc	120
gcaaataatgc	ttttaaggca	gcccattcaa	acatgcggac	ctattatttc	tgcaactgata	180
caggaaagga	aatggagttg	tggatgaaag	ccatgttaga	tgctgcccta	gtacagacag	240
aacctgtgaa	aagagtggac	aagattacat	ctgaaaatgc	accaactaaa	gaaaccaata	300
acattcccaa	ccatagagtg	ctaattaac	cagagatcca	aaacaatcaa	aaaaacaagg	360
aaatgagcaa	aattgaagaa	aaaaaggcat	tagaagctga	aaaatatgga	tttcagaagg	420
atggtcaaga	tagaccctta	acaaaaatta	atagtgtaaa	gctgaattct	ctgccatctg	480
aatatgagag	tgggtcagca	tgccctgctc	agactgtgca	ctacagacca	atcaacttga	540
gcagttcaga	gaacaaaata	gtcaatgtta	gcctggcaga	tcttagagggt	ggaaatcgcc	600
ccaatacagg	gcccttatac	acagaggccg	atcgagtcac	acagagaaca	aattcaatgc	660

```

agcagttgga acagtggatt aaaatccaga aggggagggg tcatgaagaa gaaaccaggg 720
gagtaatttc ttaccaaaca ttaccaagaa atatgccaag tcacagagcc cagattatgg 780
cccgtaccc tgaaggttat agaactactcc caagaaacag caagacaagg cctgaaagta 840
tctgcagtgt aaccctctcc actcatgaca agacattagg acccgagcg gaggagaaac 900
ggagggtccat gagagatgac acaatgtggc agctctacga atggcagcag cgtcagtttt 960
ataacaaaca gagcaccctc cctcgacaca gtactttgag tagtcccaaa accatggtaa 1020
atatctctga ccagacaatg cactctattc ccacatcacc tccacaggg tcaatagctg 1080
cttatcaggg atactccct caacgaactt acagatcgga agtgtcttca ccaattcaga 1140
gaggagatgt gacaatagac cgcagacaca gggcccatca ccctaaggta aaatagctgc 1200
tgattttggt ttaactcact acctataaaa tgctgtgtt tctttctagt atactatttt 1260
aaatgtgaga gacaaaagaa tggggataaa gtaagcaagg cagctctttt ttgttttaaa 1320
aaaaaaa 1327

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<210> 228
<211> 448
<212> DNA
<213> Homo sapiens

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```

<400> 228
agctgccctt cctgggectg ggggtctgtt ttcccaggg catggtgatg gcgagcccg 60
agatgaatcc taccatctgc tcggtgtttg aggcacatat agtcttactg tttcatgcca 120
ccaccttccg acgaggattc caggtgacag tactcgtggg caacgtacgt cagacggctg 180
tggtggaaaa gatccatgcc aaggtgagag ggacctggcc ttctatttct ccagaggtea 240
gaaaagaggg aggcctgccc cagactggca gagaactcct tgatcccaca atgggaataa 300
aaccctactt atggtgggta gggcctgat aggcctctgg aggggtggaga gcctcggtg 360
gcatagaatg ggacagaagg cactggccag gggagtgacc acttatttgc tgcaggacaa 420
actgcgga ggcgataagg cagtggtc 448

```

```

<210> 229
<211> 619
<212> DNA
<213> Homo sapiens

```

```

<400> 229
gatgataaaa atgcccaggg gataaagagg catgttaagc caacaagtgg aaatgccttc 60
accatttgta aatatccatg tggaaaaagt agggagtgtg ttgccccaaa catctgcaaa 120
tgtaaacctg gttacattgg ttctaactgc caaactgtct tttgtgacct tgattgcaaa 180
aaccatggaa aatgtattaa gcctaacatt tgtcagtgtc ttccaggaca tgggtggagca 240
acctgtgatg aagaacattg taaccocact tgtcaacatg gtggcacatg cttggctggg 300
aatctctgca cttgtcctta tggttttgta ggaccaaggt gtgaaacaat ggtttgtaac 360
aggcactgtg aaaatggagg ccagtgtcct acaccagata ttgcccagtg caaacctggc 420
tggtatggac ccacctgtag tacagcttag tgaaggcatt ctgaattcta atcatagcct 480
ctacattctt gatagagcag gagcaccgtc atcttgaca aacaccgcca ctttaaattc 540
cagctccctt tctagctttt ctaagcttag tgttatttgt aaacttaatg aacatacttt 600
caaagcgatt atccagtaa 619

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<210> 230
<211> 914
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(914)
<223> n = a,t,c or g

```



```

<400> 230
tgcagtgact ttttctgtgg tatttgcata cgtagcagat ataaccaag agcatgaaag    60
aagtatggct tatggactgg tatgtatggt tattctatac cttttgtatc tgctgagaaa    120
tgccttcttt ttaagataaa tattattata aggagtgcaa acctttgcat tacaagattt    180
ttgcgtaaaa tatattttgt aataaaatca ttcattagac tacattttaa atttttttgc    240
ggtatgagggc tatgtaagtt ttgattcttt tcatttagta gatattcata agtcacatgt    300
cagaattgaa attatagtat attttacctt gtagagttct ttttaacaga atcctaataa    360
taagaattat ttagtatgtc aagagttaaa aaaaatcact actcatttaa tgtctaactc    420
aaaatacaac aggetaacat cctagctcag ggatcagcaa acottttttg tggctttgtg    480
ggccacgtac agtctctgtc tcattctttt gtttttgcat gtgtatttat gtttataaac    540
tctttaaaaa tgtaagaaac agccagattt gagccatagt ggtaggtcgc caactcctgg    600
acactgtttt ggtaaactaa attatggcag tataatgtgt catctatcaa atctaggaat    660
taaaggaaaa aagcctagta atagaatgac tactataggc acaataatag atcactactg    720
aatagccaga aataggacag tgatgcattt cggtaaatgt gagaccaata ccctgtgata    780
ataaggactg aatattgttg tgggcngaag tagttttaa agggactgat ttcngattcc    840
aaggacgtta tagtgaagat cctaagattt ttggggagga accccctttg ggggaagttt    900
gaaaaggcgn tata                                     914

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```

<210> 231
<211> 388
<212> DNA
<213> Homo sapiens

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```

<400> 231
tttagaaaatt cttaaagtctg caaccttgta tcgtttgatg caggccttct ttgtcctgcc    60
aggcaccgct tctgctatth tttcccatct ttcaggggga tttactgggt atgttttcaa    120
agcttgttcc aaaagcttct gttctctgtg tggccaaggg gtgaaatctg tatatggacc    180
tgattaagaa aaatthttat ttgaaaactg gctttgaaca tgttctcata caagtcttgt    240
ggccacaag cattcgctaa gtgccattt caatctggga tgagtcagtt tgaaaataaa    300
cttgtcgaga tgagagatac atataccct ctgagtgta ataatagaaa aaatttcaga    360
tagctcacat cccataaaat acaaactc                                     388

```

```

<210> 232
<211> 391
<212> DNA
<213> Homo sapiens

```

```

<400> 232
agcacagtta ctggacaacc gaggcggctc ttggacacag caggacacca gcagcccttc    60
ctagagctta agatccgagc caatgagcct ggagcaggcc gggccaggag gaggaccccc    120
acctgtgagc ctgcgacccc cttatgttgc aggcgagacc attacgtaaa cttccaggaa    180
ctgggatggc gggactggat actgctgccc gaggggtacc agctgaatta ctgcagtggg    240
cagtgcctta cccacctggc tggcagccca ggcattgtct cctctttcca ttctgcccgc    300
ttcagctccc tcaaagccaa caatccttgg cctggcagga cctcctggtg tgtccctact    360
gcccgaggc cctctctctc tctctacctg g                                     391

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<210> 233
<211> 403
<212> DNA
<213> Homo sapiens

```

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<220>
<221> misc_feature
<222> (1)...(403)
<223> n = a,t,c or g

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<400> 233

atgagaatca	cctgtagtaa	ttgctattga	tgaatgaagt	aggaaacaaa	aggctttgcc	60
aggatgaaat	cacggccgac	taaaggagat	actaatatta	tttgcaagag	gttgggttag	120
gatccagtag	cggaacaagg	aaaagatgac	agtgaggagt	caaatacttc	cttctgtcgg	180
nttttattgt	tttcagatga	aatcatcatg	gcagccccc	tgaggatagc	agatgtaacc	240
tctggactga	ttgggggaga	agacggccga	gtatatgtat	ataatggcaa	agagaccacc	300
cttggtgaca	tgactggcaa	atgcaaatca	tggataactc	catgtccaga	agaaaaggta	360
aatgttctac	aaaattctat	acettattgg	gaaaggatca	ctg		403

<210> 234

<211> 518

<212> DNA

<213> Homo sapiens

<400> 234

ctgtcagaat	tgcttgatat	gtttcagcct	tatatctttt	attgtgtgct	ccctgacggc	60
aaccacatct	cccacagtat	ctgacagttc	tgtggcctga	gaggcagagt	ccatggcttc	120
cagaacatgt	gtcccaattg	gttctctctc	tttcccacct	ggactggctg	cttttgacct	180
ctaactcttt	gtcttccaga	aaacaantaag	cctcctcagg	cagatgcagt	cccagataaa	240
gagctgaccc	ttcctgtgga	tagcacaacc	ctggatggca	gcaagagctc	agatgatcag	300
aaaattatct	catatctctg	ggaaaaaaca	cagttagtat	tgacacaaaa	tccttatttt	360
tgcaaaagcct	ccagaccttt	ggaagagcaa	ggttttattt	gctattatga	gttgagttgc	420
tcttaatggc	ttatccagtg	gggtgactga	ggaagaaatg	tttgcaattc	caaacttcaa	480
ctccaagaaa	atgatattat	aatcataatt	tttctaag			518

<210> 235

<211> 896

<212> DNA

<213> Homo sapiens

<400> 235

ggatgtttta	gaggtgtatg	gcacaggcgt	ggccagcacc	aggcatgaaa	tgggcacctt	60
ggataagcac	aaggagttgg	aggaccttgt	ggctaagttc	ctgaatgtgg	aagcagctat	120
ggtcttttgg	atgggattcg	caactaactc	aatgaatata	ccagcattag	ttggaaaggg	180
atgcoctcatt	ttaagggatg	aggtaaacca	cacatcgctt	gtgcttgggg	cccgaactctt	240
agggtgcaacc	ataggaatct	tcaaacacaa	ctacgcacaa	agcctagaga	agctcctgag	300
agatgctgtc	atctatggcc	agcctcgaac	ccgcagagct	tggaaaaaga	ttctcatcct	360
ggtggagggt	gtctacagca	tggaaagggt	catcgtgcat	ctgcccacga	tcatagtctt	420
aaagaagaaa	tacaaggctt	acctctacat	agatgaagct	cacagtattg	gggccgtggg	480
cccaaccggc	cggggtgtca	cggagttctt	tggactagac	octcatgaag	ttgatgtgct	540
catgggcaca	ttcaccacaa	gtttttggagc	ttcaggagggt	tacatagctg	gaagggaaggc	600
aaggatcttg	agtcacacctg	catgcctggt	gcogaacact	ggctcccaca	gcctccacag	660
gctgaccaga	gacttgcaaa	tgaatgaagc	gatggtagcc	cttgtaactg	ataggttgca	720
gggctggaat	tctggagaag	ggaactggga	cagggcagac	aaatttgggg	acctcgtgga	780
ttattttacgg	gttctactcg	atagtgtgtg	ttatgcttca	tcctagagcc	caccgatagc	840
agagcaaatc	atcagatcac	taaaacttat	catgggactg	gatgggacca	ctcaag	896

<210> 236

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = a,t,c or g

<400> 236

aatacatogt	cctttcctgc	tcagccttcc	tcaccagctc	gcccacatctct	gccccacctt	60
tcccagcacc	cctccaatcc	cctttcttct	ctggcctctg	cagaccaccc	acaatgtggg	120
ogtttctctc	cacttcaoga	acccgaacct	ctctgtccct	ccccctctct	ctcctatccc	180
accctgggtc	cctcctgggc	ttctccatcc	agttcacatc	atggatgtcc	ccctgggtctc	240
tatcccttcc	ccacgtctcc	aaaaaccatc	caacccctcg	gcctgggtca	gcttaaaatg	300
ctttgcattc	ctcctgggog	gcagcagctg	cggggagccc	agagcatgcc	gggacatggg	360
gcgtctctcc	ctctctctct	tccccctgce	an			392

<210> 237

<211> 398

<212> DNA

<213> Homo sapiens

<400> 237

aatacattgg	ggggctctgg	gtcctgcacc	atcttgctca	ggatgctgtg	gatctgggag	60
aacctggggc	gctcacctgg	gtccttctgc	cagcagtcga	gcattagtcg	gtgcataagg	120
ttaggacagt	tcctgggggg	tggcagccgg	aagccatcct	ccacagcctt	gatcacgtct	180
tggccagaca	tgtcccagta	aggccgctcc	ccaaaggcca	tcacctccca	catgatgatg	240
ccgaagctcc	acacgtcact	ggcagagctg	aagtggccaa	actgaagtgt	ctcggggagcg	300
gcccatagcg	ctgggctccg	gccactcata	gtgggtgtaga	cagcctctga	tcgggtcccg	360
gggcccgcgc	cgaagccaga	gatcttgagc	acaaggtc			398

<210> 238

<211> 1107

<212> DNA

<213> Homo sapiens

<400> 238

tggagtccat	gtagtctcac	atgtgggggc	ggcctacaga	ccagagacgt	cttctgcagc	60
cacctgcttt	ccagagagat	gaatgaaaca	gtcatcctgg	ctgatgagct	gtgtcgccag	120
cccaagccca	gcacgggtgca	agcttgtaac	cgttttaatt	gccccccagc	ctgggtaccct	180
gcacagtggc	agccgtgttc	cagaacgtgt	ggcgggggtg	ttcagaaacg	tgagggttctt	240
tgcgaagcag	gcattggctga	tggcagcttc	ctggagcttc	ctgagacctt	ctgttcagct	300
tcaaaacctg	cctgccagca	agcatgcaag	aaagatgact	gtcccagcga	gtggcttctc	360
tcagactgga	cagagtgttc	cacaagctgc	ggggaaggca	cccagactcg	aagcgccatt	420
tgcgaaaga	tgtgaaaac	cggcctctca	acggttgctca	attccaccct	gtgcccgcgc	480
ctgcctttct	cttccctccat	caggccctgt	atgctggcaa	cctgtgcaag	gcccggggcg	540
ccatccacga	agcacagccc	gcacatcgcg	gccgccagga	aggctctacat	ccagactcgc	600
aggcagagga	agctgcactt	cgtggggggg	ggcttcgcct	acctgctccc	caagacggcg	660
gtgggtgctg	gctgcccggc	gcgcagggtc	cgcaagcccc	tcatcacctg	ggagaaggac	720
ggccagcacc	tcatcagctc	gacgcacgtc	acggtggccc	ccttcggcta	tctcaagatc	780
caccgcctca	agccctcgga	tgcaggcgct	tacaacctgt	cagcggggcc	ggcccgggag	840
cactttgtga	ttaagctcat	cggaggcaac	cgcaagctcg	tggcccggcc	cttgagcccg	900
agaagtgagg	aagaggtgct	tgcggggagg	aaggcgggcc	cgaaggaggc	cctgcagacc	960
cacaaacacc	agaacgggat	cttctccaac	ggcagcaagg	cggagaagcg	gggcctggcc	1020
gccaaaccgg	ggagccgcta	cgaagacctc	gtctcccggc	tgctggagca	gggcgctcct	1080
tgtagtccat	caaaaaaaaa	gaattag				1107

<210> 239

<211> 678

<212> DNA

<213> Homo sapiens

<400> 239

atgaagcctg	acaatat	acttgacgaa	catgggcacg	tgcacatcac	agatttcaac	60
attgctgcga	tgctgcccag	ggagacacag	attaccacca	tggctggcac	caagccttac	120
atggcacctg	agatgttcag	ctccagaaaa	ggagcaggct	attcctttgc	tgttgactgg	180
tggtcctctg	gagtgacggc	atatgaactg	ctgagaggcc	ggagaccgta	tcatattcgc	240
tccagtactt	ccagcaagga	aattgtacac	acgtttgaga	cgactgttgt	aacttaccct	300
tctgcctggt	cacaggaaat	ggtgtcactt	cttaaaaagc	tactcgaacc	taatccagac	360
caacgatttt	ctcagttatc	tgatgtccag	aacttcccgt	atatgaatga	tataaaactgg	420
gatgcagttt	ttcagaagag	gctcattcca	ggtttcattc	ctaataaagg	caggctgaat	480
tgtgatccta	ccctttgaact	tgaggaaatg	atgttgagg	ccaaacctct	acataagaaa	540
aaaaagcgct	tggcaaagaa	ggagaaggat	atgaggaaat	gcgattcttc	tcagacatgt	600
cttcttcaag	agcaccttga	ctctgtccag	aaggagtcca	taattatcaa	cagagaaaaa	660
gtaaacaggg	actgtatt					678

<210> 240

<211> 387

<212> DNA

<213> Homo sapiens

<400> 240

aatacagtg	gccatcaatt	acttggggaa	ggtaatgttc	ctggatacaa	gattccgtgt	60
aggaggctct	caactgcttc	agttccttat	ttgccatctc	catgacagtc	atttcagcaa	120
attctcgtgg	agacgtggtc	ccagagagca	agttttgttg	taaatgagaa	tttctggggg	180
tcttcaaatt	ggcaactttg	cttctgatgc	aagttttata	ttttttgatg	ttctttgaat	240
aaagggtaaa	aacatgctct	tcaatttctc	ttgcaaagtt	ttgccacaaa	tcagctttgg	300
gttgatctgt	ggaagaacta	gttaaagctg	cgtaaagaag	ctctatgcat	ttagttctca	360
tgggtgttgt	gggatccagc	aactcac				387

<210> 241

<211> 390

<212> DNA

<213> Homo sapiens

<400> 241

aatacattgc	agggagaagg	ggtgagaaaa	aggctccgat	ccagcagatg	gtttgcccg	60
aaactatccc	caggacgtta	tcaggaaatgg	caaactcctg	ctgccccag	caactgaatca	120
gcttgcaaga	ggaacagtag	gtcaccagga	gctttctagg	aaaatccacg	aagagtgtca	180
cagccaagat	gatgatgaag	tcgaagatca	tcagcttgta	catttcctgc	ccaacttggg	240
tctcccagca	cgggtagagt	ttctggttgt	agccgcaaag	gtcacatgtg	tcatcatcac	300
aggatgtgat	cttggagccc	agcgtgaaca	ccaggacaca	tatggtggcc	agccgcataa	360
agacacacct	aaggattgtc	agacggatct				390

<210> 242

<211> 408

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(408)

<223> n = a,t,c or g

<400> 242
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gacaaagatg agttccacag aagggtggct gttctttaca tccagactga tgggttcggc 120
ctcttcggtg ttggagtgc cggccacgag ctgctcgtcc tcagcactga ccagctcctg 180
cagcacggcc tccacgatgg gcatcaccat ggcgggtggg gaggtgttgg acagccacat 240
ggacagcaac gtggtacagc acatgaagca gagcagcagc atgcccgggt tggccccggc 300
catcaagacc atgcgacagag caatgcgctt atgcagggtc cacttctcca cggcagccgc 360
cacgcatatg acccccacca gcagtagcgt ggtgttcttg aagtactn 408

<210> 243
<211> 411
<212> DNA
<213> Homo sapiens

<400> 243
aatacagtct ctgaattttg tgtaatgcat ttctcattta tgacatttgc tttgaagccc 60
agaactgcaa acaccaccaa tgttgccagg acagaagtga aaaaattgat gaaggacacc 120
aggacagcat caaagtggca gttgttgtct ctcttgttgt agcttgaaaa ggcaatgaca 180
ccaccaaatc ccagacctaa ggcaaagaac acttgagtag cagcttctct ccagaccttg 240
ggctccagca ttatttcaag cttaggggta aacatgtggc gaatgccatc aattgaacca 300
tttaaaagga atgctctgat gaggaagcaa ataagtacca catatggaaa cagagaacta 360
aaatatatga tttttccaga agactgaatg cctttgatca tagccaagca c 411

<210> 244
<211> 1271
<212> DNA
<213> Homo sapiens

<400> 244
atgacaacaa cattaattgg tcttttgaag actgcccagc tectcgtct tgtgcgctg 60
gccaggaaac tggatcgata ttcagaatat ggcgctgctg ttctaattgct cttaatgtgc 120
atctttgccc tgattgctca ctggctggct tgcatttggg atgcgattgg gaatgtagaa 180
aggccttacc tgactgacaa aatcggtatg ttggattcct taggacagca aattgggaaa 240
cgttacaatg acagtgactc aagtctctgga ccatccatta aagacaaata cgtcacagca 300
ctttattttta ccttcagcag ttttaaccagt gtaggattcg ggaatgtgtc tcttaacacg 360
aattcggaga aaatcttttc aatttgtgtc atggtgattg gctcactaat gtatgcaagc 420
atttttggga atgtatctgc aattatocaa agactatact cgggaactgc caggtaaccac 480
atgcagatgc tgcagtaaaa agagttcatt cgctttcacc aaatcccaa cctctgagg 540
caacgtcttg aagaatatct ccagcacgca tggacttaca ccaatggcat tgacatgaac 600
atggtcacaa atggtacatg ttcatcttgc acaagtgatg atggtcactt catcctggtc 660
tccaaccatc atcaaggagg acttatttac agttggaatg atgctgcttc tatgcaaagg 720
ccttttaatc atatcaagtc aagcctcctg ggatccacat cagattcaaa cctcaacaaa 780
tacagcacca ttaacaagat tccacagctc actctgaatt tttcagaggt caaaactgag 840
aaaaagaatt catcacctcc ttcttcagat aaaaccatta ttgcacccaa ggttaaagat 900
cgaacacaca atgtgactga gaaagtgaac caggttctct ctttaggagc agatgtccta 960
cctgaatata aactgcaggc accacgcac cacaagttta cgatattgca ctacagccct 1020
ttcaaggcag tctgggactg gcttatcctg ctggttggtc tatacactgc tatatttact 1080
ccctactctg cagccttctc cctcaatgac agagaagaac agaaaagacg agaatgtggc 1140
tattcttgta gccctttgaa tgtggttagac ttgattgtgg atattatgtt tatcatagat 1200
attttaataa acttcagaac aacatatgta aatcagaatg aagaagtggt aagtgatccc 1260
gccagtgat t 1271

<210> 245
<211> 384
<212> DNA
<213> Homo sapiens

<400> 245
aatacatgtg ggtcaagggt gtgtattttg ttttggaaga tgctattcct catgagactg 60
ttgtggaggg aggcagagct tccacctcgc tggagacgcg gcttagccgg tagagtgggt 120
tcattcctgt ccctggctgc agatggcttt gcttgggctt ctgggtgctgt caccttgacg 180
accttattgc ggtttatcat ttgttcacc catttttcta cttggacgtt gaatttcatg 240
aaaaccacat agcaaaaata agctgttaag agaagcaagc tttcccacca catgatgaca 300
ttatccagga aaaatatgat cagcatgatc aagtcaacaa tgtagaaaga cacatctcga 360
aagacgggcc accatgtcag gttt 384

<210> 246
<211> 601
<212> DNA
<213> Homo sapiens

<400> 246
cggacgcgtg ggcaacaagt ttattcagct cattctaaat ggtcccttat ataagggccca 60
aaagtactta acttttataaa gtttagcaata taatctcttc ttgcttataa ggtcaagtct 120
tttgtgatag ccttactagc aataatagaa aattgaaaaa aagcatttta gttcccgtgt 180
ttaaaaaatat ttcttataag tgttggtatt gcaaatgaat tattaccaaa tgttaataat 240
ctattatgtc ttgtttttta aagtgaatga atttttagct tttgagggtc ccatcttgtt 300
ggatatgaga attaaacatc taatcaaac aaatcagtta agtcaagcaa ctgctctagc 360
aaagctgtgt tctgaccatc cagagattgg cataaaaagg agttttaagc aaacttacct 420
tgtctgtctt tgtacatcat caccaaatgg aaagttaac gaagagggtga gtatgttttc 480
tttcattagt aattattttt taagttgaga aattaattgt taattagaat gtctttgatg 540
atccttttct ctgatatagc taacagatca ctggcatatc ttacattttg ggaagggtcc 600
g 601

<210> 247
<211> 418
<212> DNA
<213> Homo sapiens

<400> 247
cggacgcgtg ggtaaagaat gatattatth ttaatcaaac tgagagaaaa cagaaaatat 60
cagaaaatct caaacatttg gctagtgtac gtgtcgtaca aaaaaacotc gtctttgttg 120
taggtttatc tcagcgccda gcagaccagc aggttaagtc tcttgttttc tttgtcatct 180
tgatattttt tgtttccttg tcttacttgg aaataatatt tgaccctgct caattgtgtg 240
attcctctga acacattata tcttgaagga gaaaaataaga aattactttt gaataattgc 300
taagaaacca atgaccagtc gtgatcttag gcaagcgtct taatctttct tggcttcaat 360
ttcttcagtt ctaaaaactaa ggagttgaac tagatttcta acgtgctgac aatctgtg 418

<210> 248
<211> 404
<212> DNA
<213> Homo sapiens

<400> 248
gatttcaacta ccctggctgc catgatgagg accctgttct ccttatttgg tgatgtgaga 60
tctgatgttc atcggtttctc cgtgactctc tttggagcgg ccataaagtc tgtaaaaaac 120
ccagataaga agagtataga gaaccaagtc ctggacagct tggccccact acttctgtat 180
tctcaggatg aaaatgatgc agtagctgag gagagcaggc aagtcctaac tatatgtgcc 240
cagttcctga agtggaagct gccccgagaa gtgtactcca aagatccctg gcacatcaaa 300
cctactgaag caggaacaat ctgcagattc tttgaaaaaa agtgcaaggg gaaaattaac 360

atcctagaac aaacactgat gtactccaag aacccaaaac ttcc

404

<210> 249
<211> 440
<212> DNA
<213> Homo sapiens

<400> 249
tttgcgcgcc gccggcgccg gaggagcgt gactgcgctg cgcaggcgcc taggaggcat 60
tgtgccacc tggccgagtg caagctggtc tcctttccca ttggcatcta caaggtcctg 120
cggaatgtct ctggccagat ccacctcatc accctggcta acaacgagct taagtccctc 180
accagcaagt tcatgaccac attcagtcag ctccgagagc tccacctgga ggggaacttc 240
ctacaccgcc tccccagcga ggtcagtgcc ctgcagcacc tcaaggccat tgacctgtcc 300
cggaaccagt tccaggactt ccctgagcag cttaccgccc tgcgcgcgct ggagaccatc 360
aacctggagg agaacgagat cgtagatgtg cccgtggaga agctggcgcc catgccagcc 420
ttgcgcagca tcaacctccg 440

<210> 250
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(457)
<223> n = a,t,c or g

<400> 250
gcacgaccgg tccggnnnnc cggggtcgac gatttcgtca gtttaagatc tgggcagctg 60
ctaattccca taaggcaggg gggaggaatg ggagatggag ctgcttggtt aagttgggga 120
cctagggccc ctgggagggg ggctggatgc caaggagagt tgaatatggt tgggggagct 180
ggctgtggcc ctttgtcttt caggcccatc gggagcgggtg caggcaaggga gtccttgga 240
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tttttggcag cccggctcaa gaacgtgagg gcttgggaga gagctcccag gggagggagc 360
ctccgtggag tggagggagc cctgtgtggg cattgtggcg aggggtccca gggctgagaa 420
tgtagaatgg gcaccccaag agatccagga aggaggg 457

<210> 251
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(439)
<223> n = a,t,c or g

<400> 251.
tttcgtgttt gatctgaaac tgcagatccc tgggtttgca gcgcttctga ttcattggagc 60
cagctctgtt cctggcccgag agactgtcag gctgagacag aaaagaaaaa aaaaggctcc 120
tgatcacagc tcaggcagaa aagaagagct agtgacaact cacacagtag acaaattgga 180
gacaaaagaag ccagtaggcc gtgtgctctg cgggctctca ggggagctgc tccattctct 240
tctccttccc cgaaggaaaa cagagaagcg ggctctgggc agccacagaa aagctggctt 300
tccggagcac cctgtggcac cggaaccact cagtaacagc tgccagattt ccaaggaggg 360
cagagagcag gtactaagcg aaatcggagc cgggactgct ctanctcagc cgggactgga 420

tgccctcggg tggcctgtg

439

<210> 252
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 252
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 attcagcact gccaccacag ttccgcgctg tgcaccggta caccgccccg tcgcggatct 120
 gggggcctgt gaogttcatg tggctgatgg tgggtccgctc cgacatgggtg tactggttgg 180
 tgcggtggct gccatcccg cagatgggct catcgtcagag ggcccagggtg accgtggggg 240
 gcggggcgcc cttggccgca cacatcagtg agaactgctc cccgggggttg accaccttct 300
 cgctgaagga cgagacgatg cggggcgctgc catcctcaag tgcaatgatg gcaaagtcct 360
 gggcggtctg ggccttgcgg gtagcgaagc actggtaggc cccggaatgg ctcttttggg 420
 g 421

<210> 253
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 253
 ttctgtggct gcggggaggg atcatggact cttgtttgcc gtctgcaggg gccacgcaa 60
 gtaagcctgc tgtcaatgga ggaggacatt gatacccgca aaatcaacaa cagtttctctg 120
 cactatcagc acccccacc accccttcg aggtagctac tccttcgatg accatatcac 180
 cgactccgaa gccctgagcc gcagcagtc cgtgtttacc tcccacccc ggatgctgaa 240
 gcgccagccg gcaatcgaat tacctttggg aggggaatac agttctgacg tgccacgccc 300
 cctctccact caactatcct cctctctctt aggttacttc tccaccctca tgactggagc 360
 cgccttcacc aataatattg cctcttcaac aatcattctc t 401

<210> 254
 <211> 438
 <212> DNA
 <213> Homo sapiens

<400> 254
 ttctgtcagc ttgtcagggtg cccaggggtg ggggcaggta gatgagctgc tgggagagcc 60
 ggggagctgg gggagtgcgg ggactttctc ccaaatcagc ttgatggact cctctgacaa 120
 gatgcagatc tctggagtgc tgcctccctc tcctctgca gcctccaaag gtctcagagt 180
 ttacagagca ttcttgttca ttgatcact catgcttctg actagccaga ttaccaccca 240
 ggtccttgct cacctgtcct tcccattact gattgcccac cactccatct ggaccctca 300
 ataccccacc ccaggaccag cctcccatgg cctctcacc cgtgctcct ggcaggccac 360
 aaaggctctg aagcctgggg ccacgcaaaa gccagctgg tcgatgaaag gagggctcatc 420
 ctgactatgg atctgccc 438

<210> 255
 <211> 995
 <212> DNA
 <213> Homo sapiens

<400> 255


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ctgcagaacc gagaggattc ttctgaaggc atcagaaaga agctggtgga agctgaggag 60
ctcgaagaga aacatcggga ggcccaagtc tcagcccagc acctagaagt gcacctgaaa 120
cagaaagagc agcactatga ggaaaagatt aaagtgttgg acaatcagat aaagaaagac 180
ctggctgaca aggagacact ggagaacatg atgcagagac acgaggagga ggcccatgag 240
aagggcacaaa ttctcagcga acagaaggcg atgatcaatg ctatggattc caagatcaga 300
tccttggaac agaggattgt ggaactgtct gaagccaata aacttgcagc aaatagcagt 360
ctttttaccc aaaggaacat gaaggcccaa gaagagatga tttctgaact caggcaacag 420
aaattttacc tggagacaca ggctgggaag ttggaggccc agaaccgaaa actggaggag 480
cagctggaga agatcagcca ccaagaccac agtgacaaga atcggctgct ggaactggag 540
acaagattgc gggagggtcag tctagagcac gaggagcaga aactggagct caagcgccag 600
ctcacagagc tacagctctc cctgcaggag cgcgagtcac agttgacagc cctgcaggct 660
gcacgggcgg ccctggagag ccagcttcgc caggcgaaga cagagctgga agagaccaca 720
gcagaagctg aagaggagat ccaggcactc acggtaggtc tggggagcaa catcttcagg 780
ttgctaaagg cctcagctag gatgagtgtg gaactggcac tgagtatact ggctcaccct 840
tagaaattcc aggagggaaa acatgatcca caaagatatt cagtggccag gaaattggct 900
tacataggct gctgcttcat tggaaactag agatgagctt ggttggttat attcaaactt 960
ttcttagtat cttgaatagc tctctcttta cttat 995

```

<210> 256
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (405)
 <223> n = a,t,c or g

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<400> 256
tttcgtgggc ggtcctggtg cggaccctcc ggtcgcagtc atgtgggacc cgcgggcagc 60
taggatggac ctgacagctt acgctgagct gctgaaagaa tccggcaacc aggttcttaa 120
gaatgggaac ttctcttttg ccatcagaaa gtacgatgaa gccatccaga ttctcctgca 180
gttataccag tgggggggttc ccccagggga cttggctgtg ctgctgtgca acaaatacaa 240
tgcaattttc agccttggga agtggaatga ggcatttgtt gctgccaaag aatgtctcca 300
atgggatcca acctacgtga agggatacta ccgagctggt tattccttgc tgagggttga 360
ccagccttac gaagccgctc gcatgttttt tgagggtctg cgacn 405

```

<210> 257
 <211> 399
 <212> DNA
 <213> Homo sapiens

```

<400> 257
tttcgtggaa agtgcaagct ccaggccccc gggctgtttc togggagacg ggcgtttctg 60
gctagtgtct gaagggtctc ggcgtggctg ggattttaac ccttcatttt ctttcttgga 120
cccacgttac agcgtcggcg gagatgagaa catcggcacc gttaccaccc tggcgaaacat 180
cctccgggaa ttcaaccctt ccctgaaggg cttctctgtt ggcactggga aagaaaccag 240
tcctaattgc ttcttaaac aggctgtggc aggaggccga gctgaggatc tacctgtcca 300
ggccaggagg ctggtggacc tgatgaagaa tgacacgagg atacactttc aggaagactg 360
gaagataata accctgttta taggcggcaa tgacctctg 399

```

<210> 258
 <211> 1097
 <212> DNA
 <213> Homo sapiens

<400> 258
 agtgtgggag ccaggcaagg cgaagcccgga gatcgaatca ggcgtttctt tcccaaagg 60
 gaccttgagg tcctgcaggc ccagggtggag aggattatga cccggaagga gtcctgaca 120
 gtctattctt ctgaggatgg gtctgaggaa ttcgagacca tagttttgaa ggcccttggtg 180
 aaggcctgtg ggagctcggg ggcctcagcc tacctggatg agctgcgttt ggctgtggct 240
 tggaaaccgcg tggacattgc ccagagtga ctctttcggg gggacatcca atggcggtcc 300
 ttccatctcg aagcttcctt catggacgcc ctgctgaatg accggcctga gttcgtgcgc 360
 ttgctcattt cccacggcct cagcctgggc cacttctga ccccgatgcg cctggcccaa 420
 ctctacagcg cggcgccctc caactcgtc atccgcaacc ttttggacca ggcgtccac 480
 agcgcaggca ccaaagcccc agccctaaaa gggggagctg cggagctccg gcccctgac 540
 gtggggcatg tgctgaggat gctgctgggg aagatgtgcg cggcaggga cccctccggg 600
 ggcgcctggg accctcacc aggccagggc ttcggggaga gcatgtatct gctctcggac 660
 aaggccacct cgcgcctctc gctggatgct ggcctcgggc agggccctg gagcgacctg 720
 cttctttggg cactgttct gaacagggca cagatggcca tgtactctg ggagatgggt 780
 tccaatgcag tttcctcagc tcttggggcc tgtttgctgc tccgggtgat ggcacgcctg 840
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 ggcgttgacc tctttggcga gtgctatcgc agcagtgagg tgagggctgc ccgcctctc 960
 ctccgtcgtc gcccgtctcg gggggatgcc acttgccctc agctggccat gcaagctgac 1020
 gccgtgcct tctttgccc ggatggggta cagtctctgc cgacacagaa gtggtgggga 1080
 gatatggcca gacgaaa 1097

<210> 259
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 259
 gtatacttgg gagccggccc oggcctgttt ttttccaatg agggggccaa agagggtgag 60
 aaggccaata tccccaaact tatgctgccc cgagggggct tcagccaaag agagatggtc 120
 actggggaaa ggtccccacg ccccgaggag gaggaggagg aggaggaaga gggctttggg 180
 gaaagggcct cttgtcgcg gggccttttc cgggtccgat tgacacgtgt aggcctggcg 240
 gccccttcta aagcctctcg ggggcaggag ggcgatgcag ccccaagtc ccccgtcaga 300
 gagaagtcac ccaagtccg cttcccagg gtgtccctaa gcccgaagg ccggagtggg 360
 agtggggacc aggaagaggg tggattgcgg gtgcggctgc cca 403

<210> 260
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 260
 ctctggggag ggcacctgcg ctaccatctg cagcagaatg tgcatttcac agaggggact 60
 gtgaaactct acatctgtga gctggcactg gccctggagt atcttcagag gtaccacatc 120
 atccacagag acatcaagcc agacaatata ctgctggatg aacacggaca tggtcacatt 180
 acagacttca acatagcgac ggtagtga aaaggcagaaa gggcttctc catggctggc 240
 accaagccct acatggctcc agaagtattc cagggtgtaca tggacagagg ccccggtac 300
 tegtacctg tgcactggtg gtccctgggc atcacagcct atgagctgct gcggggctgg 360
 aggccgtacg aaatccactc ggtcacgccc atcgatgaaa tcctcaacat gttcaagggtg 420
 gagcgtgtcc actactctc cactgtgtgc aaggggatgg tggccctgct gaggaag 477

<210> 261
 <211> 547
 <212> DNA
 <213> Homo sapiens

```

<400> 261
tgctgacccat cactgacttc atcctgggtgc tgtatcgcta ctacagggtcc cccctgggtcc 60
agatctatga gattgaacaa cataagattg agacctggag ggagatctac ctgcaaggct 120
gcttcaagcc tctgggtctcc atctctccta atgatatgct gtttgaagct gtctacaccc 180
tcatcaagaa ccggatccat cgcctgcctg ttcttgacct ggtgtcaggc aacgtactcc 240
acatcctcac acacaaacgc ctgctcaagt tcttcacat ctttggttcc ctgctgcccc 300
ggcctcctt cctctaccgc actatccaag atttgggcat cggcacattc cgagacttgg 360
ctgtggtgct ggagacagca cccatcctga ctgcactgga catctttgtg gaccggcgtg 420
tgtctgcaact ggctgtggtc aacgaatgtg gtaccacccc ccaagatgag aggcctcgggc 480
tgggctgggg cctgggagaa cctggaagtg aggagcgct cttcccagcc gccatcacat 540
ctaggaa 547

```

```

<210> 262
<211> 588
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(588)
<223> n = a,t,c or g

```

```

<400> 262
ccggctcggga attcccgggc tcggccaagc tegtgttccct cgacctcagc tacaacaact 60
tgacctagct gggcgccggc gccttcgct cggccgggag gctgggtgaag cttagcctgg 120
ctaacaacaa cctgggtggc gtgcacgagg acgccttcga gacctggag tcgctgcagg 180
tgctggagct caacgacaac aacctgcgca gcctcagcgt ggccgcccctg gccgcgctgc 240
ccgcgctgct ctccctgctg ctggacggga acccctggct gtgcgactgt gacttcgccc 300
acctcttctc ctggatccag gagaacgcat ccaaactgcc caaaggcctt gatgaaatcc 360
agtgtctcct gcccatggag agcaggagga tatccctgct tgcgtgtcgg aggccagctt 420
cacgagtgtg ggttcacctg tcatcacaga cctctgcac atcattttct ctggtgtggc 480
cgtgtcattg cggcatcatc tcagcttctc ctgccactgt ggtcagtgct ccagaggtgn 540
caccacaacaa agatgoggag gatgaagacg aggacgagga tgactgag 588

```

```

<210> 263
<211> 343
<212> DNA
<213> Homo sapiens

```

```

<400> 263
accggcccgga atttcggggg tcgaccaccc cgtccggaag gccacaaagg ggggggagaa 60
ctgcagtttt gaggataaca aaaattggca gtccctttgg ggattaaatg gcaacttcaa 120
tttcttcagg gagccctggg gtgggaggaa taacctgccc aagggggttc ggacaacctg 180
ggccagaagt tccagccaaa acaaccggac gtttcaaaat aacaggaatt ttttgcggtt 240
gcaaagggac agccaaaaaa agggccagtt tgcccgttta ataagcccc ttgtcaacct 300
gccccaaagc ccggggggct tggagttcca gtaccaggcc acg 343

```

```

<210> 264
<211> 245
<212> DNA
<213> Homo sapiens

```

```

<400> 264
aagagctatg ctcaagtgcc tgagagaagg gcagccccct cctcataca actggacacg 60

```

gctggatggg	cctttgccca	gtggggtagc	agtggatggg	gacactttgg	gctttccccc	120
actgaccact	gagcacagcg	gcatttacgt	ccgccatgac	accaatgagt	tctcctcaag	180
ggattctcac	gacactgtgg	atgtttctga	ccccctgaa	gactctggga	agcagggtga	240
cctat						245

<210> 265
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 265						
ggcagcgggc	gacgcgccct	tgcgcagcct	ggagcaagcc	aaccgcaccc	gctttccctt	60
cttctccgac	gtcaaggcg	accaccggct	ggtgctggcc	gcggtggaaa	caaccgtgct	120
ggtgctcatc	tttgacgtgt	cgctgctggg	caacgtgtgc	gccctgggtgc	tggtggcgcg	180
ccgacgacgc	cgcggcgcga	ctgcctgcct	ggtactcaac	ctcttctgcg	cggacctgct	240
cttcacacgc	gctatccctc	tggtgctggc	cgctgcctgg	actgaggcct	ggctgctggg	300
ccccgttgcc	tgccacctgc	tcttctacgt	gatgaccctg	agcggcagcg	tcaccatcct	360
cacgctggcc	gcggtcagcc	tgagcgcc				388

<210> 266
 <211> 486
 <212> DNA
 <213> Homo sapiens

<400> 266						
aacagggagg	cctaagatga	gttcaggcca	tggaagatct	ccagtgaggg	gatcttgga	60
gatgtgaaaa	gcatcctgga	gggggaggta	gccctgcagc	ttagcgggtcc	agtttccctc	120
actggtctta	cttggtatgg	catagagggtg	ctcacacagc	agccccaggt	atcctccac	180
ttccctaaag	gcttaaacac	accaagatgt	gtatcagttt	cttaaaagagc	acaatagcac	240
attactgaac	aaccaaaatt	gcagagaagt	ggcctcattt	cctggaagtg	tttcatggac	300
ggggagggtg	tgaggtgagg	aaatcctcat	gaccaaagaa	acatgaggcc	tgaggactgg	360
cggttggtgt	caaccacatg	gagaccacgt	cgtgccctac	aagagcaatc	tggtgggtgtg	420
gtgctgtgga	agagagaccg	ccatggcgac	aaaacttggtg	catgtattta	gaatcagagg	480
ctcctc						486

<210> 267
 <211> 714
 <212> DNA
 <213> Homo sapiens

<400> 267						
ttttttttta	aatggtgccc	aggctggtct	caaactccta	gccttaagca	atcgctctgc	60
ctcagcctcc	caaaaatacag	ggattacagg	tgtgagccac	tcacaccctg	cctgtatttt	120
aactgcatct	cattatgtta	ttaaatttgag	aactaaatga	ggatatgttg	ccttgcatgt	180
ctgttagttt	gtactaagga	tctgattagg	aagtggccac	tgagctaaga	agaaaatggt	240
gcaaagaagg	aaagaggcca	tttctggatc	caatattcat	cttttactaa	attttcacta	300
gagagttgtc	ccctgtccca	aatgagattt	gggatgtgaa	ggccagtagc	ctaacaggta	360
acaattcctg	gggaagactc	ctgagaagag	tctcatgtta	caaactcatg	agggtccctc	420
ttctttcttg	taggcaccca	ggctggagaa	gcagaacagc	acacctgaga	gtgactacga	480
caacactccc	aacgacatgg	agccagatgg	catggggtag	atgcacagga	cagcggtgcc	540
aggggagggg	ctcccagggg	ccagagacct	ggcaggcctg	ggccagcaga	agcagttcac	600
cacacacacc	ccttttctct	attttcagac	tcataaaggc	ttaaaggatt	caagcatacg	660
ctcgagggtt	acatgtcttg	gcatctcaca	atgttggcga	aagggtcttt	tctt	714

<210> 268
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 268
 atcgctgca ccttttgtgg ccaggatgag tgggtcccgg agcgaagcac acgctgcttc 60
 cgccgcaggt ctcggttcct ggcattggggc gagccggctg tgctgctgct gctcctgctg 120
 ctgagcctgg cgtggtggcct tgtgctggct gctttggggc tgttcgttca ccatcgggac 180
 agcccaactgg ttcaggcctc gggggggggcc ctggcctgct ttggcctggg gtgcctggggc 240
 ctggtctgcc tcagcgtcct cctgttcctt ggccagccca gccctgccc atgcctgggc 300
 cagcagccct tgtcccacct cccgctcacg ggctgcctga gcacactctt cctgcaggcg 360
 gccgagatct tcgtggagtc agaactgect ctgagctggg cagaa 405

<210> 269
 <211> 436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(436)
 <223> n = a,t,c or g

<400> 269
 ccacccgtcc ggcagagaag atacaatacc ttgtgctgtt ttttgttatg tccatcctt 60
 cacaggctta tgacaagtta agcttgagtg atcacttact aatagcagta ctaaatctct 120
 tgagaaggga agtttcagag catgggcgtc atttacagca gtatttcaac ctgtttgtaa 180
 tgtatgcaa tttaagtaag aatttaagtt tttcagaatt ctgttttgat gtatcatatt 240
 aaattgtgaa gccatttatg tcaagtgtg aaatataatc tgatctgaag tagaaacaat 300
 ttcccataaa acctgttgtg aattttatct gaacatggca ctttcacctt ttactttgtt 360
 tatgcatgtg tctttgcggc agacacaggt cagaatctgn gctctgatcc tttttttttc 420
 ctttaaccccc caacgg 436

<210> 270
 <211> 489
 <212> DNA
 <213> Homo sapiens

<400> 270
 gagctacaga gccagcaggc ctgcacccac accaaggaga cagaacagct gcgcagccag 60
 ctgcagaccc tcaagcagca gcaccagcag gctgtggagc agatagctaa ggcagaggag 120
 acacacagca gcctgagcca ggagctgcag gccaggctgc agacogtca tagagagaaa 180
 gaggagtgtc tgagctgtc cattgaaagg ggcaaagtgc ttcagaacaa acaggcagag 240
 atctgccagc ttgaggaaaa gttggagata gcaaatgaag acaggaagca tgcgctggag 300
 cggtttgagc aagaggcagt ggctgtggac agcaacttga gagttaggga gcttcagcgc 360
 aaagtagatg ggtatccagaa ggctacgat gaactcaggc tgcagtctga agccttcaaa 420
 aagcacagct tggatctttt aagcaaggag agagaactca atggcaaaact ccgccatctc 480
 tctccatag 489

<210> 271
 <211> 670
 <212> DNA
 <213> Homo sapiens

<400> 271
aaggagaaaa gagtgacagt acaattgcct acagaatcca tacagaagaa ccaggaagat 60
aagctcaaga tgggtccag gaagcaaaga gaatttagcg gatctgacag agggaaactt 120
ccaggaagtg aagaaaaaaa tcagggacca tcaatgattg gtcgaaaaga agagagatta 180
ataactgaaa gaaaacacga acatctgaag aataaatcag caccaaaagg cgtcaagcaa 240
aagggttatcg atgcacatct tgattcacag actcagaatt ttcagcaaac acaaatacag 300
accgctgaaa gtaaagctga acataaaaaa ttgccccagc catataatag tctgcaggaa 360
gaaaaatgtc tcgaagtcaa gggcatacaa gagaacaag tcttctctaa tactaaagat 420
tcaaagcaag agattacaca gaacaaatct ttcttttctt ctgtgaaaga atcccagcgg 480
gatgatggaa aagggtgcctt aaatatagtg gaattcttga gaaaacgtga agaactgcat 540
cagattttgt cgacagtga acagccttga tcatatcctt tcattcgtgg tctcttacac 600
ttcagatata tottagttac ttcccatata ttcatgaact gtattatcag ccttattatg 660
tagaatctcg 670

<210> 272
<211> 524
<212> DNA
<213> Homo sapiens

<400> 272
ggagcggaag tgtatgcaag gaaaatatgc aggagctatg gaatctgaac cctgtgtctg 60
cactgaggct gattttgatt gcgactatgg ttatgagcga cacagcaatg gccagtgcct 120
gocggcattt tgggtcaatc catcctctct gtcaaaggat tgcagcttgg gacagagtta 180
cctcaatagt actgggtaca ggaagggtgg ttccaataat tgcactgatg gcgtaaggga 240
acagtacact gccaaaccgc agaagtgcc agggaagcc ccgcgggggc tgcggatagt 300
cacggctgat ggaaagctga cagcggaaca aggacacaac gtcactctca tgggtgcaatt 360
agaagagggt gatgttcagc ggacactcat ccaagtggac tttggcgatg gtatcgcggt 420
gtcttacgtc aatctcagct ccatggaaga tgggatcama cagctctatc agaacgtsgg 480
catttyccgt gtsaccgtgc aggtggacaa cagtctgggt tctg 524

<210> 273
<211> 395
<212> DNA
<213> Homo sapiens

<400> 273
ccggacgcgt ggggttcagag cagcatggga cttgaaactt tgtatgttca tgactcttta 60
ttgccccatg acaccctagc aggtctaattg tgggaccccc tcagcttacc gtatggaata 120
cttccaatct gagtcatgac aaccgacgga aatacatctt tagtgatgag gaaggacaaa 180
accagctggg catccggatc caccaggaca tccccctccc tccaaggaga agagagctcc 240
ctgccttgcg gaccaccaat gggaaagcag actccctaaa tgtatctcgg aactcagtga 300
tgcaggaact ctcagagctc gagaagcaga ttcagggtgat ccgtcaggag ctgcagctgg 360
ctgtgagcag gaaaacggag ctggaggagt atcac 395

<210> 274
<211> 402
<212> DNA
<213> Homo sapiens

<400> 274
agagaagtag gttccaggaa acaaaaagggt cagaggtgta cctgtgaaag acaacagcag 60
gtgtgaaagc caagaaactg cagcgctcag ttcactcaag aaacaaagg gttcaatatg 120
gatggactgc agatctccag atggaagcgg ggcattggcca ggccagcatc ctatggctct 180

actttgagac	gggtacctgg	gtgtatcctg	tgtttgccaa	actcagtctt	ttgggtctag	240
cagctttatt	ctctttaagg	gagatattca	tcgcccgtaa	tggggtagtt	ggtgagacgc	300
tcacccattg	taagaggggt	atctggccca	ggcatggttt	taaaagtact	aagagatccc	360
ccgagtatct	tgaggcgag	agttcgcagg	tgggagaaaa	ag		402

<210> 275
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(393)
 <223> n = a,t,c or g

<400> 275						
cccacgogtc	cgaaattctc	tgagttcagg	gagatggttt	ttttattcag	gtaagatttc	60
ttatgtattt	tggcagacat	tttgtattta	gcgtatttaa	ggctgtcagt	ttacaaaaat	120
taactaggaa	ggaatattac	atgcattgag	tttagttctt	attcacagga	atatataaag	180
tcataatatg	catatttcat	tttttagggc	tctcttgcta	cttgccagtt	atctgagcca	240
ttattgtggg	tcattttgag	agtattggat	actagtgatg	ccttgaaagc	atttcattgat	300
atgggtaaga	taatatattca	ataactatca	tttaagtgtg	gttatgtgat	agtatgttac	360
attttcattt	ttgtagcctt	ttgtggaagt	tan			393

<210> 276
 <211> 694
 <212> DNA
 <213> Homo sapiens

<400> 276						
gcctcccatg	gggggttttg	gtgggacagc	aggcaggtag	gctgggaggt	ctctccatgg	60
tgetggtgac	agagcctggg	tgggcatctc	gcccacagac	tggtccccc	aggtgggtgga	120
gctgtgtaag	aagtaccagc	agcagaccgt	ggtagccatt	gacctggctg	gagatgagac	180
catcccagga	agcagcctct	tgcctggaca	tgtccaggcc	taccagggtg	gtcctgtgag	240
aagggaatgga	gaggctggcc	ctgggtgagc	ttgtctcca	cccatagttg	ggagaaatca	300
caagaaccag	ggaccatggt	gtctcctgag	ttctgaagtg	tgtctttggt	gggtcttaag	360
gcttgggaact	ggaatcccc	tgggcccaggc	gtggtgggtc	atgcctgtga	tcccagcact	420
ttgggaggcg	aggcaggagg	attgcttgag	cctaggagtt	tgagaccagc	cagggcaaca	480
tagtgagatc	catctctgca	aatacaaaaa	aaagtagtca	ggcatgggtg	tgcattgctg	540
tagtcccagc	tacttgggag	gctgagggtg	gagaattgct	tgagtcocag	aagtcaaagc	600
tgcagtgagc	tgtgataatg	cgactgcact	ccagcctggg	tgacagaggg	agaccctgtc	660
tcaaaaaaaaa	aaaaaaggaa	gaaagaagaa	agag			694

<210> 277
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(412)
 <223> n = a,t,c or g

<400> 277						
tggtcctaca	ggaaaggctg	gataatttcc	aaaggaaatg	catacagtta	gccagcagca	60

```

cagaaggaaa agtcgacaaa ctccaatga gaaacctctt cattagttat ctccacacac 120
caaaacacaa acaacatgaa gtgttacagg caatgggaag catcctgggt atcacagggg 180
aggaaatgga ggcgctgttt caggaagagc atggcactgc taccagggtg atgactgggt 240
ggcttgaagg aggatcaaaa agtgtcccta aaacaccact ggggctgaat cagcaacctg 300
cccttaatgg ttctttttca gaactttttg ttaaatttct taaaacagaa tctctttcat 360
ctactcttcc aacaagnctt cctcctcata attctccagg aaagatcaaa ct 412

```

```

<210> 278
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(457)
<223> n = a,t,c or g

```

```

<400> 278
cggaattccc ggtcgacnnn nccccagaaa tggaggagaa tgttctggcc ataagagcca 60
ccatgcaaat gcaagtcggg tgaggtgggg gcaggggcat ccaaggaagc aggagccaag 120
gcttctctct tcagggcctc tgactctcat ccacttctgt atccctctag tcttctctgc 180
tttttgacgc tagttccaga gcttcagggt ggagaagggt gatactcctg ggcatagggg 240
ttgtctggcc catcctgttc ctgcccccac tcacctctcc caaccatcat ttccaggggc 300
cagctggaga cagcctgaa gtggagggaac tatgagggtga agctgcggct gctgctgcac 360
ctggagggaac tgcagatgga gcatgatatc cggcactatg acctggagtc ggtgcccatg 420
acctgggacc ctgtggacca gaaccccagg ctgtgtcc 457

```

```

<210> 279
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(441)
<223> n = a,t,c or g

```

```

<400> 279
ggaggcagga ggcggngagg tcgggtgccg ttgggaagga accgagtcgg gaagaggcgt 60
gggagcgagg ggcaccgagg acgctggccc ggactgcggg ggcagctcgc gggagaccga 120
tgggcggctt ggaagcctgc aggattgcag atgaggattg agttcggaat ggagtgagga 180
atgatgtagg atggaggaaa gtgaaggaag gggaggggga acagaggaaa atgtgggagg 240
agtggttggg aatttgtgag tagcaggcag gaagggatgc ggaaggctgg gtaggggctg 300
cagaggattg gaatgagcgg gaaggtagc aggaatcaga ggaagtggtg ccgagagctg 360
aagggttcgg caggagtggt cattaaaagg aactggtgac ttgacatgtc ccttcgctcc 420
ggntcctgat gtctcccata t 441

```

```

<210> 280
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(447)
<223> n = a,t,c or g

```



```

<400> 280
ttgcctcggt ccggnnnaat tcccggtcga cgatttcgac cactaaccog ccctgcagcg      60
tctcagccac aggcctaaca agttggctcc cgcctccgct ggccatcgca ttggaaggct      120
acctctggct ctcccacgcg cccagtaaga ttggctactg tgaggaagcc aaatcggatc      180
cgagagtctt tttctaaagg ccagtactgg ccacactttc tcctgccgcc ttcctcaaag      240
ctgaagacac acagagcaag gcgcttctgt tttactcccc aatggtaact ccaaaccata      300
gatggttagc tccctgctca tctttccaca tccctgctat tcagtatagt ccgtggacca      360
atcacaccag catcgatagg gagagtgtaa gaaacatgaa tctgcatgtc aacgagatcc      420
ccaggtgagt cgtaagtagg tttggga                                     447

```

```

<210> 281
<211> 448
<212> DNA
<213> Homo sapiens

```

```

<400> 281
cgcggaattc tcgggtcgac gatttcgtgt gactgtgagc aggtcccttc accgctcaga      60
gtctcggttt tcccatctga aaaatgggaa cagccgtctg ggtcccaaa gagaaagaga      120
agagggacaa agccagccaa gagggagggg acgtccctgg ggccogccaa gactgcaccc      180
cctccttgaa gagcttggtc gccactggga acctgctgga cttagaggag acagctaagg      240
ccccgctgtc caccgtcagc gccaacacca ccaacatgga cgaggtgccg cggccacaag      300
ccttgagtgg cagcagtgtt gtctgggtga gtgggtgtgt ggccagcaga tcggtgatcc      360
tcagcctgac ctctgggtga gcctggggct gctccaggga ccaggccctg ggacccgaga      420
cttgtggggc tctgggagga ccaaacc                                     448

```

```

<210> 282
<211> 472
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = a,t,c or g

```

```

<400> 282
tttcgtatga ttgagaaga cagtgaagac acaaatatct gtaaaataaa aagatatctc      60
tcttattgca acagtaaaag cttttgatca ctaacatttc ttgtgacaag aattatcatt      120
gatacagtta atacatata acacacaaat acatactaat aggtagtatg gaggcagagt      180
ttttaagtag ctgtcaaaag cctgtcgcca cttcagattt ggcttaagct tgtgaacttt      240
aaacaagtca tctaaaagag gaagtaaaac tgggtagtgt taaggcatca caaagagggt      300
tacacaagtt aaagttgtac tggcttttaa ataaccaaat ggatatccaa gttcattgta      360
ctttccactg ctagtaacaa atacctgccg gcaggtatgg ggagactttc gttccaagat      420
atactgagtt aagggcgaag gttcaagttc atatttgtca naaggaagtt tg                                     472

```

```

<210> 283
<211> 463
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = a,t,c or g

```

```

<400> 283
tattcggaacc gccccggaat tatcgggctcg acgattctgt ggccgcttcg ccattcgtgc      60
cgactgcctg attctctcag ttttcttttc agaggcaggn tccaccttga ttcttggggg      120
aatagaagcc atggtgggcg tgggtgactgg tgctgactcc tcgctgctct caaccctctc      180
ccggttcttc cgcaccaactg gtgggggctg cagcttgatg gagaactgag ttgactcctc      240
aggatgcatt tggcactgca gtggtggaac catgagccct gggtaacggg gaaaagtcgg      300
aggactcaga tggtagttga acacagaaca agcttgagaa tgaaggtagt gtttcatttc      360
ctcagggttg aaggagaagc agctgctgct ggtgaaaggg ctcaagcctg gtgatgggct      420
ataagagaag atggtggggag tcagggagag ggctggtgaa act                          463

```

```

<210> 284
<211> 449
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(449)
<223> n = a,t,c or g

```

```

<400> 284
aaaaaacta ccaagaacgt tattggatat tttggcagat ggcaccattt tgaaagttgg      60
agtgggatgc tcagaagatg ccagcaagct tctgcaggat tatggcctcg ttggttagggg      120
gtgcctggac ctccgatacc tagccatgcg gcagagaaac aatttgctct gtaatgggct      180
tagcctgaag tccctcgctg agactgtttt gaactttccc cttgacaagt cctcttctact      240
tcgttgacgc aactgggatg ctgagactct cacagaggac caggtaattt atgctgccag      300
ggatgcccgag atttcagtgg ctctctttct tcatcttctt ggataccctt tctctaggaa      360
ttcacctgga gaaaaaaaaac gatgaccaca gtagctggag aaaagtcctg aaaaatccag      420
ggtgggtctn nnnnaatccg ggaggtcct                          449

```

```

<210> 285
<211> 447
<212> DNA
<213> Homo sapiens

```

```

<400> 285
gcgcaagtcc cggatctgac cgattcgacc atattattca tactcgggco ttgatagga      60
ctgctcatgg ctccactgg cgaaagcatg gttacctgac gtgatgatct tggctctgca      120
tagagtgtct gaagatggta taaaccgaca acaagctcaa gaatggtgca tcaaactgg      180
ctttgaattg gtagaactta gtccagagga gttgcctgag gaggatggta agtgtttatg      240
tgtaggaga aaatatggca cttacatatg agagattatt ttaattcatg gaagaagaat      300
cacagcaaaa ttcaagaaac ttttttgccc agctgtttca aggatttaag caaaatccat      360
tgatgtaatc ttataatctt acacttagtg gaataactca tttttttgt tttaccacct      420
ggttttagaac ttttgaaaat gtgtgtt                          447

```

```

<210> 286
<211> 493
<212> DNA
<213> Homo sapiens

```

```

<400> 286
attccctgct cgacgatttc gtagtgaacc tggatagggg tttggacaac aagcacaggg      60
aatgagggat ctgaggctgg aggatgggga gaggggagag actagagaac ccagggctga      120

```

gatgtgatgg	gtagagtag	agtgaggag	gtaactgagg	agcagtagtt	gatctttacc	180
tctttcacct	ccctagacag	cagaggatgt	gctgactgta	gcctatgagc	atggtgtaaa	240
cctgtttgac	accgccgaag	tgtacgcagc	aggaaagtaa	ggactggggg	gaaagagcta	300
agctccattt	ggaaggetga	gaggacctca	gggattatct	tctcgttttc	cctctaaaga	360
accctgggac	ttctgagaac	gtgaagttcc	aaccttttgg	cggaggggacc	cgaaagcact	420
gtaggagcta	cagtcccaac	attagtccct	ctctggctta	gaagtcaatg	ggcgtactgt	480
gcagctacat	taa					493

<210> 287
 <211> 427
 <212> DNA
 <213> Homo sapiens

<400> 287						
tttcgtggca	gaggtgaggg	gagaatgggc	caagtacatg	gaagtccatg	agaaggcctc	60
cttcaccaac	agtgaagctgc	accgtgccat	gaacctgcac	gtcggcaacc	tgcgcctgct	120
cagoggcccg	cttgaccagg	tccgggctgc	cctgcccaca	cggccctct	ccccaaagga	180
caaggccgtg	ctgcaaaacc	taaagcgcat	cctggctaag	gtgcaggaga	tgcggggacca	240
gcgcgtgtcc	ctggagcagc	agctgcgtga	gcttatccag	aaagatgaca	tcaactggctc	300
gctggtcacc	acagaccact	cacagatgaa	gaagctgttc	gaggagcagc	tgaaaaagta	360
tgaccagctg	aaggtgtacc	tggagcagaa	cctggccgcc	caggaccgtg	tactctgtgc	420
actgaca						427

<210> 288
 <211> 469
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (469)
 <223> n = a,t,c or g

<400> 288						
tttcgtcaac	ttgggtattt	tgacctgtat	agaatgttct	ggcatccata	gggaaatggg	60
ggctcatatt	tctcgcattc	agtctttgga	actagacaaa	ttaggaactt	ctgaactctt	120
gccggccaag	aatgtaggaa	acaatagttt	taatgatatt	atggaagcaa	atttaccag	180
cccctcacca	aaaccacccc	cttcaagtga	tatgactgta	cgaaaagaat	atatcactgc	240
aaagtatgta	gatcataggt	tttcaaggaa	gacctgttca	acttcatcag	ctaaactaaa	300
tgaattgctt	gaggccatca	aatccaggga	tttacttgca	ctaattcaag	tctatgcaga	360
aggggtagag	ctaattggaac	caetgctgga	acctgggcag	gagcttgngg	agacagccct	420
tcaccttgcc	gtccgaactg	cagatcagac	atctctccat	ttggttgag		469

<210> 289
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 289						
tttcgtggca	agcggcgggc	cagcgacggc	gcgaatgtcg	gactctcagt	ttttctgtgt	60
ggcggaggaa	cgcagcggcc	actgcgcgt	ggtggacgga	aacttcctct	acgtgtgggg	120
gggctacgtg	tctattgaag	acaatgaagt	atattgcct	aatgatgaaa	tttggaccta	180
tgatattgat	agtggtgtgt	ggagaatgca	cctcatggaa	ggagaactcc	cagcctccat	240
gtcaggaagc	tgtggtgctt	gcattaatgg	aaagctgtac	atttttggag	gatatgatga	300
caaaggatac	agcaatcgac	tttattttgt	taatttacga	acaagagatg	aaacctacat	360

ttgggagaaa atcaccgact ttgaagggca accacctaca ccacgtgata aactttcctg 420
ctgggtatat aaagacagac taatatattt tggt 454

<210> 290
<211> 378
<212> DNA
<213> Homo sapiens

<400> 290
tttcgtcagg gccagctgta caaggtcttt ctccacgggt cccagggcca ggtttaccac 60
tcccagcaag tggggcctcc aggcctcagcc atcagcccag acctgctgct ggacagcagt 120
ggcagtcacc tctatgtcct gactgcccac caggtggacc ggatacctgt ggcagcctgc 180
ccccagttcc ctgactgtgc cagctgcctc caggcccagg acccgctgtg tggctggtgt 240
gtcctccagg gcaggtgtac ccggaagggc cagtgcgggc gggcaggcca gctgaaccag 300
tggctgtgga gttatgagga ggacagccac tgctgcaca tccagagcct gctgccgggc 360
caccaccccc gccaggag 378

<210> 291
<211> 385
<212> DNA
<213> Homo sapiens

<400> 291
tttcgttaca tgcccaacaa cagacaacag ctactgagga aaaggcacat aggaaatgac 60
atcgtcacca tcgtcttcca ggagcctggg gcacttcctt ttactccaaa aagcatccgg 120
tctcactttc agcatgtctt tgtcatagtc aaagtgcata atccatgtac cgaaaatgtg 180
tgttatagtg ttggagtttc cagatcaaaa gatgtgccac catttggccc accgattccc 240
aaaggtgtaa cttttccaaa gtcagccgtg ttccgggact tccttttagc caaagtaatc 300
aatgcagaaa atgcggccca taaatcagaa aagtttcgag caatggccac tcgaacgagg 360
caggagtact tgaaagatct ggcgg 385

<210> 292
<211> 453
<212> DNA
<213> Homo sapiens

<400> 292
gtcgacccac gcgtccgcca cccgcgacaa cccagtcctc tgaaagcact atggatacct 60
cactgaagaa ggagaagtca gccatcctgg atctttatat tcctcctccg cctgctgttc 120
cctactctcc ccggtatgtt gctgtccatt gtcattggtat gcttgtctcc tgttggtgtc 180
atttgtaaat ggtggagtga aaagaggatc ttgagagagg aagttgctga gccacagtgt 240
gacagggctg aatcttgaac tgccgttaaa agtattatca gocttatttt ataggagtgt 300
aaggacatat ctgggttctg tggggcttga aactatacag attggtgggg aggggccttt 360
tgacaaaaaa atattggcgg gcttggccat agtggggaca ctaacacctg gtaatccaa 420
actctgggag agtgaggtct ttaatcact tga 453

<210> 293
<211> 427
<212> DNA
<213> Homo sapiens

<400> 293

agggagaaaag	aggaggagggt	ggaagaggaa	gaagataagg	tggttaagga	gacagaaaag	60
gaggctgagc	aggaaaagga	agaagacagc	ctgggagcgg	ggacceaccc	ggatgctgcc	120
atccccctcg	gggagcggac	atgtggctct	gagggtctcc	gctccgtcct	ggacctgggt	180
aactacttcc	tgtcccccca	gaagctgaca	gcagaaaacc	gctactactg	cgagtcgtgt	240
gcctccctgc	aggatgccga	gaaggtgggt	gagctgagcc	aagggccgtg	ctacctcatc	300
ctcacactgc	tgcgcttctc	tttcgacctg	cgcacctatg	ggcgccgcaa	gatcctggat	360
gaagtctcca	tccccctgct	gctccgcctg	ccactggctg	gtggccgtgg	ccaggcctat	420
gacctct						427

<210> 294
 <211> 392
 <212> DNA
 <213> Homo sapiens

<400> 294						
catatttcca	tggaacaaga	ggggtgaact	ttgaatttca	aagattcatt	actgaacagg	60
taagagtgat	gattttttgta	ttcctaggag	aatcagacaa	aatactaaca	gctttgttgt	120
ttttgtttta	gacagactac	tctgatagtt	tatatattgt	cttttattgg	aatggttatc	180
tttactttoa	cattggacct	tagatatatt	atcatcgtgt	ttgttactgg	aggggtgctt	240
gggtaagtat	cagatgtgtt	aaggaggaat	gatagcatgc	tgttataatt	ctgaagtatt	300
attactctgg	tctttaattt	tttcagttca	tccaaagttt	cttcaatatt	ttaaacttca	360
aaggattcat	tctatgcata	taaacatgta	ag			392

<210> 295
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 295						
ctctggcttc	ctcacagcat	ggaatactga	acaatctttc	tctccttttc	agtatttgca	60
aaacatgtat	tcggacaatg	gatcatcact	gcccgcgggc	gaacaattgt	gtaggagAAC	120
agaatcacag	atttttttgt	gotcttcaact	gcaagtcaaa	acatttttgc	attgaattta	180
cattgaatac	gaacttcttt	aactgcttct	tgctggagc	agagaaatct	actatcgacg	240
cgccattttc	tctccagcct	tttctccagg	attcaaaagta	taatactgog	ctgtcattgt	300
cagaaagtat	ctcccaataa	gtaacatgct	ggctcgtatt	atcttaagag	ctcacgtgta	360
tttaattctc	tcccatatgc	cctcaatcgc	tattgtttat	tt		402

<210> 296
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 296						
gtggaattcc	agagatcata	ttctaagaac	atgtttcgat	tttgttttac	attgccagtt	60
ttgttatctt	ggcacattat	cccatagact	cctaggagtg	actgccttgg	tcagaaaggT	120
ggtgtgggct	aaatggaaac	caagtttccc	tgacagggca	cccactgtca	ccccctgcct	180
agtttatggT	caggcctaac	aaatataaag	ccagtattca	catagtttgg	attatcattt	240
attgcagggt	accaaaaatc	ctttcacact	ggcgacagt	tccaatcctg	gacagacgga	300
gagactacag	gagtttagcc	agaagatgga	ccaggtaaga	ggtcactggc	cagtcagtac	360
ttagaatcct	ggggctccag	tgaacaggag	gctgcattgt	catgtcttgc	cactttttga	420
acatctaa						428

<210> 297

<211> 432
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(432)
 <223> n = a,t,c or g

<400> 297
 gtgcaattcg cggtnnacgc tggtnnttggg taccttttatt ttactgggca tccaggacaa 60
 cattttgggc ttgattctgg ccacacccccc cttcatggcg ggggggaagt tgtatagcac 120
 tatggggcgc ttccctcagag accgaaagaa cccggcgtgc cgggagatgg ctgtggtact 180
 gctggccaac ctggctcagg gggacagcct ggacagctcg gccattgcag tgcagaaagg 240
 cagtatcggc caccctcctgg gcttccctaga ggacagcctt gccgccacac agatccagca 300
 gagccaggcc agcctcctcc acatgcacaa cccacccttt gagccaacta gtgtggacat 360
 gatgcccggc gcttgccgcg cgctgcttgc cttggccaag gtggacgaca accactcaga 420
 gtttactctg tt 432

<210> 298
 <211> 595
 <212> DNA
 <213> Homo sapiens

<400> 298
 cgggaattca attattttaa attgggtttt ggtataccat aggtaaaaaa tggatgagcc 60
 ttacttaatc tgtgtaactt tatttgggta caatcaactt ataaaaactag aagtaaattt 120
 ttotcagaaa aaaatgtgta tttgttgctt ccagttctgt aaccttgagc tgattgggtca 180
 atgataatag ttcccttactt tgacatagca acttcaaaat attcacttat ttgggtcatta 240
 gaataagccc gagaggcaga atgattgcat cagtatgtga ttgtgacttt ctggtagttc 300
 tttctgtaat tctggattta ttttccctage ttcttcatga ctgggttaacct cccttgggt 360
 tttgaatttg ctgttgaaat cacttacctt gaactctgaag gtacttcacg ttggtcttctt 420
 aatgcttctg cacaggtaaa cctctgattt ctctaaacct gagatgatta ttataccaga 480
 tattctagtg agtaatgagt ttgaccatgg ttttatttgt tgttgttgtt gttgttttgt 540
 tttttggaga cagagtcctg ctcagcctgg gtgacagagc gagactctgt ttcag 595

<210> 299
 <211> 492
 <212> DNA
 <213> Homo sapiens

<400> 299
 aaaatcaaag caaagaatct caaaaactat gatctctgca gcatttttct tggaaacctct 60
 acgctcttgg tttgggttgg agtcacacaga taactgggtt atttccagge atataatgtg 120
 ctgattttta caatgcaggc ctcactgcca aaagttcttc ggttttgtgc ttgtgctggg 180
 atgatttate tgggttacac attctgtggc tggattgtct taggaccata ccatgacaag 240
 tttgaaaate tgaacacagt tgctgagtgt ctgttttctc tggtaaacgg tgatgacatg 300
 tttgcaacct ttgcccacat ccagcagaag agcatcttgg tgtggctgtt cagtcgtctg 360
 tatttatatt ccttcatcag cctttttata tatatgattc tcagtctttt tattgcactt 420
 attacagatt cttatgacac cattaagaaa ttccaacaga atgggtttcc tgaaacggat 480
 ttgcaggaat tc 492

<210> 300
 <211> 445
 <212> DNA

<213> Homo sapiens

<400> 300
 ccagtgtggt ggaattcact aaacggagct tcagaagtga cattttctgt gcatgtaaaa 60
 gatggtggct catttccaaa gacagattct acaacagtga ctgttagatt cgtgaataag 120
 gccgatttcc ctaaagtcag agccaaagaa caaacgttca tgtttcctga aaaccaacca 180
 gtcagctctc ttgtcaccac catcacagga tcctctttaa gaggagaacc tatgtcatat 240
 tatatcgcaa gtgggaatct tggcaatact ttccagattg atcagttaac agggcaggtg 300
 tctattagtc aaacctctgga ttttgaagag atacaaaaat atgttgtatg gatagaggcc 360
 agagacgggtg gtgtccctcc tttctcctct taagagaaac ttgatataac agtattagat 420
 gtcaatgata atgccccaat tttta 445

<210> 301

<211> 433

<212> DNA

<213> Homo sapiens

<400> 301
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 aagatgagtt aaatgaataa gcaaaaggag ccacttcttt ctctgctctc cactcaggcc 120
 ttgccagcca tttaaatagt accactgtgg ctgttctctg aaccctattc atttgccttc 180
 ctttgggtta ttgttttccc cttttagaca aagatttgca gctcccttcg ggattcaatt 240
 gcaacttcga ttctctcgag gagccctgtg gttggatgta tgaccatgcc aagtggctcc 300
 ggaccacctg ggccagcagc tccagcccaa acgaccggac gtttccagggt aagccagctg 360
 tgagtgaaga tatgaaagag ttaaggccag cttgttccac atacttcaac cccagattcc 420
 cttacaagct tca 433

<210> 302

<211> 412

<212> DNA

<213> Homo sapiens

<400> 302
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 gtctgtgcac atttatgtca cccagctggc tgagaagttc gacctcagga ccacctagct 180
 atacatctgc gagcggcact tccagaaagt gctgaaccgg agtctgttca cgggcctgag 240
 ctccatcacc cactttggcc gtcccccctt cgagcccttc ttcaactccc tgcaggagggt 300
 ccaccacag gtgogcaaga tcggggtgtt cagctgcggc cctccaggaa tgaccaagaa 360
 tgtagagaag gcctgtcagc tcgtcaacag gcaggaccga gcccaacttca tg 412

<210> 303

<211> 453

<212> DNA

<213> Homo sapiens

<400> 303
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 caaataataa cttacatcta ttaatttaaa acacaggaga gtaaataagag atggaatttc 120
 aatcttaaaa gagattcgaa cctatggaaa ttgagcagaa atgctttcta atggctgtta 180
 ttttgttttt cagacactca tccttgatcc tccttcattg cctttttcat ggggtcttta 240
 ttaaaggctt ctgacactta aatgagctct ctttagaaaa acagaaatag aaattaaata 300
 gatggctttt tttcttttac agctggctct ttgggacccg gctctatgag atgggtgactc 360
 taggagcacc accgtatcct gaagttcctc ctaccagcat cctagagcat ctccaaagaa 420

ggaaaatcat gaagagaccc agtagctgct cac

453

<210> 304
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 304
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 tccccacaga cacttttggg gtgttgggggt atgttgctgc aaggcctacc gccggggctt 120
 ccgcagctgc tcagacacag gatagtgagt ctgactcaga cctcctgctt ggggttgacc 180
 cgggtgtcccc tcccaggccc tcaggaaagc agagagcttg aagaaatgtc tctctgtcat 240
 ggaagccaaa gtgaaggctc agactgctcc aaacaaggat gtgcagaggg agatcgctga 300
 ccttgagagag gtagggggcg ctccctccc tccgtcctca gggcctggtg catgaaacat 360
 gcccgctctt caggaaatca tctgtg 386

<210> 305
 <211> 438
 <212> DNA
 <213> Homo sapiens

<400> 305
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 gactcttctg tgtgttctta atgagcagtt gtgaacatct ctttaggaac tcattgcctt 120
 ctgcggcagc atagggcatg ggctacctcc acgccaaggg aatcctacac aaggacctca 180
 agtcaaagaa cgtcttctat gacaacggca aagtggctcat cacggacttt ggactcttca 240
 gcatttctgg ggtgctgcag gctggcaggc gggaggacaa actgcgcac cagaatggct 300
 ggctatgcc cctggcacca gagatcatcc gccagctgtc ccccgacaca gaggaggata 360
 agtccccctt ctccaagcac tctgacgtct ttgcccttgg cacaatctgg tatgaactcc 420
 acgccaggga atggcctt 438

<210> 306
 <211> 430
 <212> DNA
 <213> Homo sapiens

<400> 306
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 cacaagttta ggggagagca gtggatgcct gtgggaaatt gggaaatggt tgagttgcag 120
 cttgctgtct ttcccttccc ccttagctgt tctcatcatc accttctgca ttgtgaccgt 180
 gcttggaaag gaggtctctc ccaaaggggc gctgtgggca gtctttctgc tcgcagggtc 240
 tgccctctc tgtgccgagg tcacgggctg catctggagg cagcccgaga gcaagaccaa 300
 gctctcattt aaggtgagca gctcggccta ggaaggaac cctggtacac agaccctggc 360
 cctcctgatg cctggccagc cctgcgtggg ctccagccgg cctgggtgct cccgaggaag 420
 gtttttgcct 430

<210> 307
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 307


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aaactatctc tgcacgcta agaacagtgc gggcagtgcc atggggaaga cgcggctggt    60
gggtgcaagtc ccaccagtga tcgagaatgg cctcccagac ctgtccacca cogaaggctc    120
ccacgccttc ttgccttgca aggcgagggg cagtcctgag cccaacatca cctgggacaa    180
agatggccag cctgtgtcgg gcgcgagggg gaagttcacc atccagcctt ctggggagtt    240
gctggtgaag aacttgaggg gccaggacgc aggcacctat acctgtaccg ctgagaacgc    300
cgtgggcccgg gccgcgcgc gcgtgcacct caccatcctg gtactgcctg tgttcaccac    360
cctgcctggg gaccgcagcc tgcgccttgg ggacaggctg tggcttcgct g          411

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<210> 308
 <211> 407
 <212> DNA
 <213> Homo sapiens

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<400> 308
cccacgcgtc cgcacgcgt cgcctttgat aatgagtttg atgcagaatc tcaaagaaaa    60
cgaacgacat ctgtcagcaa gatggaaaga atggatagct ctcttctga agaggaaaga    120
gatgaggaca aggaagctat taatggcagt ggaaacgcag aaaacagaga gaggcattct    180
gagtcacatc actggatgaa gactgttcca agttacaacc aaacaaatag ctccatggac    240
tttagaaatt atatgatgag agatgagact ctggaaccac tgcccaaaaa ctgggaaatg    300
gcctacactg acacagggat gatctacttc attgaccaca ataccaagac aaccacctgg    360
ttggatcctc gtctttgtaa gaaagccaaa gcccctgaag actgtga          407

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<210> 309
 <211> 526
 <212> DNA
 <213> Homo sapiens

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<400> 309
ccaggacttc ctgacactga cgtgacgga gccactggg cttctgtacg tgggcgcccg    60
agaggccctg tttgccttca gcatggaggc cctggagctg caaggagcgg tgagagggtg    120
ggcagtggga ggcagtcggg cctgccagag ggcaaggccc agaggggctg tgcttggtta    180
gggtgtccct cagcctggct gcccccacag aagtgtgtgt gggcatccgg ggcctgccct    240
ctgggtgggg tcagcatgcg gcattcctct cctctctggc acttactgaa ttctgtgtag    300
tgggggtggt tggggcttcc attctgtact aaaggaagtc cccagagaat agggaccatg    360
cctctgcact gggcgtccct gtgttgctgc tgcaggctgt gcttgtgaca cgtgctcagt    420
cgtacactgt aacgtggctg acatccccct cctttcccc agatctcctg ggaggcccc    480
gtggagaaga agactgagtg tatccagaaa gggaggaaca accaag          526

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<210> 310
 <211> 419
 <212> DNA
 <213> Homo sapiens

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<400> 310
caggacatga tggagcgcgc catcatcgac acttttgtgg ggcacgacgt ggtggagcca    60
ggcagctacg tgcagatgtt cccctacccc tgctacacac gcgatgactt cctgtttgtc    120
attgagcaca tgatgccgct gtgcatggtg atctcctggg tctactcctg ggccatgacc    180
atccagcaca tcgtggcgga gaaggagcac cggctcaagg aggtgatgaa gaccatgggc    240
ctgaacaacg cgggtgactg ggtggcctgg ttcatacccg gctttgtgca gctgtccatc    300
tccgtgacag cactcacgc catcctgaag tacggccagg tgcttatgca cagccacgtg    360
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<210> 311

<211> 465
 <212> DNA
 <213> Homo sapiens

<400> 311
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 gggctgggggt tccaggaggt ccagagcgga ggccttgggt ccctcacttg ctccctttct 120
 cttcaccagg ctatttgggg gttatgaagg cccagaagcc aggtgctgga gagggcatga 180
 aacctcagaa gccaggcctg cgagggacct tgaagcctca gaagtcagga cacggccatg 240
 aaaatgggce ctggccaggt ccctgcaatg cgagggtcgc tccgatgctc ctccccaggc 300
 ttcccactcc aggggtccct tcggacaaag aggggtggctg gggcctgaaa tcccagcccc 360
 cttcgcagct gcagaatggc aagttaccag ggcaccagcc tccaaatggc tatggaccgg 420
 gagcagaacc aggttttaat ggtggcctcg agccacagaa aattg 465

<210> 312
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 312
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 gtgtggtcct ctgcatcgac catogaggaa tgcacacagg aggcctgtagc ccaaaaacaa 120
 agccccacat aaaagaggaa tgcacgtac ccactccctg ctataaacc aaagagaaac 180
 ttccagtoga ggccaagttg ccatggttca aacaagctca agagctagaa gaaggagctg 240
 ctgtgtcaga ggagccctcg ttcacccag aggcctggtc ggcctgcaca gtcacctgtg 300
 gtgtggggac ccagggtcga atagtcaggt gccagggtgct cctgtcttcc tctcagtcgg 360
 tggctgacct gcctattgac gagtgtgaag ggccaagcc agcat 405

<210> 313
 <211> 430
 <212> DNA
 <213> Homo sapiens

<400> 313
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 tggactcacc aaggaaccag tgctatggac gctggtgtct aaggaacccc cagccccggc 120
 tgatggaaac tgggatgctg gctgtgacca acgccggaag gggggcctgt ctctcaactg 180
 gaaagtgcc catgtgcaag tcaaggatgt acccaacttt gagcagctct caccagagct 240
 ggaggctgca ctgaagaaag catgtacgag ggatcccagc cgggtgggcc gcttctggca 300
 ctgggggcct ggacaggtgc tgaogtacct gctgctaccc tgcacactgc ccttcgagta 360
 catctacttc cgcagcagaa ggttggtggt gtggctgccc gatgtgccgg cggacttgtg 420
 gtggatgcag 430

<210> 314
 <211> 424
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(424)
 <223> n = a,t,c or g

<400> 314

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agcaggtggg	tggcgctcag	acogtgcagg	tggtcgaagg	agaacgaggc	gagttcgttg	120
cagccagggt	agagatggct	gagcgcgcgc	aggccgtgga	aggcatgctc	gtccaagtgc	180
accaagcggt	tattgaacag	aagcagcttc	tccagcgccc	ccagcccgtc	gaggtcgtgg	240
cggccaagcg	cccgcacagt	gttagatgat	agatcgagca	gcctcaggcc	gctggcgttg	300
acgaagacgc	cgcgacccag	cgcatctagt	tcgttgtggt	ctaggtgcag	ggcgcgcagc	360
tggaagaggg	gcgccaacca	gcggggggcg	aagcgctgga	gcgcgttgtg	gctcangtcg	420
aggt						424

<210> 315
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 315						
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ctatgggtgc	gggcagcact	agaccgtgag	gccagggaat	tgtacatact	gaaggtaatg	120
gcagtgctctg	ggtccaaagc	tgagttgggg	cagcagacag	gcacagccac	cgtgagggtc	180
agcatcctca	accagaatga	acacagtccc	cgcttgtctg	aggatcccac	cttcctggct	240
gtggctgaga	accagccccc	agggaccagc	gtgggcccag	tctttgccac	tgaccgagac	300
tcaggaccca	atggacgtct	gacctacagc	ctgcaacago	tgtctgaaga	cagcaaggcc	360
ttccgcatec	acccccagac	tggagaagtg	accacactcc	aaaccctgga	ccgtgagcag	420
cagagcagct	atcagctcct	ggtgcaggtg	caggatggag	ggagcccacc	ccgcagcacc	480
acaggeactg	tgcattgtgc	agtgcctgac	ctcaacgaca	acacataaaa	aaaaaaa	537

<210> 316
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 316						
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ggttcagggt	gtcacgggga	atgtgcccaa	ggccggcact	gatgctaacy	tctacctaac	120
catctacggc	gaggagtatg	gagacacggg	cgaacgaacc	ctgaagaagt	cagacaagtc	180
caacaaattt	gagcaggggc	agacagacac	cttcaccatc	tatgccattg	acctgggggc	240
cctgaccaag	attcggattc	gccacgacaa	cacaggcaac	agagcaggct	ggttcctgga	300
cagaatagac	attactgaca	tgaacaacga	gatcacgtac	tactttccat	gccaacgttg	360
gctggcagtg	gaggaagatg	atggccagct	gtccagggag			400

<210> 317
 <211> 440
 <212> DNA
 <213> Homo sapiens

<400> 317						
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aggtcctgta	cctggcagaa	agtgataatg	tgaggctggg	ctgcccctac	gtcctggacc	120
ctgatgacta	tgggtccaat	gggtctggaca	tgcagtggat	gcaggccaac	tcaaaccctg	180
cccaccaccg	agagaacgtg	ttccttagtt	accaggacaa	gaggatcaac	catggcagcc	240
ttcccatct	gcagcatagg	gtccgctttg	cagcctcaga	ccaagccag	tacgatgcct	300
ccatcaacct	catgaacctg	caggatctct	atacagccac	ttatgagtgc	cgggtgaaga	360
agaccacat	ggccaccctg	aaggatcattg	tcactgtgca	agcacgacct	gcagtgccca	420
tgtgctggac	agagggccag					440

<210> 318
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 318
 actgaatttc caactcatca ctgttgtggc aacagtgcac gtccttctgg aaaaaacaca 60
 tctccatcaa gacgttgggtg ctgaagaacc tgagcggccc actccaaaga tccgttaatt 120
 gccagagaag gagttcccca taattagaaa atcatcttcc ttaaaagtca ccaagtgcct 180
 ttctactgaa cagcccaaac ccataatcat ttctgcgttt gcagaaaatt acgacgcgag 240
 gctcttacgg attgacattg ccaacacgct aaggaggcag gtccaggagc ttttcaataa 300
 gacatatggt aagcagcgca gaacccctgg ggaggggacat gtagctgctg tggacagaga 360
 agtggcaggt ttcccagttc cagccgaggg gatttctggg gaaacgattc accc 414

<210> 319
 <211> 508
 <212> DNA
 <213> Homo sapiens

<400> 319
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 ccagcagcac tgggtccggcc actctgcgga gatctccacg ctggccctca gccacagtgc 120
 ccaggtcctg gcctctgcct cgggcccgaag cagcaacgac gccattgtc agatccgcgt 180
 ctgggacgtg tctggcggcc tctgccagca tctcatcttc ccccatagca ccacogtgc 240
 gccctggcc ttctcaccag atgacaggct tcttgtcaca ctgggggacc acgatggccg 300
 caccctcgcc ctgtggggca cgggccacct atgacctcgt gtcctccacc cgcctcccg 360
 agccggtgca tgggtgtggcc ttcaaccctc gggacgcggg tgagctcacc tgtgtggg 420
 agggcactgt caccctctgg ctcccttcagc agcgtggggc agacatcagc cttcaggtgc 480
 gtcgagagcc ggtcccagag gcagtggg 508

<210> 320
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 320
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 acagggatat tgatctcggg gacttttttt tgtttctttg taaaaaacia ggtctcactc 120
 tgttgcccgg gctggagtgc agtgggtgcaa acccagctca ctgcagcctc caaactcctg 180
 agctgaagca atcttcctgc ccagccctt caagcagttg ggactacagg tacctaacac 240
 cacacttggc catctcaagg acattttatg acaaagagga aagtgtctgt cacacagaag 300
 gagctcaacc aatgttgggt agattggaaa aaatgggtgct ccctgcccc agccctcac 360
 cgtgatggcg tctatcttga agagggcttt ggccctgggtg ctgggtgtagg cgtcgaagcg 420
 gtacgtgatt tgggttgagg tgtcgatgga gtaggcctgg acccgcaaa tctcagtacc 480
 cagtgccaga ttctccagga tggcagcctc gtaggagga ttggagaact gcacggcctc 540
 gtccagctcg ttgagcagag tgatgtagac gctgcagaag ccctgggtga agggcgggg 600
 ctgggtcagt gccgacacat tcatcatgta gctgggtctt gtctcgtagt ccaggtaatt 660
 caggtgatg ataagccctg tgctctcgtc aat 693

<210> 321
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = a,t,c or g

<400> 321
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 atttattatc taggatagat ttggatgaac taatgaaaaa agatgaaccg cctcttgatt 180
 ttcctgatac cctggaagga ttggaatatg cttttaatga aaagggacag ctaagacaca 240
 taaaaactgg ggaaccattt gtttttaact accgcgaaca tttacacaga tggaaccaga 300
 aaagatacga ggcctctagga gagatcatca cgaaatatgt atatgagctc ctggaaaagg 360
 attgtaattc gaaaaaagta tct 383

<210> 322
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 322
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 ccagccacag catgtctctt ggtctaagta gagtgaatga gtttcatttc tcacgacagg 120
 agagggtggat tggatttgac ggcctgtgcc agtggtcatga aggattctga ggctgtgtcc 180
 aagcccgata ggagagagtg cggaaacagcc ttttccctgg gaggggagac agccagtgtg 240
 catgctgtcc atccagtcct gtgtgggtct tccttgaaac aggatttttg ttcccttggc 300
 tcttcttgca ggtggaagtg atcaagaaag cctacatgca aggtgaagtg gaatttgagg 360
 atggagaaaa cggtaaggat ggggcggcgt cccccaggaa cgtggggcac aacatctaca 420
 tattagccca tcagttggct cggcatt 447

<210> 323
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 323
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 tttttaatac cagggtatgca aaaatacaca ttocaattat tgcacagtg tctgagcatc 120
 aacctacgac ttgggtgtct ttcttctttg atctacatat tcttgtatgt accttcccag 180
 caggcctttg gttctgcatc aaaaatatca acgatgaaag agtatttggg aagagagggt 240
 tttaatgaat actttgatat ggaatagtta tttttctttt tgagattatt tactttaaat 300
 ttttggtttt ctatggttga ctctatatat tcaagataaa ttttctcctt tattttgcat 360
 aggtgcttaa ccaagaaaaa ttcactgaga ggc 393

<210> 324
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 324
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 atggagatgt aaaagaatat ttatatgtgt gcgtgtgtat gtgtgtattg aaattctttt 120
 taacctattg cataagggtt attgaaatag aaacatatat catggaaaaac attaatacca 180
 ttttggtatt gaaagtacta gataatctac aaataatccc atgaaaagag caaattttct 240
 gaaaaatata taaacctgtt aatataataa acaagatagc actcaaattg atttgtcaaa 300

attaatatat	aataactcag	taaaatgtaa	ttatatgtga	ccttacttaa	atatatttta	360
tgacatcaaa	attatTTTTc	tctccaatta	aaattagaaa	taaacaaaaa	agttaaatcaa	420
aatcttaact	atttggatat	gaagaaatat	ttctagtctg	tttctctggt	taaatacaga	480
ctggagaact	tggcttaatg	aattgtttga	ggcatgaatt	aactatgtta	tttttctgog	540
cggtatcatc	aaagaaaaat	ttttgggatt	ctctatatatt	ttacgctgtc	tgcaataaat	600
aggaaagagc	ctaatttatt	tatttactta	tttatatttt	tcgagatgga	gtctcactct	660
gtaacccatg	ctggagtgca	aagacacaat	ctcaattcac	tgcaacctct	gcctcctggg	720
ttcaagcgat	tctcctgcct	ctgotttcta	agtagctgga	attacagggg	cgcaaccacca	780
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<210> 325
 <211> 623
 <212> DNA
 <213> Homo sapiens

<400> 325						
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ccgcaaagcc	ggccaggtct	tcttggaaga	gctggggaac	cacaaggcct	tcaagaagga	120
gctgcgacaa	tgtagggtggc	aggttggggc	cttataagcc	caccttgctg	ggcacagggt	180
gctgcgggca	aaggaccatc	attgtactca	aaggatggag	cacgaagcag	caggaggcag	240
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atccttctag	ccctcttctc	tccgacaccc	ttttcccagc	ctgaatgtag	accaactgtcc	420
cttgtcttgg	agggtgggaaa	aacaaattac	tgtagtaaca	ggaaacatgt	cctcttctaa	480
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taggactatt	gtggcttcaa	aaa				623

<210> 326
 <211> 172
 <212> DNA
 <213> Homo sapiens

<400> 326						
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aggactggcc	acttttttgc	taaataaaga	ggcccttaaa	gatgaatttg	ag	172

<210> 327
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 327						
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ggagacatcc	aggagggcga	cctggtggag	gtggtgctgt	cggcctcggc	caccttcgag	240
gacttccaga	tccgcccoga	cgccttcacg	gtgcactcct	atcgggcgcc	tgccttctgt	300
gatcactgcg	gggagatgct	cttcggccta	gtgcgcccag	gcctcaagtg	cgatggctgc	360
gggctgaact	accacaagcg	ctgtg				385

<210> 328

<211> 569
 <212> DNA
 <213> Homo sapiens

<400> 328
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 ctcaacgccc acaacaaggc ggcggtggac tggggctggc aaggtttaat tgcttatgga 180
 tgtcattcac ttgtggtagt gattgattcc attactgcc aaactcttca agtttttagaa 240
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 ggctcaccat attgcttacg gttagcttct gctgatgtca atgggaagat catcgtctgg 360
 gatgtagcag caggagtagc tcagtgtgag atccaagagc atgccaaagc tatccaggat 420
 gttcagtggt tgtggaatca agatgcttcc cgcgatttac tgcttgctat ccacccgcc 480
 aattacattg tgctctggaa tgccgacact ggcaccaaac tatggaagaa gagctatgca 540
 gataacattc tttctttttc ttttgaccc 569

<210> 329
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<400> 329
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 gggagggaagc catggactct accaagtctg aaccctgaa gggatcacca gaggtgaag 180
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 aagagatctg tgagagcagc tccaagatga tcaccttcac cgacctggca ggccaccata 1080
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<210> 330
 <211> 397
 <212> DNA
 <213> Homo sapiens

<400> 330
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 tctctggggt ctcactcaac actagtggag tgggtgtggc ctggatccgt cagccccag 180
 gaaaggccct ggagtggctt gcactcattt attgggatga tgataagcgc tacagcccat 240
 ctctcaacga caggctcacc atcgccaagg acacctccag aaaccagggtg gtccttacia 300
 tgaccaacat gggcccagta gacacagcca cttactactg tgcacaattc gcaagggggg 360
 cgagggggctc caattgggtc gaccctggg gccaggg 397

<210> 331
 <211> 1537
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1) ... (1537)
 <223> n = a,t,c or g

<400> 331
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 accggggtgt caccacctc aacatttcag ggctgaagat gcccagaggg atcgccatcg 120
 actgggtggc cggaacgtg tactggaccg actcgggccg agatgtgatt gaggtggcgc 180
 agatgaaggg cgagaacgc aagacgctca tctcgggcat gattgacgag cccacgcca 240
 ttgtggtgga cccactgagg gggaccatgt actggtcaga ctggggcaac caccocaaga 300
 ttgagacggc agcgatggat gggacgcttc gggagacact ggtgcaggac aacattcagt 360
 ggcccacagg cctggccgtg gattatcaca atgagcggct gtactgggca gacgccaagc 420
 tttcagtcac cggcagcatc cggctcaatg gcacggaccc cattgtggct gctgacagca 480
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 tgacaggggg cctgagccac gcctctgacg tggctcctta ccatcagcac aagcagcccg 660
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 ggctgtctcg cacctgtccc aatgggaagc ggctggacaa cggcacatgc gtgcctgtgc 780
 cctctccaac gcccccccca gatgctcccc ggcttggaa ctgtaacctg cagtgttca 840
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 acacgggtga caagtgtgaa ctggaccagt gctgggagca ctgtcgcaat gggggcacct 960
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 aatgcaccca gcaggtgtgt gcgggtact gtgccaacaa cagcacctgc actgtcaacc 1080
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 cctgtacat gaacagcaaa atgatgcctg agtgccagtg cccacccac atgacagggc 1440
 cccggtgtga ggagcacgtc ttcagccagc agcagccagg acatatagcc tccatcctaa 1500
 tcectennnn nnnnnnnnnn nnnnnngtgc tggtggtg 1537

<210> 332
 <211> 952
 <212> DNA
 <213> Homo sapiens

<400> 332
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 accgagcagg tcctatgcgg cagataagtc tcggtggagc agtagatgaa gaagtgggtg 120
 attatttccc agagttcctt gatatgttag aagaatcacc atttctgaaa atgactttgc 180
 cctggggtac actttctagc ctccgactcc agtgtaggtc ccagagtgat gatgggccta 240
 taatgtgggt aaggccagga gaacagatga tccctacagc agatatgcca aagtcaccct 300
 tcaaaagacg acgatcaatg aatgaaataa aaaatctcca gtacctacct cggaccagtg 360
 aaccccgcca agttctcttt gaagatagga ctagagctca tgctgatcat gtcggtcagg 420
 ggtttgactg gcagagtacg gctgctgttg gagttttgaa agctgtacaa tttggtgaat 480
 ggagtgaacca acctcgata accaaagatg tgatttgttt tcatgctgag gattttactg 540
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 gggtagatga agctaaacta aaccaaatga ggcgggaagg cattcgttat gctagaattc 660
 agctttgcga caatgatata tacttcatcc ctagaaatgt cattcatcag ttcaaaacag 720
 tttcggcggt gtgcagctta gcctggcata taaggcttaa acagtaccac cctgttgtgg 780
 aagccactca aaacacagaa agcaattcta acatggactg tggtttaact ggaagcgag 840
 aattagaagt tgactcccaa tgtgtgagga taaaaactga atctgaagaa gcatgcacag 900

agattcagct gttaacaact gcttcatcat ctttcccacc tgcatacagaa ct 952

<210> 333
 <211> 526
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(526)
 <223> n = a,t,c or g

<400> 333
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 tgacggggaa cagatggaag caggttctgt ctgcggcacc agcccttttc cacgctcggg 120
 aagtcggaa cttccctgtc agacttttca ggcactgcac cctcacggcc tccaccaggc 180
 ccgcacgaat ggggccactt tccacgtctt tgatgagcat cccacacagg tgtctactgg 240
 agcactcacc gccaggtttc gagatgaaat ctccgccttg tagctccgga cgtcctccag 300
 atccagcgtg gccgtcagga cttccacgtc atccagagaa aactgggagc cttgagcaaa 360
 gacgcttccg ttcattggcg tcatggcaca gccgtcgtag tacaggcggg ccccgctcga 420
 acccttctgg ttggccggac gcgtgagoga acgctgtggt ccgaccgggt attccggccc 480
 ggtactgcag gccgatcaaa gaagggttc aaatnnggac gagccg 526

<210> 334
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 334
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 ctaaacccagc tgaccgagga caacgctgaa ctcaacaacc aaaacttcta cttgtccaaa 120
 caactcgatg aggccttctg cgccaacgac gagattgtac aactgcgaag tgaagtggac 180
 catctccgcc gggagatcac ggaacgagag atgcagctta ccagccagaa gcaagtaagg 240
 agggtaaca aggtcgtgag atccctggag gacttttaga aggattttag gagtgcttgg 300
 tgogttctcc caagggttcc aacactgaac ctcatacagt aattgggctc tttttagaag 360

<210> 335
 <211> 846
 <212> DNA
 <213> Homo sapiens

<400> 335
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 atgcagcaat catgactgcc ctccagatgc agaagatttc agagcccagc agtgctcagc 180
 ctacaatgat gtccagtatc aggggcatta ctatgaatgg cttccacgat ataatgatcc 240
 tgctgccccg tgtgcactca agtgcctatg acaaggacaa aacttggttg tggagctggc 300
 acctaaaggta ctggatggaa ctggttgcaa caggactcc ttggacatgt gtatcagtgg 360
 catctgtcag gcagtgggtc gcgacggca actgggaagc aatgccaaag aggacaactg 420
 tggagtctgt gccggcgatg gctccacctg caggcttgta cggggacaat caaagtcaca 480
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 gagaattaca gtgaaaggac ctgcccacct ctttattgaa tcaaaaacac ttcaagggaag 600
 caaaggagaa cacagcttta acagccccgg cgtctttgtc gtagaaaaca caacagtggg 660
 atttcagagg ggctccgaga ggcaaacctt taagattoca ggacctctga tggctgattt 720
 catcttcaag accaggtaca ctgcagccaa agacagcgtg gtteagttct tottttacca 780

gcccacagtc catcagtgga gacaaactga cttctttccc tgcactgtga cgtgtggagg 840
aggtta 846

<210> 336
<211> 347
<212> DNA
<213> Homo sapiens

<400> 336
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ggaaacagga agctggggct cactctgact cctgctgcct cctccacacc ccgcccaggc 120
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acgtccacgt ctgtattatg tgcctacgog ccatcatgaa ctaccaggtc agccgagggg 240
catgggactg gcgactaggg agcccagcct gtcctcactg ggggctacac aagctgccga 300
ggctctggga tccactgtcc ctttaccctg tgctgtgctg gggaact 347

<210> 337
<211> 709
<212> DNA
<213> Homo sapiens

<400> 337
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gactgttcct ccatgctggg tagaagttca acaagaacag cagcaaagga ggcatcctca 120
acatttgcat cagcaacacc atggtgatgc tgctcagcat actogaactt ggaaactaca 180
gaccgacagc aacagctggg atgaacatgt atttgaatta gtactaccta aagcttgat 240
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acaagtgaca ctgctgaaaa ataaagctcc aggattaggg aaagtcaatg gtcttagatt 360
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tggtccttgat ctatcagggc atgctggaat gttgacgtta acaagcccca aacttgtaa 480
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aggaacagaa gagatttgta atggtggtat gcgtcctgta gtaaggcttc catccctaaa 600
acaccagagt aacaagggtt attcacttgc ttcacttttg gctaaagtgt cagcaggcaa 660
ggaaaaatca tctaattgta agaataaaaa tacaagtggc acccgtaaa 709

<210> 338
<211> 384
<212> DNA
<213> Homo sapiens

<400> 338
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cagatgctgg tgacaggagg agtaagttct cagctggaac aacatttaga taaggataaa 180
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caactgttct gtggctcatt agactttttt ggaatcctgt gtgttggtt ataccgaata 360
attgatgaag aggagctcaa ccca 384

<210> 339
<211> 362
<212> DNA
<213> Homo sapiens

<400> 339
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 ctggccattg gtcttgcaag aagtcttttt tctgggcttc ttctggctct atttgtatgt 120
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 tggctatggt gcctttcaaa actatgtccc ttcttcogtg accacgatgc tctcctgggt 360
 tt 362

<210> 340
 <211> 1466
 <212> DNA
 <213> Homo sapiens

<400> 340
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 ctatagactt ggctcccaca ccacagttaa aagaaagatt agcatatgaa tttaaaggcc 180
 actcgttgct gcaagctgca cgagaagctg atgttactcg aatcaaaaaa catctctctc 240
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 catctccata tcccaaaaaga aagcaaatat gtgaactggt gctaagaaaa ggagcaaaca 360
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 gaaatgaaaa tgtacagcaa ctctccaag agggatatctc attaggtaat tcagaggcag 660
 acagacaatt gctggaagct gcaaaggctg gagatgtcga aactgtaaaa aaactgtgta 720
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 gcgataccca aggcagacat tcaacacctt tacatttagc aggttaagtga atgaagtttc 1260
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 taaactttaa aaattcaaat caggccaagc atggtggctc acacttgtaa tcccaacact 1380
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 atggcaaaac cacaccteta taaaaa 1466

<210> 341
 <211> 547
 <212> DNA
 <213> Homo sapiens

<400> 341
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 tccgaagaag agtcggtgat taacctgctc tcttataaca ttgacgggat tatactttcg 180
 gaaaaatata acaccatcag gacggtgaaa tttctgogtt cagccaccat tccggtcgtg 240
 gaattgatgg atgtacaggg agaacggctg gatattggagg tcggttttga taatcggcag 300
 gccgcttttg acatggtgtg taccatgctg gagaagcgag tcaggcacaa aattctgtat 360
 ctcggttcca aagatgacac ccgcatgaa cagcgttatc aagggtattg cgatgcgatg 420
 atgctgcata atctttcccc attacgcatg aatccacgag ccattctcat cattcattta 480
 agaatgcagt taatgcgtga tgcccttagc gcaaaacccg atttagacgg tgtattttge 540

accaatg

547

<210> 342
 <211> 461
 <212> DNA
 <213> Homo sapiens

<400> 342
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 cgtgttgccc agtttgcggc ataccgcgtc ggtagccat tcagccatca gccgataggt 120
 catcagtttg ccacgggtga tggtgataaa tccgtccaga ccatcgcggt cagcatgggtc 180
 gagcagcacg atgccacggc tgacgttacg tccgctcggg tcgtcatcgc tggcaaccag 240
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 ttcccttca cgcagcagaa tatcaacctc ttctgcgctc actcgattat cgtcaatctc 360
 gttgtaatca atacgtaaag aggtggtacc aatcagcga atggtatcgc caggcaccag 420
 aatatcggcg tcggaagggt tacggcagcg gttgatcctc t 461

<210> 343
 <211> 250
 <212> DNA
 <213> Homo sapiens

<400> 343
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 ccacccccag accaatacgt aatccgggtga ggatttccgg cagcgccagg ggcaaatga 120
 caaacacag cacctgcgca cggctggcac ccagcgactg ggccggcacga atgcgaacct 180
 gctgcacgct ttccaccccc gccagcgccg acatcgccac cggtgcaaaa atcgctaaat 240
 agatcagtaa 250

<210> 344
 <211> 138
 <212> DNA
 <213> Homo sapiens

<400> 344
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 ttctactgac ggctatccgc tggcgtgggc ggtggcgcac agtaagcett cgaccgtaa 120
 tattttatta ctactggt 138

<210> 345
 <211> 467
 <212> DNA
 <213> Homo sapiens

<400> 345
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 cgctttcggc gcacgcctgc gcgcttggtc cttcagttca ggcaacggta aggccttgcg 180
 atccagcttg ccggtggcga taagtggtaa ctgtggaagt tgcagcagaa ccacgggtac 240
 catatgtggt ggcaatgttt cacgaagctg cgcctgcaat gcgctggtat ccaacggcag 300
 gcccgattgc gacaccagat agcccaccaa ttgacgcgca tcaccaccgg tggcagcgcc 360
 ctggttaate acacaggcgt gggtaacggc ttgttcgaca tccggcagcg cctgcacac 420

gogategatt tcgcccagtt cgatacgtg cccgogaatt tttagct

467

<210> 346
<211> 403
<212> DNA
<213> Homo sapiens

<400> 346
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cattttcgcc attcgcgtca gctcttcgag attagagtag agcacatctt ccagctcctt 180
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gcgaatttcg tgagcgatat ccgctgagaa attggactgg cgggtaaaga catcctcaat 300
acgctcgatc atatggttga acgacagtac cagctgttcc agctcaatgg gcacggctctg 360
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<210> 347
<211> 340
<212> DNA
<213> Homo sapiens

<400> 347
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agtctggtca gcaggctctat atgcaactgc tgaataaaga gcaggagctg aaaatcaccg 240
aggccagcac cgtcggcgat gtgcgcattg ttgacccggc aatcactcag cctggcgctgc 300
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<210> 348
<211> 723
<212> DNA
<213> Homo sapiens

<400> 348
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cagggtatga actaccggac caagacaggc aaccgcttcc agacgcggcg attcaaggta 180
tgccagacgc acggcaacgt tagcgccgaa acggaaaacca aaggccgcga cgcgagtgtg 240
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cagaccacca cacattaata ccgtcgggaa cgggccatcg cctttcggca tatgcaaaaa 480
gccgggtgatg ggcgcaccgc cgggtacggg aaactccatc tgccgcateg tgcccggtag 540
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atctcctttc agatgaggat aggcggcaat gttgtacaac gtagccgcat gcagccagtg 660
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ggt 723

<210> 349
<211> 249
<212> DNA
<213> Homo sapiens

<400> 349

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tcaggcggtta	gggcccgtttt	cattacgcgc	gggcgtagcc	agctcgacct	taggtattgc	180
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gaatatgct						249

<210> 350

<211> 424

<212> DNA

<213> Homo sapiens

<400> 350

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atataactga	aaaaacagaa	gattctagt	ttccagaaac	tccagataat	gaaagaaaag	180
caagtatatc	atatttcaaa	aatcaaagag	gaatacagta	tattgatttg	tcttctgata	240
gtgaagatgt	cgtttcccca	aattgctcca	atacagttca	agagaaaaa	ttcaacaaaag	300
atacagtgat	tatagtttct	gagccatctg	aagatgaaga	gtoccaaaggc	cttctctacca	360
tggcacgtag	aaatgatgat	atttcagaac	tggaaagacct	ttcgggaatg	gaagacctta	420
aaga						424

<210> 351

<211> 404

<212> DNA

<213> Homo sapiens

<400> 351

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catcgagacc	gagctgtcgt	ggggcgcccta	ctacaaggcg	ccgctgtatt	ccttagctct	180
gaaatgcctt	atcagtctct	tcacgatcat	cctgctcggt	ctgacctcg	tgtaccacgc	240
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ttatgagcct	attttccctca	tctttttgga	agcactgagg	ggggtcattc	atgccacacc	360
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<210> 352

<211> 340

<212> DNA

<213> Homo sapiens

<400> 352

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ccaactcaac	gttagttcac	acaactgctc	aacaacttcc	gcgcgcgttg	ccagcccact	180
gaccacctcc	accaacttca	tcacgcgtgc	cgggttaaaa	aaatgcagcc	ccgcaacacg	240
ttcaggattt	tttatctccg	cagcaatcgc	ggttatagag	attgacgaag	tgtagtggt	300
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<210> 353

<211> 188

<212> DNA

<213> Homo sapiens

<400> 353

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<210> 354

<211> 365

<212> DNA

<213> Homo sapiens

<400> 354

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taataattgc	tgaaagaatg	aagaataagt	atctacatgt	gaccaaaggc	tggaagcatg	180
gttattacgt	gtgctattta	taaaaaccca	gggcagtgtc	catgaaagga	aaacaaggcc	240
tottacctca	gtcatgttgg	agaagggaaa	ggagcttctg	tcatacacc	agccatttac	300
acatgattcc	gtgtctgtct	cacctatgtt	gagaaatgtc	ccattcaggt	gaaagagctg	360
ceatg						365

<210> 355

<211> 1250

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (1250)

<223> n = a, t, c or g

<400> 355

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tcgcatctgt	gtggttggag	agaatggggc	tgggaagtct	accatgctga	agctgctttt	360
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gtctgggggg	tacctctctg	ggttatagat	tccccactg	ccccagctct	gactggaccc	1200
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<210> 356
 <211> 544
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(544)
 <223> n = a,t,c or g

<400> 356							
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<210> 357
 <211> 1249
 <212> DNA
 <213> Homo sapiens

<400> 357							
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tgggggtgct	gagctcgcag	ccatcactcg	ggcccggagc	ctccaacat			1249

<210> 358
 <211> 1135
 <212> DNA
 <213> Homo sapiens

<400> 358

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ccacagcaag	accccccgcc	cccaagcaca	gtagctttct	cagcgtcgag	atccctccgt	1080
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<210> 359

<211> 389

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)...(389)

<223> n = a,t,c or g

<400> 359

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attttaccgg	aaaggccgag	ataggatgac	cgttttccta	tgtgtacttc	ttctgcatgg	360
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<210> 360

<211> 785

<212> DNA

<213> Homo sapiens

<400> 360

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ttgct

785

<210> 361
 <211> 1826
 <212> DNA
 <213> Homo sapiens

<400> 361
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<210> 362
 <211> 1293
 <212> DNA
 <213> Homo sapiens

<400> 362
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 gctttgggct ttgaggaagt tggggatgga ggggatgatg cttctttagg tttctctatt 240
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 cacttggttt aagagagtct gggctttgaa agggctgatg ggcttctcag ggtggaaaga 720

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gggccccagg agaaaagaag agcaagattc accatggagg cctccagcc cctctttcag 900
ggagttaaga agataggtac tgggtgcacg gtacctgctg gtaatatcca ctgatatcat 960
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<210> 363
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 <212> DNA
 <213> Homo sapiens

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<400> 363
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<210> 364
 <211> 418
 <212> DNA
 <213> Homo sapiens

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<210> 365
 <211> 3055
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<400> 366						
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cctaca						246

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 <211> 2367
 <212> DNA
 <213> Homo sapiens

<400> 367

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<210> 368

<211> 2664

<212> DNA

<213> Homo sapiens

<400> 368

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 <211> 401
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 <213> Homo sapiens

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<210> 371
<211> 770
<212> DNA
<213> Homo sapiens

<400> 371
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<211> 381
<212> DNA
<213> Homo sapiens

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<210> 373
<211> 14887
<212> DNA
<213> Homo sapiens

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aaattgt

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<210> 374
<211> 1909
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)... (1909)
<223> n = a,t,c or g

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<400> 374
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tattttttaa ctgcaagggt aattgtaaaa tcatagtgtg aagtttgtgt ggtgtttctg 180
ctttttgtaa tgtttggaac ttgcctctgc aggtaaaate ccagaggaat ccaaagccct 240

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ctctttattg	gctcctgctc	caacccatgac	aagtctgatg	cctgggtgcag	gattgcttcc	300
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accagcagca	gcactagacc	ccaacattgc	aacacttgga	gagataccac	agccaccact	420
tatgggaaac	gtggatcctt	ccaaaataga	tgaaattagg	agaacgggtt	atgttgga	480
tctgaattcc	cagacaacga	cagctgatca	actacttgaa	ttttttaaac	aagttggaga	540
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tgaaagagaa	agacagggaa	aaggagagag	agagggaaaa	ggaacgtgaa	aaagaaaagg	1320
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aaaagggaaca	ggacaaagaa	aaggaaacgag	aaaaagacag	atccaaagag	atagatgaaa	1500
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agaaggataa	aaagagagaa	aaagaaaggg	accacatcag	tgaaagaaga	gagagagaa	1740
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acagtacttc	cttnagagaa	agagcncatt	aagaccngat	tcagtgtgac	caagaatnga	1860
tacaggatcn	cccaggctgn	gaaacaatac	acacattggg	aatgtcgct		1909

<210> 375
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 375						
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caagatcagg	acacttttgt	gagtgatgat	accagtcatt	taatccattc	ctgaaggatg	180
agggatatctg	gagatctgga	gactagggat	aaaaaagaac	caagggtcct	gggaatttaa	240
ccatgtcaat	gtagtctttt	ttgactgaag	aaaaatgggt	gccccctaaa	gattttttaa	300
gattagga	tgaagccaga	aagagccaaa	ttaggacctt	agagggtggat	gcctaataat	360
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<210> 376
 <211> 975
 <212> DNA
 <213> Homo sapiens

<400> 376						
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aagcaattct	gcctcggccg	ctcgagtagc	tggtgattaca	ggcatgtacc	accacaccgc	240
gctaattttg	tattttttatt	agagacgggg	ttctctccatg	ctggtcaggg	tggtcctcagg	300
tgaccacact	gcctcggcct	cccaaagtgc	tggtgattaca	ggcgtgagcc	acacctggcc	360
taaaaatcat	ttaatTTTTT	atgcttgctt	agttataagg	tcaaagagaa	tcaaatgact	420
gatgcagtca	gcaccttaaca	acctctgtat	atgggaaggg	ggtaatgaga	acatactatt	480
tggaataaat	aacagcctaa	gagccaagtg	ctgaagttac	atttctgcct	accacagcta	540

aagctctcct	cactgtctcc	taccagtc	tcctttccat	caattaccag	tctcttgat	600
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aactgcatgt	ataagatgg	tgtcatttgc	ttgaataccc	ccttgaaaaa	tgttgattct	780
tgagcatcag	tgggacatag	aggtgtctga	agaaccattt	tacatgat	cataaatagg	840
aggtctctgc	attaccatgt	ttgcttgcaa	agtggaaaac	ttttagatgt	gtaacttgaa	900
tgtatcaaga	tctcaagtgc	ttaatgataa	ggtgttgact	tgttaaatta	aaccatttgg	960
aatacaaaaa	aaaaa					975

<210> 377

<211> 2305

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(2305)

<223> n = a,t,c or g

<400> 377

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aagctagccg	atggcggagt	ctcttctcct	tcaactgcct	cactggcttt	tccttatagt	180
cctgttgcaa	gactcagccc	ottatagcca	atggccatta	atactcccc	gcttctctta	240
aaacctcaaa	taaagcaata	ctaaccacct	gnaaaaacag	gttacacttc	caggggctcc	300
ccactcagtc	cccagtcac	tatcgacagt	gagctgagta	cttcagaatt	ggaggatgat	360
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tccagtgtgt	catttgagttc	aggaaaaaaa	gggacatgta	gtgatcaaga	atatgaccaa	540
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tcatttttta	tttattgtca	tacatgggtt	tcatatttat	aacggcatca	tgagctcatt	2040
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aaggatgaaa	ctgtaatgtt	ttattaacaa	tgcttctgga	aatgaatgca	ttttaagca	2160
aataaatctt	tttgatagac	cttttaca	atccatttgc	actaatgaat	gcttctttat	2220
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gactctattt	cccccaaaaa	aaaaa				2305

<210> 378
 <211> 2107
 <212> DNA
 <213> Homo sapiens

<400> 378
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 gtgactgaga gccgcccctc agtgctacgg ggcgaccacc tgtttgccct tttgtcctcg 180
 gagacacacc aggaggaccc catcacatat aagggtcttg tgcacaaggt ggggaattgga 240
 ccgtgtcaag ctgagctttt ccatgagcct cctgagccgc tttgtgggat ggggctgacc 300
 tttcaagggtg aactttttacc tttcaaccgc cagccgctgc gaggttccagc accgtgccct 360
 ggagctgaca gggcgctggc tgctgtggcc catgctcttt ccttggtggca cctcgggacg 420
 tccogctgct gccctcagat gtgaaactca agctgtacga ccggagctcg gagtcaaacc 480
 cagagcagct gcaggccatg aggcacattg ttacgggcac caccogtcca gccccctaca 540
 tcctcttttg gcctccaggc accggcaaga ctgtcacgtt agtggaggca attaaagcagg 600
 tggtagaagca cttgcccata gccacatct tggcctgcgc tccatccaac tcaggggctg 660
 acctactctg tcaaaggctc cgggtccacc ttctagctc catctaccgc ctctgggccc 720
 ccagcaggga catccgcatg gtacctgagg acatcaagcc ctgctgcaac tgggacgcaa 780
 agaaggggga gtatgtatct cccgccaaga agaagctgca ggaataccgg gtcttaatta 840
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 catacagcta tcggggcaga gccagggtcac tggcagtttt tacagctttt caggcgactc 2040
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 tatgcgg 2107

<210> 379
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(432)
 <223> n = a,t,c or g

<400> 379
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 tgetqccttt tcatgcgtnn gacctggcag ctgtagcttt ttgtggggaa acttccactg 180
 ctcannggag tcaggotcna ggtagctgct ggcccgogta cccttgttgt tgetttgttt 240
 nnggagagct gtggtggtct ccactttccc gccttgacgg gngcctgcta tctgccttcc 300

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aggncactg tcancggctt cccgggtaga aagtcacttt atgnagacac anccagtgtg 360
gcccttggtt ggccttgaagc ttcctcagag gaagggcggg aaccagagtn ngaccgaggg 420
ggcagccttg gg 432

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<210> 380
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(507)
<223> n = a,t,c or g

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<400> 380
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gaggctctcc acagcgcagg aaggcagcct gtcaccctgc tctccgagcc aggggccaag 180
gtgtgggggg gcacaggcca tctcatcct gccaggcccc cgctttcagg agtggggggg 240
tgccaatgct cccactcaaa accctggact gcgggggtccc ctgagcagag ggaccatcca 300
gctccccata aacagattga agctggacag gggotgectg ggccccagge ttggggaggg 360
tagaaaaggcc ctgcantgct gctgcctggg cccggaggag ggccctggccc cgtagcatca 420
ttggaggcca gagcccaagc cagttccgga gtcacacca acggcggagg gagaacctac 480
ccatatccca ccttcagctc tggggag 507

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<210> 381
<211> 1097
<212> DNA
<213> Homo sapiens

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<400> 381
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ccttcaggag tttgacattg ccaggaacgt tctagaactg atctatgcac aaactctggg 180
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ttttcgaggt ctgacctctc tcattcactc catctacagc tggatcgaca ccctaagtac 480
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ctttttcatc ctcaccctca ttgtgcta atcatcctat ctttactggc agatcacaga 600
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ttcttccatg ccacctgtgc ctttaggaac tgcccagaag aaaatccaag gctttagcca 960
ggagcggaaa ctgactacca tgtaattatc aaagtaaaat tgggcattcc atgctatttt 1020
taatacctgg attgctgatt tttcaagaca aaatacttgg ggttttccaa taaagattgt 1080
tgtaatatgg aaatgag 1097

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<210> 382
<211> 375
<212> DNA
<213> Homo sapiens

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<400> 382

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tgacgatggt	gatggatgatg	gtgatgatga	agatgacagc	taaaacaagt	actgctaact	240
ttgatcatta	ataattatag	cttcgataat	gatactgaat	atcttgtaaa	gcgcttaata	300
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tgaatggtgt	agcctt					375

<210> 383

<211> 1541

<212> DNA

<213> Homo sapiens

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gcaggtctggc	ctgccaacaa	tcctaccctc	atgatggaga	gtcgaatccg	cgtagccag	4740

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tcctgacaag tttggcgatt ggtatacaaa aaagttctaa tgaccttggg aggtgaagtt 4800
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5725

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<210> 387
 <211> 378
 <212> DNA
 <213> Homo sapiens

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aattgcctta aatctaaaga tcgttttggg gggaaattgac atcttgttga gtcttgcagt 180
tcatgaatat ggtacgtccc tctgtttatt gaggtcctcg ttgatttatt tcataagggt 240
tttgttaatt tcagcttata gattatggac atattttaaa aatctagaca gtttcttaga 300
gggccattat atgttgtatt gagttttaaa tttcagtttg cacttgatac ttgcaattat 360
agagaaatat atccattg
378

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<210> 388
 <211> 794
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(794)
 <223> n = a,t,c or g

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<400> 388
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atctgaaaaa gtgattaatt tcttaatatc agatagtcta cattttgtct oaaaaatgtc 180
ttttaaaaaa atcttattta ttcaaatcaa atcctcacia gatctaaata ttggatttag 240
ttgttactaa catttttagaa tgttatttat tttagaagtc atttatttac atgcatttaa 300
cctttatatt aaaccaacgc agaaggatg gtcccagctc agagagggtta agaaacctta 360
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cagcactttt tgaggccgag gcaggcaaat cgcttgagtc caggagttcg aaaccagtct 600
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acacctgtag tcccagccac tggggatgcc gaggtgggag gatcacttgc gcctgggagg 720
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794

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<210> 389
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 389
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 caaatgataa acgctgacta tcagaataaa ttgactctcg actacttgct aacaactgac 180
 agagaggtct atgaaccatt taaccttact aattactgtc tacacataca taatcaaagg 240
 cttggagctt atgacctagg ttaagtatga cagaactggc acatgtgcc gtacaagtgt 300
 agcatggatt cgaccctgag gccatgttta ga 332

<210> 390
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 390
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 ccctggcttg tcggcggtc acgcggaaga tctatgaagg catcaagaaa gcgggtgaaac 180
 ccaatcatag tccgcgcggg gtgaaaaagg ttcatataatt tgtcaacaaa ggagaaaaag 240
 ggatcatggg tttggcagga gacacactcg gcattggggg gtactgcctt ctaccctgca 300
 tgtgttagga ccgaaaattg acatatgccc atatccctc tacgacggac ctgggtgcag 360
 gcgcaggcta cc 372

<210> 391
 <211> 709
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(709)
 <223> n = a,t,c or g

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 attaaccaga agtcaagagg gcatgaagtt aggagaaaat ttcttgatgt ttgccatgcc 180
 ccccgatgat tcaaaagaga gcaaaggaaa ataattttta ctgaaacaaa acagtattta 240
 gcacacctatt aatttaatat ctttggtttt gaatttataa tgctgataac tgcatttatt 300
 gaacattcac taaatccaag atacaacact aaacagttct catgtttcac aagttttgtt 360
 ttcattcagt tttaacaagaa tcctataaat cctcattaat ctcattttac agatgagaca 420
 aaaagcaagc cctgaaagtt tcagcaaatt gcgcaagtcc tgtcacatct aggaaggtgg 480
 ggattttacc taggacagag tgactctaca tcttcaccac attatagggtg gaaaggggaa 540
 aagccaggaa ggcatttggg cccctatcca tttttatctc ttaaaaaact gctgggggttc 600
 cctgctctgg aaacaggttc cctccccggg gggaaataaa taggcgggct gggggntttt 660
 ccttttttat cnggcttcag ntccatttgg gtccgggggg ntttagggg 709

<210> 392
 <211> 900

<212> DNA
<213> Homo sapiens

<400> 392
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 ggagatacaa gggattcttg gaagtgggaa gtaaacagta cacagatctc tttaaatcag 180
 gagcataatag gtcataataa aatgagctac aggcacaaaag ccagtaacac atttatggtc 240
 ogttcacctg gaaaagtttc accgcccact ccccaactcct cttccccctc ctggaagcag 300
 ccagctttat ccttggcatt ttaatttttag agaaaattta aacttccatg ctgccctgtg 360
 gcttcgggtca atggagcttc tttctccagt tatggaatga gtcagcaaaa cggggagttt 420
 ctgatccttg gaattagggg gggacagttt acagaatgtc ctcatctcac tcttttccca 480
 atcatgggaa atatccagcc aattctggtt ttaaagattc atatcaaatt caaagtcctt 540
 ccctcctttt ggcgaggaag acaacccttt agagcgaaac acaaaagagc aaatgtaaaa 600
 tccactctggg gcggggcatg gtggctcacg cctgtaatcc cagcactttg ggaggccaag 660
 gcaggcagat cacgaggtca agagatcgag accatccttg ccaacatggg gaaaccccg 720
 ctctactaaa aatacaaaaa ttagcttggc gtggtagcac atgcctgtaa tccccagcta 780
 ctccggaggc tgaggtagga gaatcgcttg aacccgggag gcagattttg cagtgaagtcg 840
 agatcatgcc actacactcc agcctggoga caggcgaga ctccgtctcc aaaaaaaaaa 900

<210> 393
<211> 383
<212> DNA
<213> Homo sapiens

<400> 393
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 tttcttctca gacaggaggt tctccaacag cttaggtgca gtgacagagg aatggcagag 180
 atccaagaag gacaattgtc ccaggaagaa gtacatgggt gtgtggaggc aagaatcagc 240
 attaatcacc accagcagca gcaggtttcc catcacagtc aggaggcaaa tcaccacgaa 300
 cagcacaaaag agcagagtct ggtctgggg gccagctgac agcccagga ggacaaactc 360
 agggacaaca ctgcggttcc tca 383

<210> 394
<211> 1345
<212> DNA
<213> Homo sapiens

<400> 394
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 gactgatttc ttggcttttt atcattttga actttatgga atacatcggc agccaaaacg 360
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gatgctgcta tctcaaccag atgccagga cagggtgctct agccattagg accacaaatg 1200
gacatgtcag ttattgctct gtctaaacaa cattcccagt agttgctata ttcttcatac 1260
aagcatagtt aacaacaaag agccaaaaga tcaaagaagg gatactttca gatgggtgtc 1320
ttgtgtgctt ctctgcattt ttaaa 1345

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<210> 395
 <211> 340
 <212> DNA
 <213> Homo sapiens

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<400> 395
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actcattcct taaaaacatt ccacagaaat tgggattggg agtctgaata tacattgttt 180
atgtcagcct tgaaggtaaa taaaaataat gccaaacttt ggaataatgt gggtcattgt 240
ctggaaaatg aaaagaactt tgagagagct ttgaaatact tcttacaggc taccatgtt 300
cagccagatg atattggtgc ccatatgaat gtaggaagaa 340

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<210> 396
 <211> 430
 <212> DNA
 <213> Homo sapiens

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<400> 396
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ctagtatatt tgacacattt taaacattaa agttaatttg ctgatttggc ttgaactgga 360
gatgtaagat aaatggttcg tgttggccga attcacggcc ttctccatg agcaacaatc 420
cttatttctg 430

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<210> 397
 <211> 401
 <212> DNA
 <213> Homo sapiens

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<400> 397
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<210> 398
 <211> 2987
 <212> DNA
 <213> Homo sapiens

<400> 398

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gtttttatata	aggcatgcca	aaggcatata	atagaatcac	atggaaacaaa	gaatttaaaa	180
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tgcaataaat	gttactat	gactacttat	gtttctacaa	aaacaccatc	gtaaaggtgc	360
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<210> 399

<211> 2789

<212> DNA

<213> Homo sapiens

<400> 399

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<211> 453

<212> DNA

<213> Homo sapiens

<400> 400

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 <212> DNA
 <213> Homo sapiens

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 <211> 1678
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<211> 447
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 <213> Homo sapiens
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 <223> n = a,t,c or g

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 <211> 409
 <212> DNA
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<210> 405
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> n = a,t,c or g

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<212> DNA
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 <223> n = a,t,c or g

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<210> 407
 <211> 2214
 <212> DNA
 <213> Homo sapiens

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<210> 408
 <211> 467
 <212> DNA
 <213> Homo sapiens
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 <222> (1)...(467)
 <223> n = a,t,c or g

<400> 408
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<210> 409
 <211> 1339
 <212> DNA
 <213> Homo sapiens

<400> 409
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 <211> 1475
 <212> DNA
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<400> 410

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 <211> 3092
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<400> 411

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 <213> Homo sapiens

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 <211> 1365
 <212> DNA
 <213> Homo sapiens

<400> 421

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 <211> 421
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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836

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 <212> DNA
 <213> Homo sapiens

<400> 424
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<212> DNA

<213> Homo sapiens

<400> 431

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gctcggttac	ccggactcca	ccggtctgga	gtccctgctg	ctgctgcgag	gtgctgaccg	300
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cttcagaag	gcagcaaaga	ggagaagcga	gtactggcgg	ggccagcgga	aggcgctgcg	420
gcagctgctt	tcagggtgtga	gctcataggg	ctcggtgggc	gcctcgctga	tccttgcttt	480
acaacaacca	atcagcacat	aacttgtctc	acttcatgcg	tatcccgctg	agccgtttgg	540
tcacccttgt	ggggtttact	ctgcctctt	g			571

<210> 432
 <211> 475
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (475)
 <223> n = a, t, c or g

<400> 432
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 ccattttgag ttttaatttt tgagaagggt gtaaagtcgt aacttagatt cttttttttt 180
 gtacatggac atccaatttt taagcaccat ttgttgaaga gactgcattc cttcatttaa 240
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 tctctcttct gaaccattga tcaatctgca tattctttca ctaatgccat gctatctcaa 360
 ttatttagct ggagagtaag tcttaaagtt gggtagtgct agtctcttga gttgttatctc 420
 ttcagcattt tgactatgag tcttttgcgt cttcatataa gctttagaat aaatg 475

<210> 433
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 433
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 ggccgtgcat cctctactac cctgcaggat ctggaggtaa gaggccctgg gccgagggtgc 180
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 ccagctgagg cagcccacac acccccacca gccctaataa ttattctctc taccctctcc 300
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 cagtagccct ggattcaagc tccgcaataa tcagtcaact cactgaaaac atcaattcac 420
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 gagaggcggc agggaggagca ggagaggctg catgccattc ttttcgggct gcggagaaca 1860

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atgtttatgt gtgtttctaa tttatagttt aaattttatt gtgtttctaa tttatagttt 2040
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aaattttatt gtgtttctaa tttataattt aaattttatt gtaaaaaggt aaatgagagt 2160
gggtctttct ctcagtgtca ctctggcatc ttttagcatt tttttaattt gataattata 2220
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<210> 434
<211> 728
<212> DNA
<213> Homo sapiens

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<400> 434
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aaaactcccg tgctgatcag tagctgggac tacaggcacc caccaccacg cccagctagt 240
ttttttgtat ttttagtata gacggggttt caccgcgtta gccagaatgg tcttgatctc 300
ctggccttgt gatctgcccc cctcagcctc ccaaagtgtc gggattacag gcgtgagaca 360
ccacgccagc cctattatat tttgagcaag agtctcactc tgtcaccacg gctggatgga 420
gtgcagtggc acaatcttgg ctactgcaa cctttgtctc tggaggatcg cttgagtcca 480
ggagtctctg gctgtagtgc gctatgccga tgggtgtgcc gcactaagtt cggcatcaat 540
atggtgacct cccgggagcg ggggaccacc aggttgccca aggaggggtg aaccggccca 600
ggtcggaaac ggagcaggtc aaaactcccg tgctgatcag tagtgggacg gcgcctgtga 660
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aaaaaaaa

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<210> 435
<211> 3163
<212> DNA
<213> Homo sapiens

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<400> 435
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ctaaattcac tactgccccg tgctcaaca tcaaaagagg ttgatgctag tctactctca 180
gtggtttcct tcctgtcctt tgcagtagag gatagccagt tggtaggagt cacaaaacag 240
gaaatcatca ccaagcttca gggtcgttat ggttgctgtc gctttctacg agatggatat 300
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acctggaatc tggcaactgg atgaatgatt atgattcaac cagtcattgct cgctgtggtg 1500
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ccctacctc acagaaggga gggctagatc ggttccaagc tgctgtgcaa acaacctgcg 1620
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<210> 436
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(398)
<223> n = a,t,c or g

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<400> 436
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ttgcaggact cactggatgg acgctattca actccttcca gctgtcttga acagcctgac 180
tcctgccggc cctatggaag atccttttat gcattggagg aaaaacatgt tatcttttct 240
cttgacgtgg gagaaacaga caacaagggg aaggggaaga ctataagggg aatataaact 300
tttaagggga gaaaaggggg aacataccaa cgggagcagc atgctaacc ccttgcccca 360
ngctcagcaa ggagctgctg gatgagaaaag ggcctgag 398

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<210> 437
<211> 5157
<212> DNA
<213> Homo sapiens

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<400> 437
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ctctttcttg ttctcagagc tcctgcagca ggcctgaatg aaccgcaagc ggggcccctg 180

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<211> 871

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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<211> 6807

<212> DNA

<213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<400> 453
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<210> 456
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 456

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 <212> DNA
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<223> n = a,t,c or g

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<212> DNA
<213> Homo sapiens

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ggcacgggtc cagagtgtca cagttcctcc ctccccaaa gccagcttgt acttgaacct 420
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tagcactttg agaggctcag gcgggcggat cactgagga tcaggagatc tagaccagcc 660
tggccagcat ggggaagacc tggctctact agaaatacag aagggtactc ggggggtgag 720
gcgtcaagcc tggggacacc cactacttcg taggggtagg ggcgaaaatt gcatgcaccc 780
gggggggggg gttaaaagag cttagatttc accggcctca acctgaggac tcatgagaat 840
gcccaagg
848

```

```

<210> 461
<211> 2490
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(2490)
<223> n = a,t,c or g

```

```

<400> 461
ogaaaaagaa gtgggggact ctaaagattt tctcctttta agaaaaaata gttccggctg 60
gggagtacaa aatggagtgt aaaaagggcc ttgggcccga gggaggcccc tgtggactaa 120
ggggagtcca tgcacccctt ctttccccag aggggctgga ctcagggtgag tatgggggtg 180
ggggctcctg cacttcgaca caggcagcgg aagggttttc tccccattcc ctctgcactc 240
ccaacttgag ctatactttt taagaaagtg attcaccctg cctttgcccc cttccccaga 300
acagaacacg ttgatcatgg gcgatatttt tcattgtgcc aaaaagtggc catgaccgtc 360
attaaacctg tttaaacacca aataataagg aaaataaaac aaaaagtctg ggcaggtg 420
agaaactcac tccaaataaa ttacctacca aaatatataa tgggtggaaat attccaaaat 480
tccatatttt gggatttata cacaaaagat aaacaaatta gaggccaaga ggctgccgga 540
agggaaaaac ggggcctgga aaggccgttg tgaggaatga gcttggccta aagaggccac 600
tggcagggcag tagctggacc tgccgaagtg gccgaaaggc aggagctttg gacggggggag 660

```



```

gccgcagtga ggcgagagct agctgggcgt ggagagtcca ctgtgaggcc aaggccaagg 720
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caccaaaagt caaaagcggg gcttgggaag gccgcgggga ggcatgagct gggctgggccc 840
gaaagaggcc actgggaggc aggaggagct gggcctggag aggtctgtga aaggcaggag 900
ctttcgctg aggatgccac agtgagacac catctgggtc tggaagggtc cactgtgagg 960
cagaggctgg gcgtgaagaa tctgctgtga ggcagatgtt gggattgtag aggcgagcgg 1020
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caaagaagca tgagctgggc ctggtgaggt cgacttgaga aagttcaggg cctggagaga 1140
aggctgggag gcaggagctg ggtctaaaga ggccattgta acgatggagc tgtgcctgtg 1200
gaggctgttg tgaggcagta ggctcatctg cgggagactgc cgtgacgtag ggtatgggccc 1260
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aatcagggaag cataaaccac tcaaaagttt aaagtggtaa aatttaatac agagaattat 2100
tcattataac aggtgaacag cataatgaga gattgactag cacaagtaa agagaactct 2160
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aggcatgatt atgccaatac agtacagcct ggtgcagag caagaccctg tctcaaaggc 2460
caaaacgcca atganttaca ccgcactttc

```

<210> 462
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (400)
 <223> n = a,t,c or g

```

<400> 462
cccacgcgtc cgcaccaagc tccgcccacg cgtccgcttt ctaccttcac aacctcctac 60
ttatgaatca agaactaaat tctggagaca agatgaaggt actacttaac taccatgacc 120
cctgctgact ctgcttctgt ggaacccaat aacttctctt tcttcataac ccagnggtc 180
actatttgaa tgaagtggga ttccaaacat tttggcattc agtcttctgt tttcagccca 240
ggttgggttt cattttttta ccacaggaga tataaaagaa tgatttagta aatcataata 300
gcagttaagt ctgaagctgt tcatcagctt ctcttcaca agtttgggta tcagctcctc 360
agtctctttt gctttcacca ttacaggct tcacttattg
400

```

<210> 463
 <211> 423
 <212> DNA
 <213> Homo sapiens

```

<400> 463
tttcgtcgag ctcttaggac gtatccgcct ccactcctcc ccggccgggg ctgccogagg 60

```

tttcgggatt	cctactgggg	atggccgggc	agaggcgaag	ggatcacggc	ctccgtggta	120
ggccgggacg	ggctccaggg	cgaaggggcg	acgctggcct	aggggtgggg	aggcgacat	180
ctgggtgctgc	tggtgggaag	gcctcggttt	ctgacccggc	catacgtcct	gatcccgga	240
gaagctgctt	ttcctcccgg	gccggagccg	cggctgggce	aggagctcag	actgcgagcc	300
cgaggttggg	gggcgctggg	gggtgcccgcc	ggagaaagga	tttctttgtc	attgcctttt	360
tggcacggcc	tgactttacc	atacgtggcc	gggaagcatc	tggacacagc	attaaaaagg	420
ctt						423

<210> 464
 <211> 2251
 <212> DNA
 <213> Homo sapiens

<400> 464						
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gggtgtcattt	taagaaatag	cagggtgcagc	tccatctccc	gagtgggggt	tatggccaac	180
agtctgaatc	taggacgtgt	gtcctcggtt	tgcagcgtcg	ggcaggcagc	gtttttttgt	240
ogtgggtggt	ggtgggatgt	ttcagaaaca	cattttaaaa	agaagagat	cagcagcgaa	300
aaaccatatg	gctggctaca	tctttggatt	actggactcc	aggacgcccc	agccaaacct	360
ttcaaacccg	ggtacaaact	tgotgctggt	aatgtcagct	gactttcaga	agtgtccagg	420
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gactgggtct	ctcctgcagg	tcgaaagccc	agcaggccga	cagattctca	ctgacttcc	540
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gacttgctcc	gggtgagtg	ggggaagctg	ggcagcagct	ggaagacctt	gcggctgggt	2160
ggttgttggg	atgtttcaga	aacacatttt	aaaaagaaag	agatcagcag	cgaaaaacca	2220
tatggctggc	tacatctttg	gattactgga	c			2251

<210> 465
 <211> 824
 <212> DNA
 <213> Homo sapiens

```

<400> 465
tctgtagatc cctagtccag ogtgggtggaa ttccacctgg gcagacacct tctctctgct      60
cttggctctt gccgttgccc tctacttggg ctactactgg gcatgtgtgc ttcagaccca      120
cagggctttt tgtgccagca atactgaaga tctagagaca gtctgaacc acataaagca      180
tcgttatccc caagctccac tgctggccgt gggcatctct tttggaggga tactggtgct      240
gaatcacctg gcacaggcca ggcaggctgc agggctgggt gcagcactga ctctgtctgc      300
atgctgggat tcctttgaga ccactcgctc cctggaaaacc ccactcaact cactgctctt      360
caatcagccc ctcactgctg ggctctgcc aacttggtaa cgcctatcct atggttaagac      420
ctgcaggccc gtacaatcog ccagtttgat gagcgctaca catctgtggc ctttggtat      480
caagactgtg ttacctacta caaagcagca agccctagaa ccaagataga tgccatccgg      540
atccctgtgc tctatctcag tgcagcagat gacccttct ccaccgtttg tgcccttccc      600
aaacaggccg cccaacactc ccgtaagtt gcgtgtctca tcacagcccg ggggtggccac      660
atcggcttcc tggaagggct gctcccgtgg cagcactggg acatgagccg cctcttgcat      720
cagtacgcca aagccatctt ccaggaccca gaggggctgc ctgacctcag ggctctctta      780
ccttctgagg acagaaacag ctgacaagag taccatttgg ggctc      824

```

```

<210> 466
<211> 435
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(435)
<223> n = a,t,c or g

```

```

<400> 466
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agcaactcac acatgcagga gattctcgat aagattatca gcaaatatct catcanaaac      120
tggggaggcc agagggcagt gtcccagtggt attcaaagtg cttaaagaaa aaaaactgtc      180
aactaagaaa tcctttggcc aaaagtaagg gagaagtga gacattocca gacaaacaaa      240
agccaggagg tttgatacca ctagacctac catccaagaa atgctaacag gagtcctgca      300
gggttgaaat gaaaggacac tgacagtaac ctgaagctgt gtgaagaaat agagatctca      360
gogaaggtaa atattatgat tgcaacgaca atgtgcaatt ccactttttg ttttctacat      420
gatttaagaa actan      435

```

```

<210> 467
<211> 2464
<212> DNA
<213> Homo sapiens

```

```

<400> 467
ogcccccggg agaccaagag aagggggaaa tggggctggg ggccgtcccc gggagacagg      60
oggccttcog agagggactg gagcaggccg tgccgagtgg gcattgcttg atgggcaggga      120
agttgagtgt tccttgcaag ggtgctgtgg caagaggagg cctggtgtat ttggcagcgt      180
tcttgaggct ggcatgatc cactgatgg ctggccgagt accccaggga gctgatcgaa      240
tagcagtc aa ggctgagatg gagggcgttt ttctggagaa cctgaggcat gcagctgggg      300
ttttggctca ggaggacctc gtgggactgc tggagcccat caacaccgc atcactgacc      360
cccagtaact cctggacacg cccagcagg cggcagccat cttacagaag gtaggaagac      420
ccaacctcca attacaaatg gacatattcc actggcagat catggatggg aacctgacag      480
gaaacatcog ggagttcctg ccattgttg ggcagtgtga ggtggcacag gtocagggtc      540
gaggggagcc cagcagcccc ggagagctga atttccccta tctgtttcaa ctgctggaag      600
atgaaggcta caaaggcttc gtgggctgag acacagtaga gggcttgagt tggctacgtt      660
catactggga taggcggggc caccagagg ctggccagt agggcccgca caccaccac      720
gtgcctccag acagcgagt acatcccatc tctcctctg cattaaagat gacctgtga      780
acattgtcat atgtctctgt aatggggctg tgggacacat agtgtctaac acttcagttt      840
ctctgctgct tccctcccat tgagaagcca gtgccagggt tgctgtgaag atgggagagc      900
ttctgaaccc acctcattaa aggatgagaa acccagggtc cgagagcaaa gggacttgac      960

```

gggtggccgca	agtgtcttcaa	aggcagagct	gggattggaa	cccaggtgtc	atctcgatgg	1020
gaatgtccag	cagtgatgtc	caagtgggaa	gtgaagaccc	gaaggctcaa	gggacacagg	1080
tggctgacag	tggtcaaagg	ctagggggca	ggattcaggc	agaggagctc	taggggggtgt	1140
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gggtgttact	gggaagggtc	ctcggaaaac	cactgtcaga	gacgtcttct	ctaagtggga	1620
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gctggcgtag	tcagccacgt	agttgtatag	ctgggtgggca	gcaatgagtg	gtgtggggag	2460
ctcc						2464

<210> 468
 <211> 1354
 <212> DNA
 <213> Homo sapiens

<400> 468						
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ttttttttgt	aattatctca	ggggaaggta	gttattaagt	gttactgat	taggattaat	120
gtttccaatt	tttgtcaaga	acagaatgta	tgtattacta	atttaaccat	aatttcaatc	180
aaaactgtgt	cattaaaaat	gttggcagtc	atgcatttcc	tgcattggta	tgaatttttt	240
catgtatcta	tagtattttt	ctaacagctc	aattttaatt	catttacttt	ctcacgaaaa	300
tgtatttttt	ttccatttca	gcatgtagta	cttgtgttac	cttttcacga	ggcccacact	360
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cttacagtgt	ccatcagctt	cctatgattg	aagaaaagct	tccacttgta	ataaaccaac	480
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tctatttgggt	tcttaggtta	cacattaatt	ccatttgcct	agtaatttaa	agaatgtact	1140
gtagtacacc	aataagctaa	caaactcggg	cccttgaccc	caagtcacca	gtgtcaccta	1200
gattcaaaaa	ccaatataac	gagtcgaagta	tgaatgcaca	atattttagc	taagcccttt	1260
ctgtcccacc	tctaataaat	ccacatgctg	ccccagggtc	tggcacatgc	tggtaaaagta	1320
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<210> 469
 <211> 4747

<212> DNA

<213> Homo sapiens

<400> 469

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taaaatata	taaaatgatt	taataaaggt	cttttattat	tttacacatc	aaatttcatt	180
caatcagtac	tccactgaag	gagaaaagga	ttatgaaaaa	acaatgaaag	cacagggtag	240
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cgcagagcca	tctgggggat	gaatgttttt	catgtgttct	actagtattg	tcagcttcac	720
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<210> 477

<211> 843

<212> DNA

<213> Homo sapiens

<400> 477

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<210> 478

<211> 1307

<212> DNA

<213> Homo sapiens

<400> 478

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<210> 479

<211> 3081

<212> DNA

<213> Homo sapiens

<400> 479

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gcaattcata tattaaaatt gcaccttacc ttgcatacgc tcatattcta gggttttttc 2940
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<210> 480
<211> 417
<212> DNA
<213> Homo sapiens

<220>
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<223> n = a,t,c or g

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acccttgta aaaaattcct tccagcatca tctgtagatt cacaatocca aacaaaatcc 300
cagcaaatta attttactga caaactgatt ttctgagttt atatagagag gaagaagatc 360
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<210> 481
<211> 332
<212> DNA
<213> Homo sapiens

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<400> 481
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cacgagacac atcttcttgc gagatttttt ctgatatag agcagggtcg ttagctggc 180
caggggctct ttctacgagc acctctgagc ttcccgcat ggcttctatg otatcaatca 240
gatcacccctg gtcattggatg atcatggcca aatctttaaa tatctgattg acatccaaaa 300
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<210> 482
<211> 371
<212> DNA
<213> Homo sapiens

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<400> 482
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ctctaattca ttaatcatca ggaaagtgca aatcaaacc acaattcttt accatcatat 180
attcaccaga aaggctaaaa tgaaaaccac agacaaaacc aagtataggt gaggatttaa 240
agcaataaca actctcatto actgctcaca ggattgtaaa ttgcaataat cacctgagaa 300
aaccatttca tgatatctcc taaagctgaa caacacataa cctatgacac aacaattcca 360
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<210> 483
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<212> DNA

<213> Homo sapiens

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aagcaacata	gcaagacccc	tctct				565

<210> 484

<211> 805

<212> DNA

<213> Homo sapiens

<400> 484

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<210> 485

<211> 275

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(275)

<223> n = a,t,c or g

<400> 485

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<210> 486

<211> 376

<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(376)
<223> n = a,t,c or g

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gtcagattcc agttcgtaat ttaaaaagtg ctggtgaatt gtcagttgta tttcaatatg 180
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gatcaatcat atctan 376

<210> 487
<211> 770
<212> DNA
<213> Homo sapiens

<400> 487
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<210> 488
<211> 781
<212> DNA
<213> Homo sapiens

<400> 488
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 <212> DNA
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 <212> DNA
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<211> 421

<212> DNA

<213> Homo sapiens

<400> 499

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<212> DNA

<213> Homo sapiens

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 <211> 1785
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <211> 1950
 <212> DNA
 <213> Homo sapiens

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 <211> 554
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 <213> Homo sapiens

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<211> 412
<212> DNA
<213> Homo sapiens

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<210> 509
<211> 453
<212> DNA
<213> Homo sapiens

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<210> 510
<211> 1108
<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<211> 1085
<212> DNA
<213> Homo sapiens

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 <211> 3038
 <212> DNA
 <213> Homo sapiens

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3038

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<211> 1356

<212> DNA

<213> Homo sapiens

<400> 517

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<211> 974

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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 gattgcttga gcccaggagt tggagacaag gctggcaaga cctgtctct acaaaaaaaaa 600
 ttgaaaagtt aaccaggcac ggtggaacac gcctgtagtc ccatatactt ggggggctaa 660
 ggtgaggatt gcttgagcct gggaggtaga ggctgcagca agctgtgatc atgccactgc 720
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 aaaaaggata ttttcaccaa aattttttgt gaaaaatagc tggagaacca ctgtgttagg 960
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 gacctgttta agtaatcccc caggggccat ttggcaggaa cttttctatg aaaagatgac 1140
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<210> 526
 <211> 512
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(512)
 <223> n = a,t,c or g

<400> 526
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 ctatcctgtg cccatataaa cccaagctc tacaagcaga ggaacagaag agcagcagag 120
 tagcaaaatg gcatggcaga ggagagaaga gaaggagcat ctgaatgtca ggaggagtcc 180
 ggctgaggac gggtgaaaag cagataagcc ggggatggct gaactccagg ggaagatcat 240
 cttcccactc catccccctt ccagctccac atccattcct ctgagagcca actccatcac 300
 tcagtataat cccacacctc actatccttc aggttgatgt gacctgattc ttcctagatg 360
 ccagacaaag gacgggatta ccaaggagga ggcaggattt taaaaagggc tgttcaccct 420
 ggattnttcc cattgagtgg gaattagggc ctccaggaa aaggcaactg gttaaagggg 480
 cattnatttg ttaaccacac ccttaggatg gt 512

<210> 527
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 527
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 cttactttga aaactgggtat ttaaattgtca agaattaagc tttctcctg tcttcccagc 180
 attgacgatt togaaaaatt tttgatacta ttctacgtaa cactgcttta gctaaggtaa 240
 gtatatcttc ttagttccaa gtatcctatc cagcctgctc tccagtcatt cctgcttaag 300
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 cacatccctg tacaaggccc tctcggcagg caccatgat ggccattcc ttcgtagtga 480
 agtacacagc cactcctca aaagccactg attcctgggg cctggttgtt aaggacacag 540
 ctgtcatcat ctgacctctt ttcttctctt ctgggtaaag gtaaaagtct cagggtctga 600
 ggatatgcc cttggggcct ctccatccag agctccccga ggaaccgagc accaggggtg 660
 ttccctcgc tocagctg 678

<210> 528
 <211> 1160
 <212> DNA
 <213> Homo sapiens

<400> 528
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 agctgaggag gagtctaaga aaacaagcca ttctcagta tccctcggga aagaaggggt 180
 gagaggacac agatatacacc aggccctggg tgactgcatt gctggggcca tgcagggtc 240
 agctctccac caagggaaag tgctgatttt ccttgctatg ggtcctggcc ttgctcccat 300
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 tcaactaat tttcacttag gggtttgaag gccgctttac cctgtcgtag tgtcagggtg 420
 ccaggggagt tgtcatcctg gcaggatggg tgaagggggg atttccctaa gtacctgtct 480
 gctgttttgg tttccatcta ttgcgcatag aaccttgaag atctgggagt ctcagggtcc 540
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ggggcaaggg	ccagcccggg	acgaggaggg	aatgccgggc	cccaattcca	cctctggatg	1140
cacaacagct	cgctcgtgcc					1160

<210> 529
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 529						
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tggaatcctc	atattttgct	gtcatagcca	ctttgaaaaa	caatttgaca	acctcgttga	180
tttaagcaga	tttaaacgat	acttaccatc	atatattcta	tcagtgaaga	acatactttt	240
cataatgcag	gagtctgact	ctcagatatt	tacccaagat	ttatgaaagg	ttatgttcac	300
actgaaatct	gtacatgaat	gtttattgca	gttttatttg	tagttgtcaa	aacctggaaa	360
caattc						366

<210> 530
 <211> 397
 <212> DNA
 <213> Homo sapiens

<400> 530						
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tcatttatgt	tttatagttt	tcagtgcata	tatttttgtc	atgttttgat	tttaatatag	240
ttattctgct	gccatatttt	cttagctgtt	taaataaaat	acttcttgag	cccttatttt	300
ttttgtctcg	agccttagtg	aatactgtaa	ctatagtatt	tccattttacc	tcaagtaact	360
aaaattggaa	attaotcaat	attatgtggg	gaaaaact			397

<210> 531
 <211> 475
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (475)
 <223> n = a,t,c or g

<400> 531						
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tattacacta	catgatttta	agatttatca	taaagccaca	gtaatcaaaa	tggtatggta	180
ctggcatagg	caataaaaaa	tcagtaagaa	tgtatagaga	gttcagaaat	agagccacac	240
atatatgacc	aattcatttt	tgacaaaggt	gaaaagataa	ttcaggagaa	aggaaacagt	300
tttttcaaca	atagtgtctg	aagaattgga	tattttacata	aaaaagaact	atccatacat	360
tatacaactg	ttaacttaga	tcattggttct	aaatataaaa	tataaaactt	cagaattttt	420
aggataaaaa	ctttgttaacc	ttgagttata	caaaataactt	actatgtatg	accn	475

<210> 532
 <211> 384
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(384)
 <223> n = a,t,c or g

<400> 532						
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gagtaattag	agaacataaa	tggaacagta	actgagaaaag	aaacaggagg	agtgtacaaa	120
gaattatcct	ccccaaaata	ctctgggtact	aggcagtttt	atgggcaaac	tatttcaaac	180
tttccaggaa	aaataatttc	tatggtatat	aaactatttc	agaataccga	aaagaaggaa	240
ggcatcctat	ttcactatat	gaatttagaa	taactctaata	aaccataccc	aacaaagata	300
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ctacctaana	caatagcaaa	atag				384

<210> 533
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 533						
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tttctacaca	ttaacaatga	acaatttgaa	aataaaaatta	aacaaatatt	catttataat	120
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cactgaaaca	ttactgagaa	aaattaaaga	agacacaaaat	aatggaaaag	acatctatgt	240
ttctgggttg	gaagactaat	attgttaaga	tgccaaaatg	atctgtatat	tcaatgcaat	300
tcctatcaaa	atgccaatga	tgtgcatggc	aaaaatagaa	aaaaattcat	cctaaaaa	357

<210> 534
 <211> 2618
 <212> DNA
 <213> Homo sapiens

<400> 534						
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taattgacct	gggctatctg	agcagcagtc	actggaactg	tggggctcct	ggccaggata	120
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gccactgcct	tgacatcttt	attaaccagg	catttgacat	gcagcgggac	ctgcagatca	300
ctcccaaacg	tctggaatat	actcgaaaaa	aggagaatga	gttgatgaa	tcattgatga	360
atattgccaa	ccgaaagcag	gaggaaatga	aggatatgat	tggtgagaca	cttaatacca	420
tgaaggagga	acttctggat	gatgctacta	acatggagtt	taaagacgto	attgtccctg	480
agaatggaga	accagtaggc	accagagaga	tcaaagtctg	catcogacag	atccaggaac	540
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gacaaaaaca	ataaactgtg	gatgtctggt	tcctgtgtgc	tgcagccagg	tatctcaggt	2460
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ccagtgtgtt	tacatttata	ggaccacata	tccttggttt	ctgggggagg	gtttcactgt	2580
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<210> 535
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 535						
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tctaccttac	tagcccatat	atgggcatta	tgcgactcaa	aggactgtgg	gaagctttca	180
aaggatcatt	ttgccttggc	ttttcactta	atcacggcag	aagttaatca	agggcattga	240
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ggtaacagag	cttacaagga	aacctgtgtg	tattattttc	aaaggaacaa	tactctggcg	360
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<210> 536
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 536						
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gatccagggg	tgtctgtgtg	aaatgatcag	cctgggcccc	caagcaggto	actcccagca	180
cagagatgtc	attgattgta	cctcogtcac	caggctgtct	tcggccctca	gggaaaagta	240
gcatgtcttc	cagcaccata	tgacaactgc	tcagcactta	ttctctgtca	ttgctccctt	300
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atgccaacag	tgaacaatct	gaaaaagata	ttaaaaagta	atctcattta	caatagccac	480
acataaaaatt	aattcctagg	tatttaacca	aagaagttaa	atatctctat	aatgaaaact	540
ataaaaacact	gatgaatgaa	attgatgaga	tcacccaaaa	tgaaaaaata	ttccatgttc	600
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cagtgcgaatc	cctataaaaa	taccaatgac	attcttcaca	gaaatatgat	cctaaaaatgt	720

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cttggaggaa	tcacattacc	tggactttaa	ataatactac	agagctgttt	aactcaatca	840
gcattgtatt	gtcttataat	cagt				864

<210> 537
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(419)
 <223> n = a,t,c or g

<400> 537						
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cccaaataca	ggagcataaa	tggatgctca	tagaagttcc	tgtccagaga	cctgttctct	180
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tgatgcacag	ccttgggaata	gatcagcaga	aaaccattga	ggtaaagtga	tcagagattt	300
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<210> 538
 <211> 549
 <212> DNA
 <213> Homo sapiens

<400> 538						
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<210> 539
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 539						
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gtcccaaggc	gcaaggccac	ttgcgtcagc	tgagtgtgcg	gcagcatgca	ccatcacgat	360
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<210> 540
 <211> 2064
 <212> DNA
 <213> Homo sapiens

<400> 540
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<210> 541
 <211> 778
 <212> DNA
 <213> Homo sapiens

<400> 541
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gaggtgcagg gogctgtgct cagtcggagt ggccgtgtcc tccaccgact ctttgggaag 720
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<210> 542
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<212> DNA
<213> Homo sapiens

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<400> 542
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<210> 543
<211> 677
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(677)
<223> n = a,t,c or g

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<210> 544
<211> 742
<212> DNA
<213> Homo sapiens

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<400> 544
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<210> 545
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 545						
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 <212> DNA
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 <223> n = a,t,c or g

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<210> 547
 <211> 3039

<212> DNA

<213> Homo sapiens

<400> 547

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<210> 548

<211> 2369

<212> DNA

<213> Homo sapiens

<220>
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 <223> n = a,t,c or g

<400> 548

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 <211> 857
 <212> DNA
 <213> Homo sapiens

<400> 549

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<210> 550
 <211> 2276
 <212> DNA
 <213> Homo sapiens

<400> 550						
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 <213> Homo sapiens

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 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<400> 559

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<211> 2633

<212> DNA

<213> Homo sapiens

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<210> 569
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 569						
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<210> 570
 <211> 1131
 <212> DNA
 <213> Homo sapiens

<400> 570						
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 <212> DNA
 <213> Homo sapiens

<220>
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<222> (1) ... (960)

<223> n = a, t, c or g

<400> 571

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<210> 572

<211> 5665

<212> DNA

<213> Homo sapiens

<400> 572

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<210> 573
 <211> 1096
 <212> DNA
 <213> Homo sapiens

<400> 573

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<210> 574
 <211> 1938
 <212> DNA
 <213> Homo sapiens

<400> 574

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<210> 575
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 <212> DNA
 <213> Homo sapiens

<400> 575						
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acaatccaaa	cagtctctct	gagaggcaag	ccaaggatgc	ctccaccagc	accctacccc	2040
ccagggcatt	ttcacagctc	cagtaggaga	accttctgaa	tctgcggcaa	gactgctcta	2100
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cg						2222

<210> 576
 <211> 500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)... (500)

<223> n = a,t,c or g

<400> 576

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cccctgtgtg	gcggccagcc	agatgcgcac	ggcggagcac	gccacagcct	cggagctggg	180
gcacagcaac	aggagagaca	cagacagggc	gaggcccca	tgcaagctct	ggacccagg	240
gcagagcccg	gcccacaagc	ccaaagccat	gccgcctgcc	agcctgagcc	agaaccaccc	300
agagtccctg	tagatccccc	ggcagcccg	gggggtgtcc	agggcagggc	agtctttccc	360
gacaccctgg	gctggcacc	catcccaaaa	cccacactcc	atggccacag	tcggggaggc	420
tcccttgtgc	ctctgaacca	ctccctctag	gagggatccg	cccaaccct	ggcctggagc	480
caaagggacg	ggatcttatg					500

<210> 577

<211> 844

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)... (844)

<223> n = a,t,c or g

<400> 577

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gtcgggtattt	tctatacaga	tgtaaaacac	acgtaaacat	gaccctgctt	ttttttctca	180
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tcattcctga	gaccaaacca	ttcgtcagga	caccaatgat	ttctgcgta	gtccctcctt	300
aatgggagcc	ttgcccgtag	ctatgtcgag	atcttgaaat	tatgtccttg	ccacaccgga	360
ttcagcccct	ttgttagggc	tgctgcaaat	gaccccatgc	aagttattca	gtcttaattg	420
gcctccttta	gggtctctct	aaagatgtaa	cgcatgggtg	tgtggattgt	aaaagacact	480
cctgaccggg	cgtggtggct	cacatctgta	atcccagcag	tttgggaggc	tgaggcgggc	540
agatcacgag	ggtcagagtt	cgagaccagc	ctggccaaca	ttgtgaaacc	ccatctctat	600
taaaaataca	aaaattatcc	gggcatgggg	gcgtgcgcct	gtaatcccag	ctactttggg	660
agttgaagca	cgagaattgc	ttgaagccca	gagggtaggg	gtggagtga	cccaaatcgc	720
gccactggac	ttcaacctgg	gggacaagaa	caagaccccg	tttttctttt	ttgggggggc	780
gcttnngggg	ggggggcccg	tttagaagac	cacgtttttt	ctcccgcggc	atgtgaaagt	840
tttc						844

<210> 578

<211> 235

<212> DNA

<213> Homo sapiens

<400> 578

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ctgggattac	aggcaccgc	cgctgcta	ttttgtattt	ttagtagaga	tgggggtttc	180
accatattgg	tcaggctggc	ctcgaactcc	tgacctcagg	tgatcaaccc	acctt	235

<210> 579

<211> 906

<212> DNA

<213> Homo sapiens

<400> 579

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atcacaggca	tgccgccacca	cacctggctc	atctttgtat	ttttagtaga	gatgggggtt	180
caccatgttg	gccaggctgg	tcttcaactc	ctgacctcaa	gtgatccgac	cacctcggcc	240
ttacccaaag	tgctgggatt	acaggcatga	gccaccacac	tcagacttaa	gtgttagtag	300
gtaaatattaa	tagaaatgga	agttccgagg	taattcttag	atacactggg	ttatggaaag	360
gcaaacaaac	tttctacacc	acagtgcacg	tcaatcttgt	gagaggttaa	tcatgtgggt	420
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cactacagac	acaatgaatg	atcacgctga	cactaaagac	acaacaaatg	atcacgctga	720
cactacagac	acaatgatga	cgctgacact	acagacacaa	tgaatgatca	cgctgacact	780
acagacacaa	cgaatgatca	cgctgacact	acagacacaa	cgaatgatca	cgctgacact	840
aaagacacaa	caaatgatca	cgctgacact	acagacacaa	tgttcacgct	gacactacag	900
acacaa						906

<210> 580

<211> 408

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(408)

<223> n = a,t,c or g

<400> 580

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ataaaatcca	cgctcatgata	tattatcctt	ttatagatcg	ctggatttaa	gctgcttgta	120
ttttgacatg	aggatttttg	tatctgtact	caagagggat	attgtactgt	agctttcttc	180
ttttgcaata	tctctgtctg	atctttgtct	caaggtaaag	ctggcttcat	aaatgagttg	240
ggaaaggcac	cctcctcttt	atctttggaag	agttcgtgta	gaatatgaca	ttattccttt	300
tttaaatatc	ttgatagagt	tccgcccgtga	aacaatctaa	gtttggaata	ttgtgtgctg	360
gaagcttttt	agctgtaaca	ttgtttgaat	aaggctttta	cctactcc		408

<210> 581

<211> 685

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(685)

<223> n = a,t,c or g

<400> 581

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ggccatgacg	ggacaactcc	ttttcggggc	tctccacccc	ctcgaggctt	gccagggtgg	180
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cccgcactcc	aaacgaccac	agcgtgtgct	tggggccatc	cttcagcagc	ccgcgcacgg	360
ccagcggagt	gtccccagct	acatcccggc	ccccacctaa	ggtgaggcca	aagcctgcgt	420

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aaccgcgaac cagctccaca gagaaatgac cagaggcctg ggatggcttc ggagcactac      480
gtgccttacc ctggatcaat tggggagggtg cgttacatgt ctctaacca cgggtgctggg      540
gccggtgata cacaatagtg gcatgaggca ggcgactgtc tgtgacctct atgtccgcag      600
agccagcac  gctaacagcc tccttcgggc gcaggcgagc aattccacca cactgcctat      660
ggacaagaac tcataanccc cgcac                                     685

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<210> 582
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(635)
<223> n = a,t,c or g

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<400> 582
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cccgccccgg cctcctgcga gtcactacca ccoctagcct ctccaaactga gctcggcgcc      180
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gggcaagact actctgccct cccaggggcc cactgcagag acccagccgg ctggtgttta      420
ccngatgtgg ccaatgccat ccattgtgtg gtggcctggg acaagcctgg gacttctgat      480
tagaggacct attcaagggt ggcctacaga gggtccccc tcccttgatt gtcaagacct      540
aatctgaaga tctttccctg ccaagacaca agagggtga gccagggttc tagctgttct      600
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<210> 583
<211> 410
<212> DNA
<213> Homo sapiens

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```

<400> 583
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gccagtgctc cgcgccccct gccctcctcc aggacacttc tgtttgagta gcacctgcca      180
cgtgcagcag gtcaccccca acctcactac caaaagtgcc actgagacag atgaggaaac      240
acacactgct ctactccat tttacagaca gggaaatgga ggcagaaagg ccgtggcgtg      300
gcctaagtcc cgctggtggc agcagtggcg caggaggtga gcccatgctg ccagctacca      360
agctcaggct cagcacccca aggggagggt tgggcggggc ctccatgctg                                     410

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<210> 584
<211> 692
<212> DNA
<213> Homo sapiens

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<400> 584
tcagccacac cccagcagcc atccgcaccc caacaccaag ggactctgaa ccagccccc      60
gtccccggca tggatgagag catgtcctac caggctcccc ctacgcagct gccgtcgggt      120
cagccccctc agccctcaaa tccccacat ggggttcaca cgctgaacag tggccctcag      180
cctgggacag ctccagccac acagcacagc caggcggggc ccgccacggg ccaggcctat      240
gggccacaca cctacaccga acctgccaag cccaagaagg gccaacagct gtggaacgcg      300
atgaaacccg ccctggggac tggaggtctc aagttcaaca tccagaagcg accctttgct      360

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gttaccaccc	agagctttgg	ctccaacgca	gagggccagc	acagtgggtt	tggcccccag	420
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<210> 585
 <211> 1749
 <212> DNA
 <213> Homo sapiens

<400> 585						
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ttaaattgtc	gatttttagc	tatttgacag	attaaaagca	aaataatcat	gccatattta	660
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aaaacatcaa	cacattcact	tagatactga	tttaatccat	ggatcaaggc	catattttca	1740
aagtatttt						1749

<210> 586
 <211> 1308
 <212> DNA
 <213> Homo sapiens

<400> 586						
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gttaaagggc	agcctggcat	tgatggctgg	tggagctctg	aagcctgcct	ctgcaggtgc	180
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aatctcagaa	acgaatctga	agtcctgcaga	ggaaacccat	actcatattt	agcagcagta	1260
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<210> 587

<211> 683

<212> DNA

<213> Homo sapiens

<400> 587

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tggggggagaa	gggaatctac	atctcctgct	tagggcttta	tatcgcatct	gctgtctgac	360
atagacttca	aaataacctat	gtcagatact	tcctgaatgc	tcctctcttg	tagctgggca	420
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ccaggagttt	aataccagcc	tgggcaacca	agtgaaaccc	tatctttaca	aaaaacaaaa	540
ttagccagat	atggcagcat	gggcctgggc	ccagctactt	tgaagctgaa	acaggcggat	600
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<210> 588

<211> 1780

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 589

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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 <211> 531
 <212> DNA
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<400> 609						
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<210> 610
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 610

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<210> 611
 <211> 1891
 <212> DNA
 <213> Homo sapiens

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<210> 612
 <211> 161
 <212> DNA
 <213> Homo sapiens

<400> 612

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<210> 613
<211> 698
<212> DNA
<213> Homo sapiens

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<400> 613
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<210> 614
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<212> DNA
<213> Homo sapiens

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<223> n = a,t,c or g

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<210> 615
<211> 414
<212> DNA
<213> Homo sapiens

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<400> 615

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<210> 616

<211> 771

<212> DNA

<213> Homo sapiens

<400> 616

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<210> 617

<211> 488

<212> DNA

<213> Homo sapiens

<400> 617

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<210> 618

<211> 2944

<212> DNA

<213> Homo sapiens

<400> 618

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<211> 1776

<212> DNA

<213> Homo sapiens

<400> 619

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<210> 620

<211> 2865

<212> DNA

<213> Homo sapiens

<400> 620

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<211> 791

<212> DNA

<213> Homo sapiens

<400> 621

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<210> 622

<211> 1484

<212> DNA

<213> Homo sapiens

<400> 622

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<210> 623
 <211> 1281
 <212> DNA
 <213> Homo sapiens

<400> 623						
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<210> 624
 <211> 757
 <212> DNA
 <213> Homo sapiens

<400> 624						
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<210> 625
<211> 502
<212> DNA
<213> Homo sapiens

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<400> 625
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<210> 626
<211> 331
<212> DNA
<213> Homo sapiens

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<210> 627
<211> 304
<212> DNA
<213> Homo sapiens

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<400> 627
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agaagcggga ataacgggcc ccggccccc ccccggttaa attttggaa ttttaaggga 180
aacggggttc ccccaggtgg ggcgggetag cctcgacccc cggacctaa gggaccccc 240
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tgaa 304

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<210> 628
<211> 1596

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<212> DNA
<213> Homo sapiens

<400> 628

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<210> 629
<211> 2029
<212> DNA
<213> Homo sapiens

<400> 629

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tcagctatta	actgtgctgt	gtatttatca	agttggtatg	ttgtatgtac	agtgttatcc	1500
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tctacccttc	tgctctagat	tgtctggact	caggagattg	tggcagttac	tggatagtta	1860
tttttaagat	aatgattgct	tttctctgtt	tatataagtc	atgtgtactt	attgtagaaa	1920
gtttgtaaga	tgcaaaaagt	ataaaaatta	aagttatgca	ctactaacat	ttcaatatat	1980
tttctcccag	attttcaata	aagactttca	ggcagtgaaa	aaaaaaaaa		2029

<210> 630

<211> 423

<212> DNA

<213> Homo sapiens

<400> 630

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cctgaatggc	tgggactaca	ggcgcccgcc	accacacctg	gctaattttt	ttgtattgtt	180
ggtggagacg	gggtttcacg	atgttgcca	ggatggtctt	gatctcctga	cctcgtgatc	240
cacccctca	gcctcccaaa	gtgctgagat	tacaggcgtg	agccactgca	cccggctgaa	300
aaagattaga	tttgcaaagg	ggcatgtgga	attttttttt	gaaagtcag	tagaatagtt	360
tataagccag	ccctttcaga	aagaaaaacc	accacacaaa	actttctttt	acttgtaaat	420
tac						423

<210> 631

<211> 1009

<212> DNA

<213> Homo sapiens

<400> 631

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tcctctgcct	ggaactctct	ccctctgctc	tcacagggtt	ccctaagtgt	cgttctctcc	120
aagaagccct	ccctgatgag	ttgagccact	ttagtttgtg	ctcagggtca	ccctgcacgt	180
cttggttgct	ctcatcactg	taatgatcta	aaacacacgt	ctgctcatga	gaccgcgcatc	240
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gctccggaaa	tgtctgctgg	gggctcggaa	tacccacctt	tctggtaatg	cagcccagcg	360
ggtcccagcc	tcgttttcca	gcctcactc	aaaatggagt	cgctctgggt	cgaacgcctc	420
tgacaagtgt	gtacctacgt	gtcaggccca	tccttctctg	aggcctttgt	cttgggtgtca	480
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aggagcctgc	tcacatgacc	gtgtggagaa	agttcttttc	ctgaggacca	tctggagtgg	600
acgogtgcac	taacctctct	tgaatacacc	ctccccaoga	ggccctctgg	agcatcctgt	660
agagccagcc	cctacccaga	gacctgagc	ccagagaatg	cgctgggtgg	tgagccctgg	720
ggaogaatgc	agagccctag	gtctctctct	cagaaagacc	ggattttgcc	atgttggtccc	780
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gggattgcag	gtgtgagcca	ctgcacccgg	cctcaggcag	gtatttttac	cagccgaata	900
ctcttgacat	gtgcactctt	cgtgttcac	atcagtcctc	cggatgggtg	tttaaggcat	960
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<210> 632

<211> 488

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(488)
 <223> n = a,t,c or g

<400> 632
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 tcaaccagct ttggcttcat gggccatctc ctgcgggttg aatttgaaat cctcccttcc 120
 acaccaate cctagcttcc ctcctaccag ggggaggcag caggctcttc attgataagc 180
 catttgacaga catttagccc tgacttgaag ggtgtctact gcacattccc tgcctcaggg 240
 ctggetccag tgcccaccca ctggacagtc tcagagctca gcaggagccc tgtggccaca 300
 gccacattct gctaaaactg ggatagagga acaagcccag cccaagagc agctatgact 360
 tttgttttta agaattggaca tttcacatct gtgcaatact gaagacctca ctttgtcatg 420
 ttgccccagt gacatagtga gaggtcacca ggcttgcaaa tgaacttcac acagacctca 480
 ggggtangt 488

<210> 633
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 633
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 tcttccggcc tgctgcaggc ggaggtgctg gatctggacg aggaagagga cgacctggag 180
 gtgttcagca aggatgcctc attgatggac atgaactcct tcagccctat gatgccaaca 240
 tcccctttat caatgataaa ccaaatcaag tttgaggatg aaccagattt aaaggatctc 300
 ttcatcacag ttgatgaacc tgaaagtcac gtactacaa tagaaacttt cattagctat 360
 aggattatta ctaagacatc tcgtggggaa ttgactcca gtgaatttga agttaggaga 420
 cgatatcaag atttcttttg gttgaaggga aaactggaag aagcacacce cactctgatt 480
 attccaccat tgccagaaaa gtttatagta aaaggatgg tggaacgctt taacgatgac 540
 ttcattgaga cagcgaggaa ggctttacat aaatttttga accgaattgc tgatcatcca 600
 actttaacat ttaatgaaga cttcaaaatt tttctcactg cacaagcttg ggaactctct 660
 tctcacaaga agcaaggctc tggcttgcta agcaggatgg ggcaaacgt cagagctgtt 720
 gcgtctcaa tgagaggagt taaaaaccgc ccagaggagt tcatggaaat gaataacttt 780
 attgaactat ttagccagaa aataaatttg atagataaaa tatctcagag aatttataag 840
 gaagaaaggg aatattttga tgaaatgaaa gaatatggcc caattcatat tctgtgtgca 900
 gcgtcagaag aggatctggt tgatactcta aaggatgttg ccagctgcat tgacagatgc 960
 tgtaaggcca ctgaaaagcg gatgtctgga ctctcagagg cctgcttcc tgttgtacat 1020
 gagtacgtgc tttatagtga aatgttaatg ggtgttatga aaagaagaga ccaaatataa 1080
 gcagaactgg attccaaagt tgaagttttg acctataaaa aggcagatac tgatctgctt 1140
 ccagaggaga ttggaaaact tgaagataaa gtggaatgtg ctaataatgc cctgaaagca 1200
 gattgggaga gatggaaaca aaatatgcaa atgatatca agttagcatt tacagatatg 1260
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 cgtgtcctta taaagtggat gaaaaatgtt ttgtacccat ctggaaaacc aacaacttga 1500
 aatctcaggt attccaggtc actgacatga atttgaagat atatctatct gtatggatat 1560
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 ttcttaaat tgtgtgcaa taattgcata tagatttttt tcttaaatat ttgactgtgg 1680
 aacatgccat tttaaatatg ttgtaaggac tgttttaata aaaagtttag tatg 1734

<210> 634
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(420)
 <223> n = a,t,c or g

<400> 634
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 ccttgaagga gaataaaaat attaaaatag cttattttatt tatttttttg actgccctaa 120
 attatgaggg atgaatttta caaactttac ttatattagt ggtaacaggg gaactggaga 180
 gttttgcgcc ttctctaagc tggccggcaa gaaccaccaa tagcatgggg gaacatacgg 240
 tccttttcaa gcccatggct ctttcggcct gtagatgtca gccacacat ctccctgtgc 300
 ttatagactg ctttgagat ccattgggtg tcaggatttc ttctgatagc tttatggaat 360
 ggatcaatga ggataacctc aaaaaatttg tatgtgtaat cttcaccaac ccaataagaa 420

<210> 635
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 635
 cccacgcgtg cggagcagcc gccgaattac acttcctata gtacattaaa caacctgacg 60
 caaaggaag aagaagaact gtctactgga aaaaagaaac agagtccgag gcctcagaaa 120
 ttactattcc tcccagcacc cgggggtac cacaggctcc cggccactgg gaagactacg 180
 gaagaggtga caacttttat ctcccacact gagaccctgg ggggattgtg ctatggaaca 240
 tctttaaccg aatgccaaata gcaaggaaga acattacgga cggggagcac catgaatatc 300
 tcattgaagt acccagacta ttccacactt ctgaagactg agggcccaca ctggaattgt 360
 gaaaccact gcgtcccgta acaggacgtc gaaagggtaa aggagcctgg gttg 414

<210> 636
 <211> 398
 <212> DNA
 <213> Homo sapiens

<400> 636
 ggaaaaaccg gaccactttt tccctgaggg cacttccttc ataatgaac cccgcgcgcc 60
 gaactgagga gacttggtac attgcttggg tggcattagc cgetcaacta ctgtgactgt 120
 ggcttaactt atgcaaaagc tcaatttgct gatgaacgat gcctattaca ttgtcattat 180
 gaaaatgtcc agcatatccc ctaacttcaa ctccatggat cagcccctgg acttccaaag 240
 gacgctggga ctacggagcc catgttacaa cagggttcct gcccaaaaaa tgtattttac 300
 caccctctcc aaccataatg cctaccaggt ggactctgtg caatctacgt gaaagagccc 360
 acaccctcc ttgctagaat gtgtctggcc ctctagct 398

<210> 637
 <211> 943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(943)
 <223> n = a,t,c or g

<400> 637
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gagcctcagc	ctccatcgct	ctgtaacctg	cgggtattgg	atgattcgt	gctaagactt	120
cgcgacaccc	ttgaagctga	gaaatggaac	ccttaacatt	cagggatgtg	gccatagaat	180
tctctccaga	agagtggaaa	tgcttggaac	ctgcccagca	gaatttgat	agagatgtga	240
tggttgagaa	ctacagaaac	ctggtctccc	taggcccggc	atggtggctc	acgctgtaa	300
tcccagcact	tcgggaggtc	gaggcgggtg	gatcacctga	ggtcaggagt	tcaagaccag	360
cctagccggc	atggagaaac	cctgtctcca	ctaaaaaaa	aaaaattagc	caggcgtgat	420
ggtgcacacc	cgtaattcca	gctgctcggg	aggatgaggg	ggaagaatcg	cttgagcctg	480
ggaggcggga	gttgcaagtga	gccgagatca	ggcgcgtgaa	ctccagcctg	ggtgacagag	540
taagaaacctg	gaaactctca	gacttcaa	ggtcctgcaa	caggagtatc	aacctatatt	600
cttcccttct	gtacaactgt	gtttctccac	atttctctg	gatactgcaa	gtcaaacctg	660
tgttttacta	ctggctcttc	tggtgtgagc	aagtcatttt	tctctgtggc	tctgttctct	720
cctctaggga	gaccagggtt	ctgtagttct	ccaacatcac	atctctatac	aaattctgct	780
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tttaagggttc	catttctcag	cttcaagggt	gtcgcgaagt	cttagctacg	aagaattccn	900
ccngnctgtc	tagagagtag	tcagtcaaan	nnngggggcc	att		943

<210> 638
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 638						
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agcgggggca	ctggaacaac	aagatggagt	ttgtgctgtc	agtggctggg	gagatcattg	180
gcttagggca	cgtctggagg	tttccctatc	tctgctacaa	aaatggggga	ggtgccttct	240
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ttgtgttggc	ctgggcccctg	ttctacctct	tcagcagctt	caccatcgac	ctgccctggg	480
gcggctgcta	ccatgagtgg	aacacagAAC	actgtatgga	gttcagagaag	accaacggct	540
ccctgaatgg	tacctctgag	aatgccacct	ctcctgtcat	cgagttctgg	ga	592

<210> 639
 <211> 1038
 <212> DNA
 <213> Homo sapiens

<400> 639						
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tcgcctaacc	tacagaggtg	tcatgtaggt	tcaatgaaat	aatgcatgga	aagcccttca	180
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actttatttt	ttaaccatct	cccatcttcc	ctttgctttt	tcagctccag	ggtttgagcc	300
acaatgtgat	cttcaccttg	gattctttgt	taaaaggaga	cctaaaggga	gtcaaaggag	360
taagtgttca	gaaatttgat	tttcacttta	acttgaaagg	attaattttt	tttttctct	420
ttcaagatca	tagtagtact	tgtatttgaa	agactctttg	aacattttca	gcgttaaaaa	480
tgtctttgga	aaatgatcat	tggaaaaaat	gtgctctctc	acataatggt	attgacagag	540
gaatgagatt	aggcactttc	aagaagattg	ggaaggctct	ccatgggtgg	ggagagagaa	600
gctaagcccc	agtcttggct	cccacagtgt	gaccactggg	gaccagcccc	ttctgaacct	660
cgggctcctg	cttcacagc	atgaccaggg	gcgcttaacc	ttcttttctc	ctcctcagge	720
cttcttgtgt	atataacaca	tggtttgatg	ttgccagggc	acagtggta	tgccctataa	780
tctgagcact	ttgggagacc	atggcggcgg	gtaaattgct	tgagcccagg	agttcaagac	840
cagcctgggg	aacataataa	gacccccatg	tctacagaag	aagtacaaga	attagccagg	900
ggtggtgggt	agtgcctgta	gttctagcta	ctcaggaagc	tgaggtggga	agatcaattg	960
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acagagtgag	accctgtc					1038

<210> 640
 <211> 643
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(643)
 <223> n = a,t,c or g

<400> 640
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 ggccacctgc tgttccctgg gattcatgtc cttctgggga ggagggagga ccaggacaa 120
 tggctgctgt tcatgatctg gagatggaga gcatgaatct gtagtcccgg gaggctgagg 180
 caggagaatt gcctgaacct gggaggcggg ggttgagta agccgagatc gtgccattgc 240
 actccaggct gggggacaag agtgagactc catctgcagt cccagctact tgggaggctg 300
 acgaaggagg atcgctttga gtccaggagt ctgagaccag cctgggcaac atagagagtg 360
 ctgcagaggt ccgatctctc tgttcattct caagcaacct gaaggcaggc aggggtctgcg 420
 tcggatccag ttctgtgccc cttggtaggc acccaggaca ctgcaggcat caataaatat 480
 cggttgggca agtacagttg caggatgagg acaatcaatt cttcctcaaa tgccgggaga 540
 gcattcccat agcgggtgctc tgggagcccg gaagaaggca ggggagcggc tcgtgcgaat 600
 tcgacgagcc gtcaataant caattttcac ccggcccccgg ccg 643

<210> 641
 <211> 494
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = a,t,c or g

<400> 641
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 gggctggccc cagagttgag ttctgagctc agctctccac ctcttcctgc ccgtctccag 120
 ctgcgtgcct cccctacttt ttcccacagc tgggcagaaat gccctcagcc tgtgcccggc 180
 ggcacacatg ccacatgggtg cctgggcgcg gtctgggcaa ggatgacgcc cccaggaccg 240
 gctgggatac caagccaccc gctgcctccc ccacctccag aacggagcgt ccccatccca 300
 tcccctttcc cagccaggga ctcggggagc aggcaggac acagcacaga cagatacaaa 360
 cacacagatg caccagagga cgcccacagg cgtgtgcccc agagggacac agacacaggc 420
 gttcacacag gctcgggtac acacacgcac gctcacaccc cccagagaa anttatgagt 480
 ggtcaccact tgcg 494

<210> 642
 <211> 487
 <212> DNA
 <213> Homo sapiens

<400> 642
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 gcacgtacct gctggcttta ttactttctc aaattttatt agctattaga tacgatcttt 120
 tttgttctgc gcaagaaaaa tagccaagtg actttccttc atgtattoca tcataccatc 180
 atgcogtgga cctggtggtt tggagtcaaa tttgctgcag gtggtttggg aacattccat 240
 gcccttctaa atacagctgt acatgtagtc atgtattcct actatggact ttctgcattg 300

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gggccagcct accagaagta tttgtggtgg aaaaaatatt tgacatcatt acagcttgtc 360
cagtttggtta ttgtcgccat ccacataagc cagttctttt tcatggagga ttgcaagtat 420
cagtttccag tctttgcgtg catcattatg agttacagtt tcatgtttct gctgctcttt 480
ctccatt 487

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<210> 643
<211> 489
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(489)
<223> n = a,t,c or g

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<400> 643
cttaatggca ttcatgaaa tgcatacttc tggttcttta gtgtatttaa aaataaaaac 60
aaagatctat tcttattttt caatgcttaa ttttttactt caggaaattc cactttcaga 120
aattctccgc atatcttcac cagcagattt cacaaacatt tcacaaggca gcaatccaca 180
ctgttttgaa atcattactg atactatggt atacttogg ttgtgagaaca atggggacag 240
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aaaagcaatt cgccaagccc tcatgcctgt tactcctcaa gcaagtgttt gcactttctc 360
agggcaaggg aaagatcaca gtaagcaatg agcttcttga tggctttttc tcctctttaa 420
ttcttaagca ttttgtgggt atggttgngn ttcctgcgac gcagtagttt tcattgggng 480
nggcctggc 489

```

```

<210> 644
<211> 489
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(489)
<223> n = a,t,c or g

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<400> 644
gggcgcggnn nnnccaccta gagegtacgt agngacgcgc annctctgtt tgetgtccat 60
cctgtgcaca ccgagtgtgt tgcgtggtgt gtcggccgtg catacctcct gtgtgccctg 120
ttcttcttgt tatctttcct tggctactgt aaagcattta gagaaagtaa caaggaggga 180
gcgcattctt ccaccttctg ggtgctgctg agtatctttc tgggagcagt ggccatgctg 240
tgcaaagagc aagggatcac tgtgctggtg agagccgcaa catggctggg gcctgctttt 300
tctgtgtgtc cttttccctc ctataaagac atctggggct ggccctgcct ctgtggcgtt 360
ctccacgcct acatccatt gctggtctga ggtgatagac ctttctggac aaatggcttt 420
cgctgtcaca attctggcat tgcagatgga gaattgactg acttccttga cagtcattgtg 480
caactgggg 489

```

```

<210> 645
<211> 456
<212> DNA
<213> Homo sapiens

```

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<400> 645
tttttttttt ggtgtttcaa ttgttttatt acaatccaaa agttggggcg ggggttctg 60
tgccaccaca caccatccag gatgagaggg tcagaagtca aaggtccaag ctgcaggagg 120

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gtcagccctt	gcctggcatg	ttgatgtaga	ctttgccatc	ttcttgggog	gggctgcggc	180
gtgggcgtgc	gcacaggaac	accgccccca	cgatgagcag	cgatgccacc	gcatcagcag	240
ccacgaggcc	tgccaggagc	ggcagagaga	gggaccacaa	tcgggaacaa	gagcctgaag	300
tgccagggtg	aaaggcaggg	agtgatgac	tctctcctgg	agtcgtctga	gctgcagcca	360
ctgggagcaa	aagcaggaag	aggatgtgac	ccagatggat	catggtggac	tggggctctg	420
caggggtctg	gcagaggact	gtggtccaga	gaagtc			456

<210> 646

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 646

tggaagaagg	gagtggagact	gctcagagag	gcaggattcc	tgctgactcc	agggggacac	60
ctggcacctc	agcttccttt	cccacttctc	caggctgcat	ggagggtgc	cgggcagggg	120
cctcctggaa	gggaacctcc	tgcagcctca	agcaccaggt	catgacatga	catctatccc	180
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<210> 647

<211> 1043

<212> DNA

<213> Homo sapiens

<400> 647

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1043

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 <211> 2061
 <212> DNA
 <213> Homo sapiens

<400> 648

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 <211> 1287
 <212> DNA
 <213> Homo sapiens

<400> 649

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<210> 650
 <211> 442
 <212> DNA
 <213> Homo sapiens

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<210> 651
 <211> 1699
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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<210> 653
 <211> 1968
 <212> DNA
 <213> Homo sapiens

<400> 653	
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 <212> DNA
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 <211> 397
 <212> DNA
 <213> Homo sapiens

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<210> 656
 <211> 633
 <212> DNA
 <213> Homo sapiens

<400> 656						
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<212> DNA
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tacaccaata	tttctatgaa	cagatcttac	aactgagagt	gatctgcaga	tttttcagag	1260
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<210> 659
 <211> 934
 <212> DNA
 <213> Homo sapiens

<400> 659						
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cttttgggtc	gtttctactt	agctgactcc	tcaattgggt	agaaacattc	ttcatcaata	660
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<210> 660
 <211> 642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (642)
 <223> n = a, t, c or g

<400> 660						
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tggcggecca	gcattgattc	tggactattg	taggggttgc	tgcctcatc	ctgttctctg	180
tagcaactgt	ggctcgtgtc	ctcgtcaaaa	gaaaaccacc	ccgggaccca	ctgttctatg	240
tgtatgcagt	ttttggattt	accagcgtgg	tgaacctcat	cataggactg	gagcaagatg	300
gaatcattga	cgggttcatg	acacactact	tgagagaggg	tgaaccgtat	ctgaacaccg	360
catatgggca	catgatctgc	tactgggatg	gctctgctca	ttatctgatg	tacctggtga	420
tgggtggcag	ccatagcatg	ggaggaaact	ttattaggaa	ccattggcct	atattgggtt	480
ggatctatta	ttatgagtg	tgttggtttt	gtgccaggaa	acattgtagg	gnagtatggg	540
acaacgaatt	gccctgcttt	tttcttaagc	ataccatata	cttgtcttcc	tgtctgggct	600
ggttttcagaa	nctataatca	gccatcagaa	aattataatt	ac		642

<210> 661
 <211> 955
 <212> DNA
 <213> Homo sapiens

<400> 661
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gaaatattaa taacttgaac attaaaaccc atccatttac agttaattta ttttagagat 180
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aattaggtag tcaatggctg aattttatag tagttggtaa atactatagg acatacgggc 300
ttattttatat aaatgttcta atacttatat ttggtagcca ttattaaagt cttcgaatca 360
tagttaagtc tccatggtag cagtgggttc gtgattatgt tttaatggat gcagtatacg 420
ataaagttaa ttcatagtta aagtttggtta ctgattttaa ttaaatcatt tgagaggcca 480
ggcacgatgg ctccacgctg taatcctagc actttgggag gcggagggtg gaggatggct 540
tgagcccagg agttcagagc tagcctgggc aaaataggga gaccctgtct ctgcaaaaga 600
aaagatagct agacgtggtg gcacgtgcct gtggtcccgg ctatttggga ggctgagttg 660
ggaggactgc ttgagccccg gaggtgaga ctgcagtggg ccataatgaa accactgcac 720
tttagcctgg gtggaagagc aagactgtct tcaaaaaaga aaaaaagggc gggccgctct 780
aggggatcca gttttcggtc cggggcggg gagggaaacg tttttttta ggggacccaa 840
gatgagattg gcggcggcgc gtttaaacag tcaagacgtg gaagacacca cacacgacta 900
gtgaggagat gacgacgcg cagtgtcgac gagcggagat gcgcgacccc ccccc 955

<210> 662
<211> 766
<212> DNA
<213> Homo sapiens

<400> 662
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atcgatcacc actacatgaa gcagcaagtc aaggctcgct tcttgctctg agaacattat 180
tatcacaggg ttataatgta aatgcagtaa ccttagacca tgtcacccca ttgcacgaag 240
cctgccttgg agatcacgtg gcatgtgcca gaactctgct ggaagcagga gctaattgtaa 300
atgcaatcac gatagatggc gtgactcogt tattcaacgc atgctcccaa ggcagtccaa 360
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ccccaacgca tgagggcgcc agtaaaggtc accatgaatg tottgacato ctgatatcct 480
ggggcataga tgttgaccaa gaaattcctc attcgggaac tcctctctat gtactgtgca 540
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gcaaatattg ggatacccca ttaccgggtg ctggccacca atccacacaa aaactggaat 660
agttaccggc tcaattggag acgaatgcat ggccacatcc cgggcttcgg cgactattta 720
tctagtgtcg ccaacgcacg ggaacaacga tttctccctc gctccc 766

<210> 663
<211> 951
<212> DNA
<213> Homo sapiens

<400> 663
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aaacacacag tgaagtttaa tcaggaaccc aacctccggt cctctgctac aaccacggaa 120
acggctccaa acttgagggg ggacccccc aagcctgctt ttggcccaaa gctotgcctt 180
ccagccctcc tcataccccc tggccacctg ggaccaggaa aggggggtag agccctgaga 240
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cccaggggtg ggcaatocct gacagcgtg gccggcactt gggagctcct gctcagccac 360
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cccgctcag atcgactgcc ttcagaaaca aaaagtccc gcgcaaaggc gttcccggag 480
tggcagcctg gccctgcacc cagctgtgct gccctgcag agccccagca gcgaggcaca 540
cccaggtcag gggagggggc ttgggtacca ggggcctcac tggctcttca ccaggaccct 600
gtagagttag aagctgagga ctgcggccac ggcgccccc acaaccccca gcagcccccg 660
gagccagaag gaagagggat gcagctctgc gtggaccaaa tgtgggaagg cggccatggg 720
ggcgagctgg gtgaagatgg tgggtgctgg ctcggtggg ccagcacagg agaacggcac 780
gggagcgggt agcgggtgct tgccggcaaaa ctcgccgggt gatgggcccag acaccggac 840

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accttcgggc aggtcggcct tggaggagac aaagaggcag ggggtctgcc cgtccatgta 900
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<210> 664
<211> 571
<212> DNA
<213> Homo sapiens

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<400> 664
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tgagcactga gttagcgagt gggttacaga tggccatata gcgatcatag cccatggctg 180
ccagcaggaa ggagtgagag gagccaaaga agaggaagga aaacatttgg atggcacagc 240
ccaggaaaga aatggctctt ttctgggaca gcaggtcaac cagcatcttg ggtacaatga 300
caaagggtata gcaaattctc gagcaagaaa ggatggcaag gaagaagtac atgggagtat 360
gaagggctct gtccagcaca atgggtggaaa tgatgattgc attgggtgcc agagtgaaca 420
ggtagaggag caggaagata acaaagagca gctgctgcag cctggccagg gatgagaagc 480
cgaggacgac gaactctctc accacagtct tattgacttg ctccatggag agcacttcta 540
taaaggagag tcaaggacag aggtagaaac c 571

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<210> 665
<211> 694
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(694)
<223> n = a,t,c or g

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<400> 665
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gcagagagct cttgaggttg aggggggagg tgacagggct aatgcctca cagccattgc 120
ctgcctcccg gataacgctg ttgaaccttg ggctgcagat ggtcacatcg acagtcctct 180
tgcttttcag ggtaggcctc tcctcagccg ggtggctcgt gacatcttct ccaaagggtg 240
cgaaagtccg tttggtgggg ccgcagtcgt cataagcctc gacatcagca gcagtagctt 300
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gaaatccttc attctgatca tgatcaggca tctgagatcc catggaggtc aactgggtgt 480
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caagttggac actctctca tgtccactat ccttcaggct gtggccctct aaanaattga 600
aggaggggcaa gcctctttga atttaaaggg ggcttcgggc tatttcaacg ggagggtggg 660
agggccaaaa agaaataggt tttcaagccc tttt 694

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<210> 666
<211> 503
<212> DNA
<213> Homo sapiens

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<400> 666
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ctttatgcat cttataacca aaaaagcctt cagtagagca agtctgagcc agaggtttta 120
tcacactttg tctcaggggt ccaccaggaa ccaggctctg gctcacagcc aggctggaaa 180
cagtccttcac agttctgagc ctggagtttg agatctgcct cccctttcaa ggaagatcca 240
gaggtcacct gcgctttag agacatggct gaagctgcag gectgaaagc tgagccttgg 300

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gccctaccag	agggggccca	gtcttttga	aatcaaaca	gaagaaatgg	ctgtctttgg	360
tgctgctttg	gaaatatact	cagctactgg	tgctcaagag	cattatttat	aaatcactgg	420
tcaaagcaag	ggtggccatg	agttattgct	gaagaatgca	ggacaacttc	tgtaaaggat	480
gtagaatagc	aaaacatgct	aag				503

<210> 667
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 667						
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gcccctagga	cctgaccaac	agccatttct	tcctgtttga	tttccaaaag	actggggccc	180
ctctgggggg	gcccaggct	cagttttcaa	gcctgcagct	tcagccatgt	gtctactagc	240
gcagggtgacc	tctggagctt	ccttgaaagg	tgaggcagat	ctcaaaactac	aggctcagaa	300
ctgcgtttac	tggtgccaga	ctggcttga	gccaccacct	ggttcctggg	gggccctgag	360
gaccagagg	gaaaaaacct	ttttgtcaac	actggggggg	gctgatt		407

<210> 668
 <211> 872
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(872)
 <223> n = a,t,c or g

<400> 668						
tttttttaat	tttaatagta	tattttattt	aatgcaaaat	atccaaaaca	ttattttcaat	60
gtggagtc	aatat	tactgagatg	ttttacatct	tcatactgtt	ttctaataat	120
atatgaatta	ttgaatgaag	tacgtatttt	acacttacac	tgtatcagaa	tttggactag	180
ccacatttca	agtgcctctg	gacagcacag	gtctattatt	ctccaggcct	cagtcatttt	240
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caataagctg	tgcgattggg	ttggatttaa	atacatctct	tccttcataa	tcctctgcat	480
tttctgcatg	aactcctgca	tatttcaggc	atattgccag	ctgcttatct	tcagataaact	540
tcacaaatcac	actttgatct	gcacaggtct	cagagttatc	gagaagtctg	ttaagtcttt	600
tcacaaatcac	tctgcttaag	acaatccctc	cttccacagt	caogtattcg	aggtctccaa	660
atataacagt	gtggcccaga	tagaagggt	gggatgcac	ccttgtaa	aaaaggta	720
ttaaattttc	aatgtcagca	aacgtagtgg	gaagtgcacg	gaagaccag	ttgtagtgtg	780
cgccattctt	ttaaaaaag	tatttgtaag	cggtctta	ctgtaccac	ctgtcattac	840
tttttatatt	ganetaatgg	atttggtgta	gg			872

<210> 669
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 669						
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gctggcccca	gctgcgattc	acttgctcaa	ccgggtgcgt	caggagtgtg	agttcaacat	120
gacagccacc	caccacttct	ctgtggatct	caatgcctct	cggagcctgt	cccaggtage	180

catggacctc	cacgaggctg	tcagcatgaa	gctgcaccgt	gtccgagagg	ccctggctct	240
gatgggcttc	accacgcctc	tgctgcttgt	gcttctctac	ctccaagccc	tattttaccg	300
gtattgttac	ctgaactggg	accattatga	caatatctac	atcactagcc	gattcctgcg	360
catggaggct	gtgcgctcca	cggcagggct	gcccacagt	ctacogctca	gtgctcacga	420
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<210> 670

<211> 1589

<212> DNA

<213> Homo sapiens

<400> 670

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tgtgctgcac	tccagctgac	ccaagtagga	agccagacga	gctgtaaaac	atgaacggaa	120
gagtggatta	tttggctact	gaggaagaga	tcaatcttac	cagaggggccc	tcaggggctgg	180
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agatcccttc	ggtaaatggc	caagacctaa	agaacctgct	gcaccaggat	gctgtagacc	360
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atggacctat	aggacatcga	ggtgaagggg	acccaagtgg	tattcccata	tttatgggtgc	480
tggtgccagt	gtttgccctc	accatggtag	cagcctgggc	tttcatgaga	taccgggcaac	540
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cacccctgct	attctgccat	gtctttccct	ctctctgcat	agccagattt	gaagtgactg	660
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aaagggtattg	tttgaaggaa	aactgaagaa	aagacttggc	ttagaacaaa	tgaggagtta	780
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tcttccctgct	accataggca	ataccttttt	tcttagctgg	catgccataa	aggccagcta	900
tgtgatatta	gaggaagaaa	ggatttttct	ttttaatgat	cttccttggg	aaattattgt	960
ggcctttatt	taattttctaa	ctaogtacct	gggtgcctat	atcgacaaag	agtgagaaga	1020
gcatttttac	ttttttaaaa	aagcaaatac	atatatacac	atacgtatgc	aatattata	1080
gtataatagt	gatccctatg	gagaattaaa	ggtgagaaag	ctactttgtg	gtgatctagg	1140
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tgtagttaga	acaaggaggt	gagccttata	agaggacgtt	cagtcctcatt	tattaaaata	1260
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aacaatatatt	attcttataa	cagccaacta	tggggagtta	ttataaggta	aattgccata	1500
atccagcgt	gctcacatct	aaaaaaacttt	gaggggtaaa	ggtaaatcgt	accaatctct	1560
gggctgcct	agtgaactttt	ttgatacct				1589

<210> 671

<211> 672

<212> DNA

<213> Homo sapiens

<400> 671

tttttttttt	ttacttgtca	caagcaagga	gagcgtctgg	aatactctcc	aaagcgggtgt	60
ctctgaagga	aagtgcacag	aggggttttat	ggggtgatgg	agaggggaga	agagtgcatt	120
ggtgcatgta	ggaaaggggt	cccagtggcg	cagccgcagt	gagtcgtcct	gccagcacac	180
aggtcacatg	ttacggtcac	gaagctatag	ctccccctgg	ggtagtgcct	tcaggatggg	240
aatgaggaaa	gttcacttgg	gttcatctag	aagttgccgg	ggtctgtcag	gagctgggtc	300
caggtgacta	ggtcaccaca	ttccacacga	aacaagggaa	gaaacaggca	gcaaggcagg	360
aagctttcct	tcctggctgc	aggtgcctct	tgggattcag	ttgcattcat	cttcctccta	420
gtcttccatc	ctatttgtgg	tcacacctcc	agcctcttcc	aagtcacccc	agagagcttt	480
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agggggccgag	gagcagatcc	tgggaaggaa	cgtgggctct	tgctgcagac	acagttcttc	660
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<210> 672
 <211> 399
 <212> DNA
 <213> Homo sapiens

<400> 672
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 atgataagtg aataatata ttctcctaca acattttttt aaagataact gaactgctta 120
 atgatgtgga aagattaaaa caggcactca acggccttcc ccaactcacc tacacaagtg 180
 ggaacccccc caagaggcag agccagctga ttgacactct gcagcaccac gtgaaatctc 240
 tggagcaaca gctggccgtg agtaaccagg cacacggggc tttgcaggaa tatgtgctgg 300
 ctccctgtag ttagtttgga aggtcattt agaaattaaa gggatctgta gctatgttcg 360
 gatcccgaa tataattatt tttatatgcy aaaagttac 399

<210> 673
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 673
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 tacttactga taacataacg aagcatgggt cctatatcaa tccctatatg tccagaacta 120
 ccaaaactatg atgaattcga tcaaagatct aaatggagat cctttgagct gcaaggtaaa 180
 aaatttaata aaaataaata agtacatgaa gagagattct atgttcacga ataggaagac 240
 tcaatattgt ttagatgtca ctttttccca acttgacctg tagattgaat gcaattccca 300
 tcaaaatccc tgcaaatcat tttgtggaag tcacg 335

<210> 674
 <211> 2954
 <212> DNA
 <213> Homo sapiens

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<211> 3181

<212> DNA

<213> Homo sapiens

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<211> 2052

<212> DNA

<213> Homo sapiens

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 <211> 593
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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<211> 677

<212> DNA

<213> Homo sapiens

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<210> 683

<211> 528

<212> DNA

<213> Homo sapiens

<400> 683

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<210> 684

<211> 404

<212> DNA

<213> Homo sapiens

<400> 684

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<210> 685
 <211> 440
 <212> DNA
 <213> Homo sapiens

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 <211> 508
 <212> DNA
 <213> Homo sapiens

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 <211> 614
 <212> DNA
 <213> Homo sapiens

<400> 687
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<400> 688

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 <212> DNA
 <213> Homo sapiens

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<211> 304

<212> DNA

<213> Homo sapiens

<400> 690

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<210> 691

<211> 231

<212> DNA

<213> Homo sapiens

<400> 691

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<211> 1306

<212> DNA

<213> Homo sapiens

<400> 692

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aaaagatgat	gatctgtttc	atagctatac	aacaataatg	gcactcatac	atctgggggtc	1260
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<210> 693
 <211> 1781
 <212> DNA
 <213> Homo sapiens

<400> 693						
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<210> 694
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 694
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 aacatgcacg aggagaacct gaagaccaag aagcagcatc ggaaggagcg gctgtaccgc 180
 ctgcggaagt acgcgggccaa ggccctgaggg gcgcctggtc aataaagcac agctggctga 240
 gaaagaaaag atatgatgca atgatctaaa accctggggg gcgtttttta tataaccgta 300
 gggggggccga ctgtttattgg gttaagcaaa ctattaattt tcttctttat taggcgacaa 360
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 gacaag 426

<210> 695
 <211> 2546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (2546)
 <223> n = a, t, c or g

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<210> 696
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(1476)
 <223> n = a,t,c or g

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gttctgctcc	ccactcacag	tagccacogt	tctaccattt	acaaacgtgt	caagtcagtc	360
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cggtcatggc	tttcttctcg	tgatcactga	ggcacaattt	cctcatataa	ttataaatgt	540
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ttctattgtt	ccctgagaac	tggaaagtct	caacaatttg	gtgtgtatgt	ctgaaatttc	1440
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<210> 697
 <211> 520
 <212> DNA
 <213> Homo sapiens

<400> 697						
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tttattcttt	gggcttctct	gaattttcct	atattttgaa	aaagcacctg	cattattttg	180
taattataaa	aaagtataaa	taagaattat	acacactatt	atttcttcac	tgctatgaca	240

tgactagatt	acaatttttt	tctttttgag	atgactttcg	gtcttgtttc	ccaggctgga	300
gtgcagtggc	acgacctcgg	ctcattgcaa	cctccacctc	ccgggttcaa	gcaattctcc	360
tgccctcagcc	tccccagtag	ctgggattac	aggcaacctgc	caccacacct	ggctaatttt	420
agtagagaag	gggtttcgcc	aaactggcca	ggctgggtctc	gaactcctga	cttcagggtga	480
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<210> 698
 <211> 1586
 <212> DNA
 <213> Homo sapiens

<400> 698						
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acgtccgcga	ggacttgaag	tcctgagcgc	tcaagtttgt	ccgtaggctg	agagaaggcc	180
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gcatagttag	gtagctaaag	ccatgggctg	gctctaaagg	ctttaaatcc	cagccatgtg	1560
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<210> 699
 <211> 763
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(763)
 <223> n = a,t,c or g

<400> 699						
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gcttttaaga	aacatcatga	agtataacaa	ctttggcata	tacaagtaca	ttttttcttg	420

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cgtgggttttg	atccccctttt	gtttttggac	aaatgtttct	acaaatacag	attcagcaaa	600
cccaaaggct	gcaaattttac	ttgcacagta	atctgccagc	ccatttactc	cacttaatcc	660
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<210> 700
 <211> 614
 <212> DNA
 <213> Homo sapiens

<400> 700						
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<210> 701
 <211> 1927
 <212> DNA
 <213> Homo sapiens

<400> 701						
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<210> 702

<211> 2502

<212> DNA

<213> Homo sapiens

<400> 702

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<210> 703

<211> 657

<212> DNA

<213> Homo sapiens

<400> 703

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ccacgtggct	ctgcagtgtt	ggtgaacagg	agttgcaggg	aactgaaagc	ccgggatccc	180
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agacctggca	aagatgataa	gagagtatga	acaggtcatc	attgaagatc	gtatagaaaa	540
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<210> 704

<211> 1417

<212> DNA

<213> Homo sapiens

<400> 704

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aggaattgcc	cccctccagg	cttcaccctc	cctgcctaag	cagggtgggg	gcagagccat	1320
gacatttttg	gttttaaagg	gccttctcat	ctctggccga	gaacactgct	gggctcccag	1380
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<210> 705

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 705

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cactttacag	acttgaatca	aaggaaacct	tcctgtctgt	tggggggtat	gtccttgact	180
atgattacta	cagagatgat	ttctacaato	ggttatttga	ttaccacggg	cgtgtgcctc	240
cacctccccg	tgcagtaatt	ccgctgaagc	gtcccagagt	ggcagtcaca	acgactcgca	300


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ctaaaattga ctccgtgcta gggcgccctgg acaagattga gaaacacgag aaggcggagg 480
cagaagctca gaagaagcta ttggaagaga gtctagtgtc gatccaagag gaatgtgtgt 540
cagagattgc agatcactct acagaggagc ctgctgaagg agggccagat gccgatggag 600
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taaaacaaaa aaaaaa 1636

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<210> 706
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (388)
 <223> n = a,t,c or g

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<400> 706
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gtgttatgga ttttagctct gagtgagctg gaaaactagg tcattatcta gatgatttca 180
gacttgaccc taattgacca tatatgacca ggaaacactt ctgagtttac agctccgtgg 240
agatgacctc aacactgcct cttgatttgt ttgatgcacg tcactttcat taattttccc 300
cctccttttt gaaagtcctg tggcagactc aatattttca ttttatgtaa tctctggtgc 360
tgctttccag tcactgtatg aagtgtcn 388

```

<210> 707
 <211> 660
 <212> DNA
 <213> Homo sapiens

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<400> 707
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ggaaggthtt catagagctg aatcacatta aaaagtgcac tacagttcga ggcgtcttht 120
tcctggagga atttggtaat tacactatth tgctcttagg tctggactca catggcagta 180
actcaaacct cggagctcca gaggaggggc taggggcagg gagaaaaaga acctctgtag 240
agaagtacgg aggagcagga gtgacaagga agaaaaaggga ccctgagat gagagccggg 300
atgtggaagg gaaagataga taatggatcg cagaagagca aatggggcct caggtgggtt 360
tcgagtttag aggtggtcct gaagcagctc agtgaagtag caccacctcc ccgtgctggg 420
ccagccagtg gtcagaaagt ttgggacaca gcagactggc gaccccccaag ctccactatg 480
tccatgtcac ctgctgcaat ctctctagca gccagtgcg ctageccagc tcctgggcgc 540

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cgctctgggc  tccacctggc  ctctgtgcc  gacaaagggg  caccgggcgt  cgcaggcaga  600
ctcacttgag  ggacagagga  gtctagcggg  acagctgtag  ccggaagctg  ggagccagcg  660
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<210> 708
<211> 313
<212> DNA
<213> Homo sapiens
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<400> 708
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ttcataataa  atcgtgctgc  tgctcattct  ttgggtccac  accaacttta  agagccataa  120
cactcaccgt  gagggctctg  ggcttcattc  ctgaagtcag  caagaccaca  aaccactctg  180
gaagaacaaa  caactctgga  tgcaccatct  ttaagactgt  aacactcact  gcgagggtcca  240
cggcttcatt  gttgaagtca  gtgagaccaa  gaacgcacca  gaaggaataa  agtccggata  300
cattttggcg  acc  313
```

```
<210> 709
<211> 693
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(693)
<223> n = a,t,c or g
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<400> 709
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ctgtaaaagc  cacactgagg  tcgcggcggc  gagtccctgc  aaggtegecc  ttctgtgcga  180
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tttttctttg  gtgtgtcttc  ctctgatgtc  ctctgcctc  ggccccggga  ccctcttttt  660
tcctcgtgcc  gaattcgtca  tcgcaagntc  aat  693
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```
<210> 710
<211> 1112
<212> DNA
<213> Homo sapiens
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<400> 710
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gaagggtatta  ttttggtttt  gaacatatgt  gaggatgatg  gttgaaaaat  tcaatcacat  180
tacaatcttg  aaaaaaaaaa  ctcagtgcc  gccctctctc  ccccagggt  gataccaccg  240
caatacaatt  caacaatatg  caacatgcc  tcaattttat  ttgtttttgg  gggaaatgtg  300
ctgaagaacc  tagagctttt  tttgttttag  accttatatc  aaagtaatga  aaatgggtat  360
gatgattaca  tgtgcaaatg  tacaaaatca  ttaactctac  aaagatacat  cattccaaaa  420
ttacagaaaa  aatttaaagc  atgcatttaa  ttctttttct  ttaaagggtt  gctgaatgct  480
tcccctgaaa  aaaggtgggt  gttttcaaaa  tcagcaactg  ctgggtgagg  tttcttggca  540
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cagttatgac	cagcatgtta	ttgctgcac	ttcctgataa	tctcagccga	caccggggga	600
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<210> 711
 <211> 1429
 <212> DNA
 <213> Homo sapiens

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cacgggtttc	catagccagg	cagttggtat	gtacaattca	gttcagcgta	tgaacttgta	1260
tctctaattct	gatgtccatt	tttataat	ttgaaactga	gcacaatgaa	atcctttctt	1320
gaatcatttt	ccttttggat	tataaaaata	tgggggaaag	tgctatgatg	aattttatgc	1380
aataaatgta	tacatgtgtg	cacatgcacc	catgctgtga	aaaaaaaa		1429

<210> 712
 <211> 782
 <212> DNA
 <213> Homo sapiens

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gctcctcggt	ggcaagccgc	cccatgatga	aggcctacac	ctgggcacgg	agacttttgg	120
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ctacaggatca	gggtggaagc	tctgtctgag	gaggaaatct	ggtccctcct	gttcctggcc	240
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gctgctcctt	tcaaggcccc	tgaactgcta	caggacaga	gtgaggatga	gcagcctgat	420
gcactctcaga	tgcatgtcta	ttcttttagga	atgaccctct	actggctcagc	agggtttcat	480
gttccgcac	atcagccccct	gcagctctgc	gagccccctgc	actccatcct	gctgaccatg	540
tgtgaagacc	agcctcacag	goggtgcaog	ttgcagtcgg	ttctggaagc	ttgtcgggtt	600

```

catgagaaag aagtgtctgt ctaccagcc cctgctggtc tccacatcag aaggctggtt 660
ggcttggttc tgggtaccat ttctgaggtc agtagagaac cgtgcttttc aagcagtagc 720
tgctgggtcat gtgtggctat taaaatttga attagttata ttatcattaa ctaaaataaa 780
at 782

```

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<210> 713
<211> 478
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(478)
<223> n = a,t,c or g

```

```

<400> 713
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accagctcca tccccagct gctctacaac cttaatggat gtgacaagac catcagctac 180
atgggtctgt ccatccagct cttcctgttc ctgggtctgt gtggtgtgga gtgcctgctt 240
ctggctgtca tggcctatga cgggtgtgtg gctatctgca agccctgca ctacatggtg 300
atcatgaacc ccaggtctct cgggggcttg gtgtcagtga cctggggctg tgggggtggc 360
aactccttgg ccatgtctcc tgtgaccctg cgtttacccc gctgtgggca ccacgaggtg 420
gaccacttcc tgtgtgagat gcccgccctg atccggatgg cctgcatcag cactgtgg 478

```

```

<210> 714
<211> 493
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(493)
<223> n = a,t,c or g

```

```

<400> 714
natcgagacc ctaggcagtg tggngcaatt cgtccatatt ggtgtgaaaa taatataata 60
ggaataggaa aattgtocac ggctgatggg aaagcctttg cagatcctga agtacttcgg 120
aggttgacat cgtctgttag ttgtgcttg gatgaagctg ctgctgcact taccgctatg 180
agagctgaaa gcacagcaaa tgcagggcag tcggacaagt aagtacattt ttgctgccat 240
cagtatgaaa tcattttctt aaaaataata acaaatagct aacatttact gagcatttat 300
tttgtgcctg gctggcactg tgctaaccac ttaacatgtg atgtcttatt tagattcaca 360
aaaactttat aaggtataga ttttgttttt actcccattt tacagatgan aagttaaaga 420
gagatgagta acttaataca gatcaaatag ataataagtg gcagagcacc agtgtctttc 480
cgactggcag gcg 493

```

```

<210> 715
<211> 1909
<212> DNA
<213> Homo sapiens

```

```

<400> 715
gcaaggtgac cgcccccagg cggccccagc gctacagcag cggccatggc agcgacaaca 60
gcagcgtgct gagggtgagag ctgcccgcgc ccatggggcg caccgcccct ttccaccaca 120
cggtggcag cagtggctat gagagcctgc ggcgcgacag cgaggccacc ggcagcgcct 180

```

cttcgcccc	tgactccatg	agcgagagtg	gggctgcctc	cccaggcgcc	cgcaccogca	240
gcctcaagtc	ccccaagaag	agggccacag	gtctgcagcg	gcggcgctg	attcccgccc	300
cactgcccga	caccactgcc	ctggggccga	agcccagcct	ccccgggcag	tgggtggacc	360
tgcccccgcc	cctggctggc	tccctgaagg	agccgttcga	gatcaagggtg	tacgagatcg	420
atgacgtgga	gcgccttcag	cgcccccgcc	ccaccccgag	ggaggccccc	accagagggtc	480
tggcgctgctg	cagtacaagg	ctgcggctgg	cggagcgag	gcagcagcgg	ctgcgggagg	540
tgcaggccaa	gcacaagcac	ctgtgtgagg	agctggccga	gaccaggggc	cggtgatgac	600
tggagcctgg	ccgctggctg	gagcagtttg	aggtggaccc	ggagctggag	cccagtgagg	660
ccgagtaoct	ggcgccctcg	gagcgagcca	cggcgccct	ggagcagtc	gtgaacctgt	720
gcaaggcgca	cgctcatgatg	gtcacctgct	tgcacatcag	cgttgccagcc	agtgtgccca	780
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cagcgggctg	gaggacggga	cgtgggacgg	agcgaggatg	tgggtgggggc	tgcgggggga	900
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gggaggggccg	gccacgcggt	ggacagagcg	aggggtgccag	ggtgaccgca	agaccgtcac	1020
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cttcccgaga	accgcctctg	tccccagggc	agctaacaag	ggctgagccc	caggtagagg	1440
ttgcctctc	caoggcagga	atttttacca	aaaccacaag	caaaaaacaa	aacagaccac	1500
cacgaccaac	aacaaagatg	gggggtaggg	ttttgtaaag	gttctgttag	gttcataatt	1560
ttatatcatt	ttgccataa	atgcggaatt	tgcogtggga	atltgaagac	aaatgatota	1620
tgtttttatg	gttttctagg	gaaggtgttc	tgggggcccg	gctctctcca	gctgtgggag	1680
gcctgtctcc	tctggggggc	accctgggca	gggtgggggg	gccttgggag	gcgcttcttg	1740
ccaaatgcag	aogaggggtg	agcctgccag	cgtttgcgac	gtccccgcac	gacaggtcca	1800
tactttctga	ggatcgtgca	tagcatagga	cgtctgaacc	tttgtacaaa	tgtgtagatg	1860
acatcttgct	acagctttta	tttgtgaatt	aaagatgcat	cgatgggtta		1909

<210> 716

<211> 1664

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)...(1664)

<223> n = a,t,c or g

<400> 716

taacttattt	aagctgaact	gggtatatct	attataagca	gaagtagtct	tttcttggtg	60
aataatccag	ttagcaaac	tgaatagtat	ttatgtctta	tgaatcctgc	cagttgtttc	120
ccaagttagt	gtaaagtaac	atagattaga	tatcaaaagg	actagaccag	aatcagttgt	180
tttcttcttt	tctgttagag	tacctaacag	aaatagttag	aatatatggc	aacaagatta	240
gacacaaatg	tgtggaagtc	tcccagaaaa	atggtagcac	cagatcagca	ccaggaggcc	300
agtgttgagt	aatagaacca	gaaggccaac	atccagacag	gcagattagt	ctgaggctat	360
tttaagtgtc	agaagggtgtg	acttctcttc	atcttctctg	ttctatctta	agtgcataaa	420
aaaatgttat	aatagctttt	ctctttcttg	tttttattct	cctggatatg	gagaaaaaaa	480
gtttactgtc	actagtanaa	atattgcagt	acctctttgt	gaaatgaaca	agatttatte	540
ctattatttc	gattctctcca	gcagtgaag	gactatggat	ctggtttttg	aaatgtgcaa	600
taccaattcc	atccactggt	gtggaatttc	aggaagacag	ctgggaaagc	tgcattccaa	660
ttcttcgctc	tgtcttgccc	ttactctgct	ttcttcagta	cagggactgc	aaagcatctc	720
tggcttaaga	ctaacagaca	cattcttaaa	gagaacatat	gaatatgatg	acatcgacac	780
agtctgtgtg	gtatcttctg	ccattaaagt	ggaaagctga	aggaaacttc	caatgttagg	840
cttttcattt	agtttcacag	aactgctctt	tttgttacct	ttgtaaaatg	atgacgtcaa	900
caacgaagta	aatatgttac	ttaaattttc	tttctctgtg	aatgggttaa	atattaaata	960
ttgtttttga	agagatctga	ttttatcttg	taatttatat	ttgaaatgaa	catgtgtata	1020
ttttctacac	ctattattta	atttcatttc	atttttagatg	accattggac	tttgttctcc	1080
aaaagctgtg	tatctgagac	catttgtccc	tagcaagtta	tctagaacac	gagtcagcac	1140
actttttatg	taagggtacaa	gataactaaat	attttaggct	ttgcaggccg	taagggtttc	1200

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gtcacaaata ctgaactctg ccatcgctact tcaagagcag ccagtaggca aaaaaagtac 1260
agtgggtgtac acaaaaagaa gcagttggac tcgggaagct gaggcaggag aatcacttga 1320
accggggagg cagagggtgc agttaagccg agatcatgct actgcaactct agcctgagcg 1380
acagagttag actctgtctc agaaaaaaag aggcagctgg gcagatttgg cctgcagggt 1440
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tagaaatatt cagttantcc agtttttctt actatcggnc acagaaaaag tttcttaaan 1560
caaaggggta gtcctcttat acctgatatt gncacacagt ataanttcta gttgtttcaa 1620
aattctgtaa tggttgtgct gattgatata tcctcaacat cata 1664

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<210> 717
<211> 620
<212> DNA
<213> Homo sapiens

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<400> 717
ggaattcgga agatctgctc aagtaacttca atccagagtc atggcaagaa gatcttgata 60
atatgtatct ggacaccocct cggatctgag gcaggtcata ccatgaccgg aagtcaaaaag 120
ttgacctgga taggctcaat gatgatgcca agcgttacag ttgcactccc aggaattact 180
cgggtcaatat aagagaagag ctgaagttgg ccaatgtgggt cttctttcca cgttgccctcc 240
tcgtgcagcg ctgtggagga aattgtggct gtggaactgt caactggagg tcctgcacat 300
gcaattcagg gaaaaaccgtg aaaaagtatc atgagggtatt acagtttgag cctggccaca 360
tcaagaggag gggtagagct aagaccatgg ctctagttga catccagttg gatcaccatg 420
aacgatgtga ttgtatctgc agctcaagac cacctcgata agagaatgtg cacatcctta 480
cattaagcct gaaagaacca ttagtttaag gagggtgaga taagagaccc ttttcctacc 540
agcaaccaga cttactacta gcctgcaatg caatgaacac aagtgggtgc tgagtctcag 600
ccttgctttg ttaatgccat
620

```

```

<210> 718
<211> 407
<212> DNA
<213> Homo sapiens

```

```

<400> 718
atgaatgtaa actgcttagc acctcacctg tgagagcaag cattctgaag gtgctagctt 60
tcattattac tttggcatct ctggacttac gcgttttctt gggctgcctc ttcggctttt 120
gagaccttcc tgtagcaata tatcatctcg atgagcagcc acaaggtgag gaagaccaga 180
aggatgtaca tcatgatttc tgagaccaca gaggtgaagt cctctccagc tgaaagaaag 240
agaatgaggt tcagaatatg caaatccagc aaacctagag ccgtcattgg agccatattt 300
ttaagtacag cttaaataaa gactgagtaa agaaactcaa gaagatgtca aaggtattcc 360
aaatcctgac tctcccgccc attggcttcc tcaactgactg tcatcac 407

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```

<210> 719
<211> 330
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(330)
<223> n = a,t,c or g

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<400> 719
aaaaattgtg caaatgaagc tgtgggtcaa aagatttttg acaggggtgct gtcaagatac 60
gatgtccgcc tgagaccgaa ttttggannn atgcttgcta ctaacagtac ccggggcctt 120
aatgaagatg agctcatggc ccatggccaa gagaaggaca gtagctcaga gtctgaggat 180

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agttgcccc	caagccctgg	gtgctccttc	actgaagggt	tctccttcga	tctccttaat	240
cctgactacg	tcccaaaggt	cgacaagtgg	tcccgggttc	tcttccctct	ggcctttggg	300
ttgttcaaca	ttgtagcggc	ogaacgatgc				330

<210> 720
 <211> 1104
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(1104)
 <223> n = a,t,c or g

<400> 720						
tttttttttc	gtgaggaagg	gctcatgccc	cttattttatg	ggaaccattt	cattctaaca	60
gaataaaccg	agaagggaaa	ccagagctgg	gactgctgcc	gtctgtccgg	tagagtgaag	120
caaggggggt	ggaatagggc	ctgttcagcc	cctgtccctg	ctgaaaecggc	tgtgggaggg	180
tgggcccctg	gagccctctt	catagcgtcc	agcgatccag	acaaatagga	gagccgtgac	240
ggcctgaatg	ccagccagca	ggaagaagta	gaggtccatc	cggcaattgt	tgatgttccc	300
aaagtccttg	gggcagtgca	gccagccccc	gggcaaggac	agcagtgcca	ctaggctgga	360
gccaacacgt	gagcccaccc	ccgacaggca	gaagaagatg	cccatgatgg	cgccctgcat	420
ggagcgcggt	gcctctgagt	aggcaaaactc	caggcctggg	atgctggcaa	agatctcact	480
gatcccaatg	agcaggtact	gagggatctg	ccaccagatg	gacagtgggt	ccgcgttgta	540
caggacctcc	ccaatctgct	gggacacggt	ctcgttgtgg	tggatgtagt	gtaagcgctc	600
catctccagg	actcctgcc	caatgacgga	ggtaaaacca	aagaacatcc	ccagcgccat	660
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cttcagaggg	accagaatca	gcaccaccac	aacattggcc	aggaggagcc	aggcttccgg	780
gatctgggca	ggaggaagtc	aggagaggca	ggctagcaga	gtgcaaggag	cctggctgca	840
gtcaggagac	ctggactcta	gactggccct	gggtgaccct	ggggtccagc	tcctttccct	900
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ataggttcct	cttgattctt	aacttttato	aattggtagt	ggctgattat	ggaacattta	1020
tgggctcagc	ataaaaaaag	tcatgattga	ctagtgatgt	ctccgaattc	ccccactgga	1080
tacgaactcg	agnnnngccg	ctcc				1104

<210> 721
 <211> 2716
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(2716)
 <223> n = a,t,c or g

<400> 721						
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agtgtgtctg	aatgcagctt	gatgaatgtc	tgtctttatc	gtgagaaagt	tgaggagtgc	180
agagcttact	ctctctctct	aattgcctac	tgttttgggg	gccaaogtga	atgcggcaca	240
gcttcattag	actgcccttc	accacgcggc	caaggtcaag	aatgttgacc	tcatcgagat	300
gcttatcgag	tttggcggca	acatctaagc	ccgggacaac	cgcgggaaga	agccgtctga	360
ctacacgtgg	agcagcagcg	ctcccgcaca	gtgcttcgag	tactacgaaa	agacacctct	420
gactctgtca	cagctctgca	gggtgaactt	gaggaaggcc	actggcgctc	gagggctgga	480
gaagattgcc	aagttaaaaa	tcccgcctcg	gctcattgat	tacctctcct	acaactgaat	540
tgcagggtgg	gtccgggacg	tgactgcccc	ogtgtgtccc	agcattgccc	gggtgagggc	600
tctgcctgtt	cctctgaagc	agcgtgattg	ctgtagatag	aacaacgctc	cttcgagctc	660
cttcctgcga	tcctgttttag	gcttctctcc	tggatcctgg	ataatgtttc	caggggtgtg	720

ggaaggcctg	cgtctcaggt	cacagttgtg	ggtgtggccc	tgcgctgttc	tacagaacct	780
accctctcaa	tgggcatggg	cccaaccatc	cagttttcct	cttttacgga	ccatccctcaa	840
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agggcattgt	tgctgattct	cactcaccgg	ggcagcctgc	cgcagatgca	caggccccag	960
gtgcaggcca	ccacctccgg	gtcggcacca	ggactgccct	cgggtgctcat	agggaatggc	1020
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gtggatgctt	ttcctggagc	actttccaag	gcattccccca	gccccaaagg	tgccgcgcatc	1140
tgctactcag	ggacttttcta	tgggtctttg	tgggggaagg	ccctgggcttt	gtattcccca	1200
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gttctggaga	acaggtcacg	cctgtcctgg	agacagtgtg	ccgggaaaag	ggaacgtggg	1980
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cccatctctt	ccccaggctc	cctgatgcca	acttcagcac	cccccttatg	tggactattc	2640
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ccttatgcag	ggctgt					2716

<210> 722
 <211> 3806
 <212> DNA
 <213> Homo sapiens

<400> 722						
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gccacaccga	atgcctgggg	ggctgcagcc	agccagaaga	ccctcgtgcc	tgtgtagctt	660
gccgccacct	ctacttccag	ggtgcctgcc	tgtgggcctg	cccgccaggc	acctaccagt	720
atgagtctcg	gcgtgtgttc	acagctgagc	gctgtgccag	cctgcactct	gtgcccgccc	780
gtgcctccac	cttcggcata	caccagggca	gttgccctgg	ccagtgcctt	tctggcttca	840
ccgtaataag	cagcagcata	ttctgccaca	agtcgaggg	gctgtgcctt	aaagagtga	900
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<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

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<211> 431
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 <211> 820
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 <213> Homo sapiens

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<210> 738
 <211> 1811
 <212> DNA
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<220>
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 <223> n = a,t,c or g

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<210> 739
<211> 939
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(939)
<223> n = a,t,c or g

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<211> 2492
<212> DNA
<213> Homo sapiens

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<210> 741
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (413)
 <223> n = a, t, c or g

<400> 741						
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agaaagagga	ggaggaggag	gaagaagagc	cattacctga	aatatttatt	ccgtcaaccc	360
cctctcccat	cctctgtgga	ttttactcag	agccagggaa	gttctgggtt	ttt	413

<210> 742
 <211> 482
 <212> DNA
 <213> Homo sapiens

<400> 742
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 cactgcatcc ctgtgcacaa acctcccgcc tcagccagga agctgcaggg cagcgtgtgc 420
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 ag

<210> 743
 <211> 1824
 <212> DNA
 <213> Homo sapiens

<400> 743
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 cttcaccagc ctcaagtggc agcaatcttc attatttctt actttctgat cttctttttg 480
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 gagatttaaa aagagctagt gtgataatcc taactctact acgcattata tatttaaatc 1620
 cattgctttt tgtggctttg cacttcaaat ttttcaaaga atgttctaaa taaaacattt 1680
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<210> 744
 <211> 416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(416)
 <223> n = a,t,c or g

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<400> 744
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tctctgtttg ccttcttcat gttgatgac ccatgtttgt gtttctcatt atgcaggatc    180
atcaggctgc cgggctgggg ctggggctgg ggctgtggct ctggggatct cagctgtggc    240
tctatatgat taccaaggag gtaggttggg agtggcccgga ggagcctggg acatggaggc    300
ccctgatata agacaggggg acatgtgaaa agagattcat gtctgaccat tctaatatcc    360
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<210> 745
 <211> 1416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(1416)
 <223> n = a,t,c or g

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tggggggttc aggcggggct gacttccacc tcaccccccgc cccgtccacg gcagagctcc    180
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atgggtgcct gggtgcacag tgggtgggtg tgaatgcaat gtcccctgca ggccctcaga    360
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gcagggaacc ctggccagca gccccctgtc cctgccctc cttctagccg gagtgaacgg    540
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acttctnct tctttttaaa acattattan ttatta      1416

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<210> 746
 <211> 2304
 <212> DNA
 <213> Homo sapiens

<400> 746

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cctgtcagag	gagctgtttg	gcttctcagg	accatactg	tggatggcat	agctccaggg	180
gctgtgtgga	tatcagggga	tctgggtgga	ctgatgtgga	tcaggctggg	aaccaggaa	240
ccatggagca	tggtagctgc	caagatggag	ctactgggag	tcagtctggc	cctggggatt	300
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<210> 747
 <211> 1182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (1182)
 <223> n = a,t,c or g

<400> 747						
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ccagcggggtg	ttgttctcag	gcagttcaga	tcactctgtc	atcatgtggg	acatcggtgg	240
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tgatcagcct	ttcttctgga	acttcaagca	aatgtgggac	agtaagaaaa	ttggtctaa	480
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<210> 748

<211> 1922

<212> DNA

<213> Homo sapiens

<400> 748

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<210> 749

<211> 447

<212> DNA

<213> Homo sapiens

<400> 749

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cttggaaaact	cctccaactg	cagatca				447

<210> 750
 <211> 427
 <212> DNA
 <213> Homo sapiens

<400> 750						
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<210> 751
 <211> 1839
 <212> DNA
 <213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
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<211> 650

<212> DNA

<213> Homo sapiens

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<211> 2249

<212> DNA

<213> Homo sapiens

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<212> DNA

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<210> 766

<211> 1145

<212> DNA

<213> Homo sapiens

<400> 766

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<210> 767

<211> 827

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (827)

<223> n = a, t, c or g

<400> 767

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<210> 768

<211> 440

<212> DNA

<213> Homo sapiens

<400> 768

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<210> 769

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 769

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<210> 770
 <211> 653
 <212> DNA
 <213> Homo sapiens

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<210> 771
 <211> 908
 <212> DNA
 <213> Homo sapiens

<400> 771
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<210> 772
 <211> 1791
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc feature
 <222> (1)...(1791)
 <223> n = a,t,c or g

<400> 772

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<210> 773
 <211> 1088
 <212> DNA
 <213> Homo sapiens

<400> 773						
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 <211> 859

<212> DNA

<213> Homo sapiens

<400> 774

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<210> 775

<211> 404

<212> DNA

<213> Homo sapiens

<400> 775

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<210> 776

<211> 925

<212> DNA

<213> Homo sapiens

<400> 776

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<210> 777
 <211> 1402
 <212> DNA
 <213> Homo sapiens

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 <222> (1) ... (1402)
 <223> n = a,t,c or g

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<210> 778
 <211> 1378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (1378)
 <223> n = a,t,c or g

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<210> 779
<211> 471
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(471)
<223> n = a,t,c or g

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<210> 780
<211> 1383
<212> DNA
<213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <212> DNA
 <213> Homo sapiens

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 3367

<212> DNA

<213> Homo sapiens

<400> 811

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<212> DNA

<213> Homo sapiens

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<211> 1585

<212> DNA

<213> Homo sapiens

<400> 835

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<210> 836

<211> 530

<212> DNA

<213> Homo sapiens

<400> 836

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<210> 837

<211> 5999

<212> DNA

<213> Homo sapiens

<400> 837

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Gly Asp Ser Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
  65      70      75      80
Gly His Leu Leu Gly Phe Leu Glu Asp Ser Leu Ala Ala Thr Gln Ile
      85      90      95
Gln Gln Ser Gln Ala Ser Leu Leu His Met His Asn Pro Pro Phe Glu
      100      105      110
Pro Thr Ser Val Asp Met Met Arg Arg Ala Cys Arg Ala Leu Leu Ala
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Leu Ala Lys Val Asp Asp Asn His Ser Glu Phe
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<210> 1648
<211> 45
<212> PRT
<213> Homo sapiens

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Ser Ser Gly Leu Leu Asn Ala Ser Ala Gln Val Asn Leu
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<210> 1649
<211> 164
<212> PRT
<213> Homo sapiens

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Leu Gly Thr Ser Thr Leu Leu Val Trp Val Gly Val Ile Arg Tyr Leu
      20      25      30
Gly Tyr Phe Gln Ala Tyr Asn Val Leu Ile Leu Thr Met Gln Ala Ser
      35      40      45
Leu Pro Lys Val Leu Arg Phe Cys Ala Cys Ala Gly Met Ile Tyr Leu
      50      55      60
Gly Tyr Thr Phe Cys Gly Trp Ile Val Leu Gly Pro Tyr His Asp Lys
      65      70      75      80
Phe Glu Asn Leu Asn Thr Val Ala Glu Cys Leu Phe Ser Leu Val Asn
      85      90      95
Gly Asp Asp Met Phe Ala Thr Phe Ala Gln Ile Gln Gln Lys Ser Ile
      100      105      110
Leu Val Trp Leu Phe Ser Arg Leu Tyr Leu Tyr Ser Phe Ile Ser Leu
      115      120      125
Phe Ile Tyr Met Ile Leu Ser Leu Phe Ile Ala Leu Ile Thr Asp Ser
      130      135      140
Tyr Asp Thr Ile Lys Lys Phe Gln Gln Asn Gly Phe Pro Glu Thr Asp
      145      150      155      160
Leu Gln Glu Phe
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<210> 1650

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<210> 1645
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1645
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 Ser Ile Cys Lys Thr Cys Ile Arg Thr Met Asp His His Cys Pro Arg
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 Ala Asn Asn Cys Val Gly Glu Gln Asn His Arg Phe Phe Cys Ala Leu
 35 40 45
 His Cys Lys Ser Lys His Phe Cys Ile Glu Phe Thr Leu Asn Thr Asn
 50 55 60
 Phe Phe Asn Cys Phe Leu Pro Gly Ala Glu Lys Ser Thr Ile Asp Ala
 65 70 75 80
 Pro Phe Ser Leu Gln Pro Phe Leu Gln Asp Ser Lys Tyr Asn Thr Ala
 85 90 95
 Leu Ser Leu Ser Glu Ser Ile Ser Gln
 100 105

<210> 1646
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1646
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 Asn Pro Phe Thr Leu Gly Asp Ser Ser Asn Pro Gly Gln Thr Glu Arg
 20 25 30
 Leu Gln Glu Phe Ser Gln Lys Met Asp Gln Val Arg Gly His Trp Pro
 35 40 45
 Val Ser Thr
 50 51

<210> 1647
 <211> 139
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1) ... (139)
 <223> Xaa = any amino acid or nothing

<400> 1647
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 Asp Asn Ile Leu Val Leu Ile Leu Ala Thr Pro Pro Phe Met Ala Gly
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 Gly Lys Leu Tyr Ser Thr Met Gly Arg Phe Leu Arg Asp Arg Lys Asn
 35 40 45

Arg Ala Met Ala Thr Arg Thr Arg Gln Glu Tyr Leu Lys Asp Leu Ala
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<210> 1642
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 1642
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 Ile Pro Pro Pro Pro Ala Val Pro Tyr Ser Pro Arg Tyr Val Ala Val
 35 40 45
 His Cys His Gly Met Leu Val Ser Cys Trp Cys His Leu
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<210> 1643
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1643
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 Glu Thr Glu Lys Glu Ala Glu Gln Glu Lys Glu Glu Asp Ser Leu Gly
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 Ala Gly Thr His Pro Asp Ala Ala Ile Pro Ser Gly Glu Arg Thr Cys
 35 40 45
 Gly Ser Glu Gly Ser Arg Ser Val Leu Asp Leu Val Asn Tyr Phe Leu
 50 55 60
 Ser Pro Glu Lys Leu Thr Ala Glu Asn Arg Tyr Tyr Cys Glu Ser Cys
 65 70 75 80
 Ala Ser Leu Gln Asp Ala Glu Lys Val Val Glu Leu Ser Gln Gly Pro
 85 90 95
 Cys Tyr Leu Ile Leu Thr Leu Leu Arg Phe Ser Phe Asp Leu Arg Thr
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 Met Arg Arg Arg Lys Ile Leu Asp Asp Val Ser Ile Pro Leu Leu Leu
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 Arg Leu Pro Leu Ala Gly Gly Arg Gly Gln Ala Tyr Asp Leu
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<210> 1644
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 1644
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Glu Val Tyr Leu Pro Asn Asp Glu Ile Trp Thr Tyr Asp Ile Asp Ser
 50 55 60
 Gly Leu Trp Arg Met His Leu Met Glu Gly Glu Leu Pro Ala Ser Met
 65 70 75 80
 Ser Gly Ser Cys Gly Ala Cys Ile Asn Gly Lys Leu Tyr Ile Phe Gly
 85 90 95
 Gly Tyr Asp Asp Lys Gly Tyr Ser Asn Arg Leu Tyr Phe Val Asn Leu
 100 105 110
 Arg Thr Arg Asp Glu Thr Tyr Ile Trp Glu Lys Ile Thr Asp Phe Glu
 115 120 125
 Gly Gln Pro Pro Thr Pro Arg Asp Lys Leu Ser Cys Trp Val Tyr Lys
 130 135 140
 Asp Arg Leu Ile Tyr Phe Gly
 145 150 151

<210> 1640
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 1640
 Phe Arg Gln Gly Gln Leu Tyr Lys Val Phe Leu His Gly Ser Gln Gly
 1 5 10 15
 Gln Val Tyr His Ser Gln Gln Val Gly Pro Pro Gly Ser Ala Ile Ser
 20 25 30
 Pro Asp Leu Leu Asp Ser Ser Gly Ser His Leu Tyr Val Leu Thr
 35 40 45
 Ala His Gln Val Asp Arg Ile Pro Val Ala Ala Cys Pro Gln Phe Pro
 50 55 60
 Asp Cys Ala Ser Cys Leu Gln Ala Gln Asp Pro Leu Cys Gly Trp Cys
 65 70 75 80
 Val Leu Gln Gly Arg Cys Thr Arg Lys Gly Gln Cys Gly Arg Ala Gly
 85 90 95
 Gln Leu Asn Gln Trp Leu Trp Ser Tyr Glu Glu Asp Ser His Cys Leu
 100 105 110
 His Ile Gln Ser Leu Leu Pro Gly His His Pro Arg Gln Glu
 115 120 125 126

<210> 1641
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1641
 Phe Arg Tyr Met Pro Asn Asn Arg Gln Gln Leu Leu Arg Lys Arg His
 1 5 10 15
 Ile Gly Asn Asp Ile Val Thr Ile Val Phe Gln Glu Pro Gly Ala Leu
 20 25 30
 Pro Phe Thr Pro Lys Ser Ile Arg Ser His Phe Gln His Val Phe Val
 35 40 45
 Ile Val Lys Val His Asn Pro Cys Thr Glu Asn Val Cys Tyr Ser Val
 50 55 60
 Gly Val Ser Arg Ser Lys Asp Val Pro Pro Phe Gly Pro Pro Ile Pro
 65 70 75 80
 Lys Gly Val Thr Phe Pro Lys Ser Ala Val Phe Arg Asp Phe Leu Leu
 85 90 95
 Ala Lys Val Ile Asn Ala Glu Asn Ala Ala His Lys Ser Glu Lys Phe
 100 105 110


```

Phe Val Ala Glu Val Arg Arg Glu Trp Ala Lys Tyr Met Glu Val His
 1           5           10           15
Glu Lys Ala Ser Phe Thr Asn Ser Glu Leu His Arg Ala Met Asn Leu
          20           25           30
His Val Gly Asn Leu Arg Leu Leu Ser Gly Pro Leu Asp Gln Val Arg
          35           40           45
Ala Ala Leu Pro Thr Pro Ala Leu Ser Pro Lys Asp Lys Ala Val Leu
          50           55           60
Gln Asn Leu Lys Arg Ile Leu Ala Lys Val Gln Glu Met Arg Asp Gln
          65           70           75           80
Arg Val Ser Leu Glu Gln Gln Leu Arg Glu Leu Ile Gln Lys Asp Asp
          85           90           95
Ile Thr Gly Ser Leu Val Thr Thr Asp His Ser Gln Met Lys Lys Leu
          100          105          110
Phe Glu Glu Gln Leu Lys Lys Tyr Asp Gln Leu Lys Val Tyr Leu Glu
          115          120          125
Gln Asn Leu Ala Ala Gln Asp Arg Val Leu Cys Ala Leu Thr
          130          135          140          142

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<210> 1638
<211> 156
<212> PRT
<213> Homo sapiens

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<400> 1638
Phe Val Asn Leu Gly Ile Leu Thr Cys Ile Glu Cys Ser Gly Ile His
 1           5           10           15
Arg Glu Met Gly Ala His Ile Ser Arg Ile Gln Ser Leu Glu Leu Asp
          20           25           30
Lys Leu Gly Thr Ser Glu Leu Leu Pro Ala Lys Asn Val Gly Asn Asn
          35           40           45
Ser Phe Asn Asp Ile Met Glu Ala Asn Leu Pro Ser Pro Ser Pro Lys
          50           55           60
Pro Thr Pro Ser Ser Asp Met Thr Val Arg Lys Glu Tyr Ile Thr Ala
          65           70           75           80
Lys Tyr Val Asp His Arg Phe Ser Arg Lys Thr Cys Ser Thr Ser Ser
          85           90           95
Ala Lys Leu Asn Glu Leu Leu Glu Ala Ile Lys Ser Arg Asp Leu Leu
          100          105          110
Ala Leu Ile Gln Val Tyr Ala Glu Gly Val Glu Leu Met Glu Pro Leu
          115          120          125
Leu Glu Pro Gly Gln Glu Leu Ala Glu Thr Ala Leu His Leu Ala Val
          130          135          140
Arg Thr Ala Asp Gln Thr Ser Leu His Leu Val Glu
          145          150          155 156

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<210> 1639
<211> 151
<212> PRT
<213> Homo sapiens

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<400> 1639
Phe Val Ala Ser Gly Gly Pro Ala Thr Ala Arg Met Ser Asp Ser Gln
 1           5           10           15
Phe Phe Cys Val Ala Glu Glu Arg Ser Gly His Cys Ala Val Val Asp
          20           25           30
Gly Asn Phe Leu Tyr Val Trp Gly Gly Tyr Val Ser Ile Glu Asp Asn
          35           40           45

```

<400> 1634

```

Lys Thr Leu Pro Arg Thr Leu Leu Asp Ile Leu Ala Asp Gly Thr Ile
 1          5          10          15
Leu Lys Val Gly Val Gly Cys Ser Glu Asp Ala Ser Lys Leu Leu Gln
          20          25          30
Asp Tyr Gly Leu Val Val Arg Gly Cys Leu Asp Leu Arg Tyr Leu Ala
          35          40          45
Met Arg Gln Arg Asn Asn Leu Leu Cys Asn Gly Leu Ser Leu Lys Ser
          50          55          60
Leu Ala Glu Thr Val Leu Asn Phe Pro Leu Asp Lys Ser Leu Leu Leu
          65          70          75          80
Arg Cys Ser Asn Trp Asp Ala Glu Thr Leu Thr Glu Asp Gln Val Ile
          85          90          95
Tyr Ala Ala Arg Asp Ala Gln Ile Ser Val Ala Leu Phe Leu His Leu
          100          105          110
Leu Gly Tyr Pro Phe Ser Arg Asn Ser Pro Gly Glu Lys Lys Arg
          115          120          125          127

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<210> 1635

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1635

```

Pro Ile Arg Pro Tyr Tyr Ser Tyr Ser Gly Leu Asp Arg Asp Cys Ser
 1          5          10          15
Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Asp Val Met Ile Leu Val
          20          25          30
Cys Asp Arg Val Ser Glu Asp Gly Ile Asn Arg Gln Gln Ala Gln Glu
          35          40          45
Trp Cys Ile Lys His Gly Phe Glu Leu Val Glu Leu Ser Pro Glu Glu
          50          55          60
Leu Pro Glu Glu Asp Gly Lys Cys Leu Cys Val Arg Arg Lys Tyr Gly
          65          70          75          80
Thr Tyr Ile
          83

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<210> 1636

<211> 27

<212> PRT

<213> Homo sapiens

<400> 1636

```

Thr Ala Glu Asp Val Leu Thr Val Ala Tyr Glu His Gly Val Asn Leu
 1          5          10          15
Phe Asp Thr Ala Glu Val Tyr Ala Ala Gly Lys
          20          25          27

```

<210> 1637

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1637

Val Trp Val Ser Gly Cys Val Ala Ser Arg Ser Val Ile Leu Ser Leu
 85 90 95
 Thr Ser Gly
 99

<210> 1632
 <211> 104
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(104)
 <223> Xaa = any amino acid or nothing

<400> 1632
 Lys Leu Pro Xaa Asp Lys Tyr Glu Leu Glu Pro Ser Pro Leu Thr Gln
 1 5 10 15
 Tyr Ile Leu Glu Arg Lys Ser Pro His Thr Cys Trp Gln Val Phe Val
 20 25 30
 Thr Ser Ser Gly Lys Tyr Asn Glu Leu Gly Tyr Pro Phe Gly Tyr Leu
 35 40 45
 Lys Ala Ser Thr Thr Leu Thr Cys Val Asn Leu Phe Val Met Pro Tyr
 50 55 60
 Asn Tyr Pro Val Leu Leu Pro Leu Leu Asp Asp Leu Phe Lys Val His
 65 70 75 80
 Lys Leu Lys Pro Asn Leu Lys Trp Arg Gln Ala Phe Asp Ser Tyr Leu
 85 90 95
 Lys Thr Leu Pro Pro Tyr Tyr Leu
 100 104

<210> 1633
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1633
 Val Ser Pro Ala Leu Ser Leu Thr Pro Thr Ile Phe Ser Tyr Ser Pro
 1 5 10 15
 Ser Pro Gly Leu Ser Pro Phe Thr Ser Ser Ser Cys Phe Ser Phe Asn
 20 25 30
 Pro Glu Glu Met Lys His Tyr Leu His Ser Gln Ala Cys Ser Val Phe
 35 40 45
 Asn Tyr His Leu Ser Pro Arg Thr Phe Pro Arg Tyr Pro Gly Leu Met
 50 55 60
 Val Pro Pro Leu Gln Cys Gln Met His Pro Glu Glu Ser Thr Gln Phe
 65 70 75 80
 Ser Ile Lys Leu Gln Pro Pro Pro Val Gly Arg Lys Asn Arg Glu Arg
 85 90 95
 Val Glu Ser Ser Glu Glu Ser Ala Pro
 100 105

<210> 1634
 <211> 127
 <212> PRT
 <213> Homo sapiens

<213> Homo sapiens

<221> misc_feature

<222> (1)...(114)

<223> Xaa = any amino acid or nothing

<400> 1629

```

Pro Leu Ile Pro Ala Asn Leu Pro Ala His Ser Asn Pro Leu Gln Pro
 1           5           10           15
Leu Pro Ser Leu Pro His Pro Phe Leu Pro Ala Thr His Lys Phe Pro
 20           25           30
Thr Thr Pro Pro Thr Phe Ser Ser Val Pro Pro Pro Leu Pro Ser Leu
 35           40           45
Ser Ser Ile Leu His His Ser Pro Leu His Ser Glu Leu Asn Pro His
 50           55           60
Leu Gln Ser Cys Arg Leu Pro Ser Arg Pro Ser Val Ser Arg Glu Leu
 65           70           75           80
Pro Pro Gln Ser Gly Pro Ala Ser Ser Val Pro Leu Ala Pro Thr Pro
 85           90           95
Leu Pro Asp Ser Val Pro Ser Gln Arg His Pro Thr Xaa Pro Pro Pro
 100          105          110
Ala Ser
114

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<210> 1630

<211> 76

<212> PRT

<213> Homo sapiens

<400> 1630

```

Pro Ser Met Val Trp Ser Tyr His Trp Gly Val Lys Gln Lys Arg Leu
 1           5           10           15
Ala Leu Cys Val Phe Ser Phe Glu Glu Gly Gly Arg Arg Lys Cys Gly
 20           25           30
Gln Tyr Trp Pro Leu Glu Lys Asp Ser Arg Ile Arg Phe Gly Phe Leu
 35           40           45
Thr Val Thr Asn Leu Thr Gly Ala Val Gly Glu Pro Gly Val Ala Phe
 50           55           60
Gln Cys Asp Gly Gln Arg Arg Arg Glu Pro Thr Cys
 65           70           75           76

```

<210> 1631

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1631

```

Lys Met Gly Thr Ala Val Trp Val Pro Lys Glu Lys Glu Lys Arg Asp
 1           5           10           15
Lys Ala Ser Gln Glu Gly Gly Asp Val Leu Gly Ala Arg Gln Asp Cys
 20           25           30
Thr Pro Ser Leu Lys Ser Leu Val Ala Thr Gly Asn Leu Asp Leu
 35           40           45
Glu Glu Thr Ala Lys Ala Pro Leu Ser Thr Val Ser Ala Asn Thr Thr
 50           55           60
Asn Met Asp Glu Val Pro Arg Pro Gln Ala Leu Ser Gly Ser Ser Val
 65           70           75           80

```

Gln Gln Gln Thr Val Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile
 35 40 45
 Pro Gly Ser Ser Leu Leu Pro Gly His Val Gln Ala Tyr Gln Val Gly
 50 55 60
 Pro Val Arg Arg Asn Gly Glu Ala Gly Pro Gly
 65 70 75

<210> 1627
 <211> 136
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(136)
 <223> Xaa = any amino acid or nothing

<400> 1627
 Val Leu Gln Glu Arg Leu Asp Asn Phe Gln Arg Lys Cys Ile Gln Leu
 1 5 10 15
 Ala Ser Ser Thr Glu Gly Lys Val Asp Lys Leu Leu Met Arg Asn Leu
 20 25 30
 Phe Ile Ser Tyr Leu His Thr Pro Lys His Lys Gln His Glu Val Leu
 35 40 45
 Gln Ala Met Gly Ser Ile Leu Gly Ile Thr Gly Glu Glu Met Glu Pro
 50 55 60
 Leu Phe Gln Glu Glu His Gly Thr Ala Thr Arg Trp Met Thr Gly Trp
 65 70 75 80
 Leu Glu Gly Gly Ser Lys Ser Val Pro Lys Thr Pro Leu Gly Leu Asn
 85 90 95
 Gln Gln Pro Ala Leu Asn Gly Ser Phe Ser Glu Leu Phe Val Lys Phe
 100 105 110
 Leu Lys Thr Glu Ser Leu Ser Ser Thr Leu Pro Thr Xaa Leu Pro Pro
 115 120 125
 His Asn Ser Pro Gly Lys Ile Lys
 130 135 136

<210> 1628
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1628
 Gly Leu Ser Gly Pro Ser Cys Ser Cys Pro His Ser Pro Leu Pro Thr
 1 5 10 15
 Ile Ile Ser Arg Ala Gln Leu Glu Thr Ala Leu Lys Trp Arg Asn Tyr
 20 25 30
 Glu Val Lys Leu Arg Leu Leu Leu His Leu Glu Glu Leu Gln Met Glu
 35 40 45
 His Asp Ile Arg His Tyr Asp Leu Glu Ser Val Pro Met Thr Trp Asp
 50 55 60
 Pro Val Asp Gln Asn Pro Arg Leu Val
 65 70 73

<210> 1629
 <211> 114
 <212> PRT

<400> 1623
 His Pro Ser Arg Ser Asn Val Gly Pro Arg Gln Leu Thr Val Trp Asn
 1 5 10 15
 Thr Ser Asn Leu Ser His Asp Asn Arg Arg Lys Tyr Ile Phe Ser Asp
 20 25 30
 Glu Glu Gly Gln Asn Gln Leu Gly Ile Arg Ile His Gln Asp Ile Pro
 35 40 45
 Leu Pro Pro Arg Arg Arg Glu Leu Pro Ala Leu Arg Thr Thr Asn Gly
 50 55 60
 Lys Ala Asp Ser Leu Asn Val Ser Arg Asn Ser Val Met Gln Glu Leu
 65 70 75 80
 Ser Glu Leu Glu Lys Gln Ile Gln Val Ile Arg Gln Glu Leu Gln Leu
 85 90 95
 Ala Val Ser Arg Lys Thr Glu Leu Glu Glu Tyr His
 100 105 108

<210> 1624
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1624
 Ile Leu Trp Leu Tyr Phe Glu Thr Gly Thr Trp Val Tyr Pro Val Phe
 1 5 10 15
 Ala Lys Leu Ser Leu Leu Gly Leu Ala Ala Leu Phe Ser Leu Arg Glu
 20 25 30
 Ile Phe Ile Ala Arg Asn Gly Val Val Gly Glu Thr Leu Thr His Cys
 35 40 45
 Lys Arg Val
 50 51

<210> 1625
 <211> 38
 <212> PRT
 <213> Homo sapiens

<400> 1625
 Gly Ser Leu Ala Thr Cys Gln Leu Ser Glu Pro Leu Leu Trp Phe Ile
 1 5 10 15
 Leu Arg Val Leu Asp Thr Ser Asp Ala Leu Lys Ala Phe His Asp Met
 20 25 30
 Gly Lys Ile Ile Phe Gln
 35 38

<210> 1626
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 1626
 Ala Gly Arg Ser Leu His Gly Ala Gly Asp Arg Ala Trp Val Gly Ile
 1 5 10 15
 Ser Pro Thr Asp Trp Ser Pro Lys Val Val Glu Leu Cys Lys Lys Tyr
 20 25 30

```

Ser Gly Ser Asp Arg Gly Lys Leu Pro Gly Ser Glu Glu Lys Asn Gln
    35          40          45
Gly Pro Ser Met Ile Gly Arg Lys Glu Glu Arg Leu Ile Thr Glu Arg
    50          55          60
Lys His Glu His Leu Lys Asn Lys Ser Ala Pro Lys Val Val Lys Gln
    65          70          75          80
Lys Val Ile Asp Ala His Leu Asp Ser Gln Thr Gln Asn Phe Gln Gln
    85          90          95
Thr Gln Ile Gln Thr Ala Glu Ser Lys Ala Glu His Lys Lys Leu Pro
    100          105          110
Gln Pro Tyr Asn Ser Leu Gln Glu Lys Cys Leu Glu Val Lys Gly
    115          120          125
Ile Gln Glu Lys Gln Val Phe Ser Asn Thr Lys Asp Ser Lys Gln Glu
    130          135          140
Ile Thr Gln Asn Lys Ser Phe Phe Ser Ser Val Lys Glu Ser Gln Arg
    145          150          155          160
Asp Asp Gly Lys Gly Ala Leu Asn Ile Val Glu Phe Leu Arg Lys Arg
    165          170          175
Glu Glu Leu His Gln Ile Leu Ser Thr Val Lys Gln Pro
    180          185          189

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<210> 1622
<211> 172
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(172)
<223> Xaa = any amino acid or nothing

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```

<400> 1622
Lys Cys Met Gln Gly Lys Tyr Ala Gly Ala Met Glu Ser Glu Pro Cys
  1          5          10          15
Val Cys Thr Glu Ala Asp Phe Asp Cys Asp Tyr Gly Tyr Glu Arg His
    20          25          30
Ser Asn Gly Gln Cys Leu Pro Ala Phe Trp Phe Asn Pro Ser Ser Leu
    35          40          45
Ser Lys Asp Cys Ser Leu Gly Gln Ser Tyr Leu Asn Ser Thr Gly Tyr
    50          55          60
Arg Lys Val Val Ser Asn Asn Cys Thr Asp Gly Val Arg Glu Gln Tyr
    65          70          75          80
Thr Ala Lys Pro Gln Lys Cys Pro Gly Lys Ala Pro Arg Gly Leu Arg
    85          90          95
Ile Val Thr Ala Asp Gly Lys Leu Thr Ala Glu Gln Gly His Asn Val
    100          105          110
Thr Leu Met Val Gln Leu Glu Glu Gly Asp Val Gln Arg Thr Leu Ile
    115          120          125
Gln Val Asp Phe Gly Asp Gly Ile Ala Val Ser Tyr Val Asn Leu Ser
    130          135          140
Ser Met Glu Asp Gly Ile Xaa His Val Tyr Gln Asn Xaa Gly Ile Xaa
    145          150          155          160
Arg Xaa Thr Val Gln Val Asp Asn Ser Leu Gly Ser
    165          170          172

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<210> 1623
<211> 108
<212> PRT
<213> Homo sapiens

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<210> 1619
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 1619
 Thr Arg Pro Ala Glu Lys Ile Gln Tyr Leu Val Leu Phe Phe Val Met
 1 5 10 15
 Ser His Pro Ser Gln Ala Tyr Asp Lys Leu Ser Leu Ser Asp His Leu
 20 25 30
 Leu Ile Ala Val Leu Asn Leu Leu Arg Arg Glu Val Ser Glu His Gly
 35 40 45
 Arg His Leu Gln Gln Tyr Phe Asn Leu Phe Val Met Tyr Ala Asn Leu
 50 55 60
 Ser Lys Asn Leu Ser Phe Ser Glu Phe Cys Phe Asp Val Ser Tyr
 65 70 75 79

<210> 1620
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 1620
 Glu Leu Gln Ser Gln Gln Ala Cys Thr His Thr Lys Glu Thr Glu Gln
 1 5 10 15
 Leu Arg Ser Gln Leu Gln Thr Leu Lys Gln Gln His Gln Gln Ala Val
 20 25 30
 Glu Gln Ile Ala Lys Ala Glu Glu Thr His Ser Ser Leu Ser Gln Glu
 35 40 45
 Leu Gln Ala Arg Leu Gln Thr Val Thr Arg Glu Lys Glu Glu Leu Leu
 50 55 60
 Gln Leu Ser Ile Glu Arg Gly Lys Val Leu Gln Asn Lys Gln Ala Glu
 65 70 75 80
 Ile Cys Gln Leu Glu Glu Lys Leu Glu Ile Ala Asn Glu Asp Arg Lys
 85 90 95
 His Ala Leu Glu Arg Phe Glu Gln Glu Ala Val Ala Val Asp Ser Asn
 100 105 110
 Leu Arg Val Arg Glu Leu Gln Arg Lys Val Asp Gly Ile Gln Lys Ala
 115 120 125
 Tyr Asp Glu Leu Arg Leu Gln Ser Glu Ala Phe Lys Lys His Ser Leu
 130 135 140
 Asp Leu Leu Ser Lys Glu Arg Glu Leu Asn Gly Lys Leu Arg His Leu
 145 150 155 160
 Ser Pro
 162

<210> 1621
 <211> 189
 <212> PRT
 <213> Homo sapiens

<400> 1621
 Lys Glu Lys Arg Val Thr Val Gln Leu Pro Thr Glu Ser Ile Gln Lys
 1 5 10 15
 Asn Gln Glu Asp Lys Leu Lys Met Val Pro Arg Lys Gln Arg Glu Phe
 20 25 30

<400> 1616

```

Ala Phe Arg Glu Val Gly Gly Tyr Trp Gly Leu Leu Cys Glu His Leu
 1           5           10           15
Tyr Ala Ile Pro Ser Lys Thr Ser Glu Gly Asn Trp Thr Ala Lys Leu
          20           25           30
Gln Gly Tyr Leu Pro Leu Gln Asp Ala Phe His Ile Phe Gln Asp Pro
          35           40           45
Leu Thr Gly Asp Leu Pro Trp Pro Glu Leu Ile Leu Gly Leu Pro Val
          50           55           60           64

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<210> 1617

<211> 93

<212> PRT

<213> Homo sapiens

<400> 1617

```

Ala Ser Arg Leu Glu Lys Gln Asn Ser Thr Pro Glu Ser Asp Tyr Asp
 1           5           10           15
Asn Thr Pro Asn Asp Met Glu Pro Asp Gly Met Gly Tyr Met His Arg
          20           25           30
Thr Ser Val Pro Gly Glu Gly Leu Pro Arg Ala Arg Asp Leu Ala Gly
          35           40           45
Leu Gly Gln Gln Lys Gln Phe Thr Thr His Thr Pro Phe Leu Tyr Phe
          50           55           60
Gln Thr His Lys Gly Leu Lys Asp Ser Ser Ile Arg Ser Glu Val Thr
          65           70           75           80
Cys Leu Gly Ile Ser Gln Cys Trp Arg Lys Gly Phe Phe
          85           90           93

```

<210> 1618

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1618

```

Ile Ala Cys Thr Phe Cys Gly Gln Asp Glu Trp Ser Pro Glu Arg Ser
 1           5           10           15
Thr Arg Cys Phe Arg Arg Arg Ser Arg Phe Leu Ala Trp Gly Glu Pro
          20           25           30
Ala Val Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Gly Leu Val
          35           40           45
Leu Ala Ala Leu Gly Leu Phe Val His His Arg Asp Ser Pro Leu Val
          50           55           60
Gln Ala Ser Gly Gly Pro Leu Ala Cys Phe Gly Leu Val Cys Leu Gly
          65           70           75           80
Leu Val Cys Leu Ser Val Leu Leu Phe Pro Gly Gln Pro Ser Pro Ala
          85           90           95
Arg Cys Leu Ala Gln Gln Pro Leu Ser His Leu Pro Leu Thr Gly Cys
          100          105          110
Leu Ser Thr Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu
          115          120          125
Leu Pro Leu Ser Trp Ala Glu
          130          135

```

Gln Arg Asp Ser Gln Lys Lys Gly Gln Phe Ala Arg Leu Ile Ser Pro
 85 90 95
 Leu Val Asn Leu Pro Gln Ser Pro Gly Gly Leu Glu Phe Gln Tyr Gln
 100 105 110
 Ala Thr
 114

<210> 1614
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 1614
 Arg Ala Met Leu Lys Cys Leu Arg Glu Gly Gln Pro Pro Pro Ser Tyr
 1 5 10 15
 Asn Trp Thr Arg Leu Asp Gly Pro Leu Pro Ser Gly Val Arg Val Asp
 20 25 30
 Gly Asp Thr Leu Gly Phe Pro Pro Leu Thr Thr Glu His Ser Gly Ile
 35 40 45
 Tyr Val Arg His Asp Thr Asn Glu Phe Ser Ser Arg Asp Ser His Asp
 50 55 60
 Thr Val Asp Val Leu Asp Pro Pro Glu Asp Ser Gly Lys Gln Val Asp
 65 70 75 80
 Leu
 81

<210> 1615
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1615
 Ala Ala Gly Asp Ala Pro Leu Arg Ser Leu Glu Gln Ala Asn Arg Thr
 1 5 10 15
 Arg Phe Pro Phe Phe Ser Asp Val Lys Gly Asp His Arg Leu Val Leu
 20 25 30
 Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe Ala Val Ser Leu
 35 40 45
 Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg Arg Arg Arg Arg
 50 55 60
 Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys Ala Asp Leu Leu
 65 70 75 80
 Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg Trp Thr Glu Ala
 85 90 95
 Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe Tyr Val Met Thr
 100 105 110
 Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala Val Ser Leu Glu
 115 120 125
 Arg
 129

<210> 1616
 <211> 64
 <212> PRT
 <213> Homo sapiens

```

Ile His Arg Leu Pro Val Leu Asp Pro Val Ser Gly Asn Val Leu His
65          70          75          80
Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu His Ile Phe Gly Ser
85          90          95
Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr Ile Gln Asp Leu Gly
100         105         110
Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu Glu Thr Ala Pro Ile
115         120         125
Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg Val Ser Ala Leu Ala
130         135         140
Val Val Asn Glu Cys Gly Thr His Pro Gln Asp Glu Arg Leu Gly Leu
145         150         155         160
Gly Trp Gly Leu Gly Glu Pro Gly Ser Glu Glu Arg Leu Phe Pro Ala
165         170         175
Ala Ile Thr Ser Arg
180 181

```

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<210> 1612
<211> 142
<212> PRT
<213> Homo sapiens

```

```

<400> 1612
Gly Pro Glu Phe Pro Gly Ser Ala Lys Leu Val Phe Leu Asp Leu Ser
1          5          10          15
Tyr Asn Asn Leu Thr Gln Leu Gly Ala Gly Ala Phe Arg Ser Ala Gly
20         25         30
Arg Leu Val Lys Leu Ser Leu Ala Asn Asn Asn Leu Val Gly Val His
35         40         45
Glu Asp Ala Phe Glu Thr Leu Glu Ser Leu Gln Val Leu Glu Leu Asn
50         55         60
Asp Asn Asn Leu Arg Ser Leu Ser Val Ala Ala Leu Ala Ala Leu Pro
65         70         75         80
Ala Leu Arg Ser Leu Arg Leu Asp Gly Asn Pro Trp Leu Cys Asp Cys
85         90         95
Asp Phe Ala His Leu Phe Ser Trp Ile Gln Glu Asn Ala Ser Lys Leu
100        105        110
Pro Lys Gly Leu Asp Glu Ile Gln Cys Ser Leu Pro Met Glu Ser Arg
115        120        125
Arg Ile Ser Leu Arg Ala Cys Arg Arg Pro Ala Ser Arg Val
130        135        140        142

```

```

<210> 1613
<211> 114
<212> PRT
<213> Homo sapiens

```

```

<400> 1613
Pro Ala Arg Ile Ser Gly Val Asp Pro Pro Val Arg Lys Ala Thr Lys
1          5          10          15
Gly Gly Glu Asn Cys Ser Phe Glu Asp Asn Lys Asn Trp Gln Phe Leu
20         25         30
Trp Gly Leu Asn Gly Asn Phe Asn Phe Phe Lys Glu Pro Trp Gly Gly
35         40         45
Arg Asn Asn His Ala Lys Gly Phe Arg Thr Thr Trp Ala Arg Ser Ser
50         55         60
Ser Gln Asn Asn Arg Thr Phe Gln Asn Asn Arg Asn Phe Leu Arg Leu
65         70         75         80

```

Lys Glu Gly Glu Lys Ala Asn Ile Pro Lys Leu Met Leu Pro Arg Gly
 20 25 30
 Gly Phe Ser Gln Arg Glu Met Val Thr Gly Glu Arg Ser Pro Ser Pro
 35 40 45
 Glu Glu Glu Glu Glu Glu Glu Glu Gly Phe Gly Glu Arg Ala Ser
 50 55 60
 Cys Arg Arg Gly Leu Phe Arg Val Arg Leu Thr Arg Val Gly Leu Ala
 65 70 75 80
 Ala Pro Ser Lys Ala Ser Arg Gly Gln Glu Gly Asp Ala Ala Pro Lys
 85 90 95
 Ser Pro Val Arg Glu Lys Ser Pro Lys Phe Arg Phe Pro Arg Val Ser
 100 105 110
 Leu Ser Pro Lys Ala Arg Ser Gly Ser Gly Asp Gln Glu Glu Gly Gly
 115 120 125
 Leu Arg Val Arg Leu Pro
 130 134

<210> 1610
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1610
 Leu Leu Gly Gly Asp Leu Arg Tyr His Leu Gln Gln Asn Val His Phe
 1 5 10 15
 Thr Glu Gly Thr Val Lys Leu Tyr Ile Cys Glu Leu Ala Leu Ala Leu
 20 25 30
 Glu Tyr Leu Gln Arg Tyr His Ile Ile His Arg Asp Ile Lys Pro Asp
 35 40 45
 Asn Ile Leu Leu Asp Glu His Gly His Val His Ile Thr Asp Phe Asn
 50 55 60
 Ile Ala Thr Val Val Lys Gly Ala Glu Arg Ala Ser Ser Met Ala Gly
 65 70 75 80
 Thr Lys Pro Tyr Met Ala Pro Glu Val Phe Gln Val Tyr Met Asp Arg
 85 90 95
 Gly Pro Gly Tyr Ser Tyr Pro Val Asp Trp Trp Ser Leu Gly Ile Thr
 100 105 110
 Ala Tyr Glu Leu Leu Arg Gly Trp Arg Pro Tyr Glu Ile His Ser Val
 115 120 125
 Thr Pro Ile Asp Glu Ile Leu Asn Met Phe Lys Val Glu Arg Val His
 130 135 140
 Tyr Ser Ser Thr Trp Cys Lys Gly Met Val Ala Leu Leu Arg Lys
 145 150 155 159

<210> 1611
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 1611
 Leu Thr Ile Thr Asp Phe Ile Leu Val Leu Tyr Arg Tyr Tyr Arg Ser
 1 5 10 15
 Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His Lys Ile Glu Thr Trp
 20 25 30
 Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro Leu Val Ser Ile Ser
 35 40 45
 Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr Leu Ile Lys Asn Arg
 50 55 60

<211> 365
 <212> PRT
 <213> Homo sapiens

<400> 1608

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Ser Val Gly Ala Arg Gln Gly Glu Ala Arg Asp Arg Ile Arg Arg Phe
 1           5           10           15
Phe Pro Lys Gly Asp Leu Glu Val Leu Gln Ala Gln Val Glu Arg Ile
           20           25           30
Met Thr Arg Lys Glu Leu Leu Thr Val Tyr Ser Ser Glu Asp Gly Ser
           35           40           45
Glu Glu Phe Glu Thr Ile Val Leu Lys Ala Leu Val Lys Ala Cys Gly
           50           55           60
Ser Ser Glu Ala Ser Ala Tyr Leu Asp Glu Leu Arg Leu Ala Val Ala
           65           70           75           80
Trp Asn Arg Val Asp Ile Ala Gln Ser Glu Leu Phe Arg Gly Asp Ile
           85           90           95
Gln Trp Arg Ser Phe His Leu Glu Ala Ser Leu Met Asp Ala Leu Leu
           100          105          110
Asn Asp Arg Pro Glu Phe Val Arg Leu Leu Ile Ser His Gly Leu Ser
           115          120          125
Leu Gly His Phe Leu Thr Pro Met Arg Leu Ala Gln Leu Tyr Ser Ala
           130          135          140
Ala Pro Ser Asn Ser Leu Ile Arg Asn Leu Leu Asp Gln Ala Ser His
           145          150          155          160
Ser Ala Gly Thr Lys Ala Pro Ala Leu Lys Gly Gly Ala Ala Glu Leu
           165          170          175
Arg Pro Pro Asp Val Gly His Val Leu Arg Met Leu Leu Gly Lys Met
           180          185          190
Cys Ala Pro Arg Tyr Pro Ser Gly Glu Ala Trp Asp Pro His Pro Gly
           195          200          205
Gln Gly Phe Gly Glu Ser Met Tyr Leu Leu Ser Asp Lys Ala Thr Ser
           210          215          220
Pro Leu Ser Leu Asp Ala Gly Leu Gly Gln Ala Pro Trp Ser Asp Leu
           225          230          235          240
Leu Leu Trp Ala Leu Leu Asn Arg Ala Gln Met Ala Met Tyr Phe
           245          250          255
Trp Glu Met Gly Ser Asn Ala Val Ser Ser Ala Leu Gly Ala Cys Leu
           260          265          270
Leu Leu Arg Val Met Ala Arg Leu Glu Pro Asp Ala Glu Glu Ala Ala
           275          280          285
Arg Arg Lys Asp Leu Ala Phe Lys Phe Glu Gly Met Gly Val Asp Leu
           290          295          300
Phe Gly Glu Cys Tyr Arg Ser Ser Glu Val Arg Ala Ala Arg Leu Leu
           305          310          315          320
Leu Arg Arg Cys Pro Leu Trp Gly Asp Ala Thr Cys Leu Gln Leu Ala
           325          330          335
Met Gln Ala Asp Ala Arg Ala Phe Phe Ala Gln Asp Gly Val Gln Ser
           340          345          350
Leu Pro Thr Gln Lys Trp Trp Gly Asp Met Ala Arg Arg
           355          360          365

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<210> 1609
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1609

```

Val Tyr Leu Gly Ala Gly Pro Gly Leu Phe Phe Ser Asn Glu Gly Ala
 1           5           10           15

```

Asn Ile Phe Arg Leu Leu Lys Ala Ser Ala Arg Met Ser Val Glu Leu
 260 265 270
 Ala Leu Ser Ile Leu Ala His Pro
 275 280

<210> 1606
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1606
 Phe Val Gly Gly Pro Gly Ala Asp Pro Pro Val Ala Val Met Trp Asp
 1 5 10 15
 Pro Arg Ala Ala Arg Met Asp Leu Thr Ala Tyr Ala Glu Leu Leu Lys
 20 25 30
 Glu Ser Gly Asn Gln Val Leu Lys Asn Gly Asn Phe Ser Leu Ala Ile
 35 40 45
 Arg Lys Tyr Asp Glu Ala Ile Gln Ile Leu Leu Gln Leu Tyr Gln Trp
 50 55 60
 Gly Val Pro Pro Arg Asp Leu Ala Val Leu Leu Cys Asn Lys Ser Asn
 65 70 75 80
 Ala Phe Phe Ser Leu Gly Lys Trp Asn Glu Ala Phe Val Ala Ala Lys
 85 90 95
 Glu Cys Leu Gln Trp Asp Pro Thr Tyr Val Lys Gly Tyr Tyr Arg Ala
 100 105 110
 Gly Tyr Ser Leu Leu Arg Leu His Gln Pro Tyr Glu Ala Ala Arg Met
 115 120 125
 Phe Phe Glu Gly Leu Arg
 130 134

<210> 1607
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 1607
 Phe Val Glu Ser Ala Ser Ser Arg Pro Pro Gly Cys Phe Ser Gly Asp
 1 5 10 15
 Gly Arg Phe Trp Leu Val Ser Glu Gly Ser Arg Arg Gly Trp Asp Phe
 20 25 30
 Asn Pro Ser Phe Ser Phe Leu Asp Pro Arg Tyr Ser Val Gly Gly Asp
 35 40 45
 Glu Asn Ile Gly Thr Val Thr Thr Leu Ala Asn Ile Leu Arg Glu Phe
 50 55 60
 Asn Pro Ser Leu Lys Gly Phe Ser Val Gly Thr Gly Lys Glu Thr Ser
 65 70 75 80
 Pro Asn Ala Phe Leu Asn Gln Ala Val Ala Gly Gly Arg Ala Glu Asp
 85 90 95
 Leu Pro Val Gln Ala Arg Arg Leu Val Asp Leu Met Lys Asn Asp Thr
 100 105 110
 Arg Ile His Phe Gln Glu Asp Trp Lys Ile Ile Thr Leu Phe Ile Gly
 115 120 125
 Gly Asn Asp Leu
 130 132

<210> 1608

Ser Thr Gln Leu Ser Ser Ser Leu Leu Gly Tyr Phe Ser Thr Leu Met
 85 90 95
 Thr Gly Ala Ala Phe Thr Asn Asn Ile Ala Ser Ser Thr Ile Ile Leu
 100 105 110 112

<210> 1604
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 1604
 Gly Gln Ile His Ser Gln Asp Asp Pro Pro Phe Ile Asp Gln Leu Gly
 1 5 10 15
 Phe Gly Val Ala Pro Gly Phe Gln Thr Phe Val Ala Cys Gln Glu Gln
 20 25 30
 Arg Val Arg Gly Pro Trp Glu Ala Gly Pro Gly Val Gly Tyr
 35 40 45 46

<210> 1605
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 1605
 Leu Gln Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys Lys Leu Val
 1 5 10 15
 Glu Ala Glu Glu Leu Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala
 20 25 30
 Gln His Leu Glu Val His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu
 35 40 45
 Lys Ile Lys Val Leu Asp Asn Gln Ile Lys Lys Asp Leu Ala Asp Lys
 50 55 60
 Glu Thr Leu Glu Asn Met Met Gln Arg His Glu Glu Ala His Glu
 65 70 75 80
 Lys Gly Lys Ile Leu Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp
 85 90 95
 Ser Lys Ile Arg Ser Leu Glu Gln Arg Ile Val Glu Leu Ser Glu Ala
 100 105 110
 Asn Lys Leu Ala Ala Asn Ser Ser Leu Phe Thr Gln Arg Asn Met Lys
 115 120 125
 Ala Gln Glu Glu Met Ile Ser Glu Leu Arg Gln Gln Lys Phe Tyr Leu
 130 135 140
 Glu Thr Gln Ala Gly Lys Leu Glu Ala Gln Asn Arg Lys Leu Glu Glu
 145 150 155 160
 Gln Leu Glu Lys Ile Ser His Gln Asp His Ser Asp Lys Asn Arg Leu
 165 170 175
 Leu Glu Leu Glu Thr Arg Leu Arg Glu Val Ser Leu Glu His Glu Glu
 180 185 190
 Gln Lys Leu Glu Leu Lys Arg Gln Leu Thr Glu Leu Gln Leu Ser Leu
 195 200 205
 Gln Glu Arg Glu Ser Gln Leu Thr Ala Leu Gln Ala Ala Arg Ala Ala
 210 215 220
 Leu Glu Ser Gln Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr
 225 230 235 240
 Ala Glu Ala Glu Glu Glu Ile Gln Ala Leu Thr Val Gly Leu Gly Ser
 245 250 255

```

Ile His Gly Ala Ser Ser Val Pro Gly Pro Glu Thr Val Arg Leu Arg
      20      25      30
Gln Lys Arg Lys Lys Lys Ala Pro Asp His Ser Ser Gly Arg Lys Glu
      35      40      45
Glu Leu Val Thr Thr His Thr Val Asp Lys Leu Glu Thr Lys Lys Pro
      50      55      60
Val Gly Arg Val Leu Cys Gly Leu Ser Gly Glu Leu Leu His Ser Leu
      65      70      75      80
Leu Leu Pro Arg Arg Lys Thr Glu Lys Arg Ala Leu Gly Ser His Arg
      85      90      95
Lys Ala Gly Phe Pro Glu His Pro Val Ala Pro Glu Pro Leu Ser Asn
      100      105      110
Ser Cys Gln Ile Ser Lys Glu Gly Arg Glu Gln Val Leu Ser Glu Ile
      115      120      125
Gly Ala Gly Asp Cys Leu
      130      134

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<210> 1602
<211> 140
<212> PRT
<213> Homo sapiens

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<400> 1602
Pro Gln Lys Ser His Ser Gly Ala Tyr Gln Cys Phe Ala Thr Arg Lys
  1      5      10      15
Ala Gln Thr Ala Gln Asp Phe Ala Ile Ile Ala Leu Glu Asp Gly Thr
      20      25      30
Pro Arg Ile Val Ser Ser Phe Ser Glu Lys Val Val Asn Pro Gly Glu
      35      40      45
Gln Phe Ser Leu Met Cys Ala Ala Lys Gly Ala Pro Pro Pro Thr Val
      50      55      60
Thr Trp Ala Leu Asp Asp Glu Pro Ile Val Arg Asp Gly Ser His Arg
      65      70      75      80
Thr Asn Gln Tyr Thr Met Ser Asp Gly Thr Thr Ile Ser His Met Asn
      85      90      95
Val Thr Gly Pro Gln Ile Arg Asp Gly Gly Val Tyr Arg Cys Thr Ala
      100      105      110
Arg Asn Leu Val Gly Ser Ala Glu Tyr Gln Ala Arg Ile Asn Val Arg
      115      120      125
Gly Pro Pro Ser Ile Arg Ala Met Arg Asn Ile Thr
      130      135      140

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<210> 1603
<211> 112
<212> PRT
<213> Homo sapiens

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<400> 1603
Ala Cys Cys Gln Trp Arg Arg Thr Leu Ile Pro Ala Lys Ser Thr Thr
  1      5      10      15
Val Ser Cys Thr Ile Ser Thr Pro His His Pro Phe Arg Gly Ser Tyr
      20      25      30
Ser Phe Asp Asp His Ile Thr Asp Ser Glu Ala Leu Ser Arg Ser Ser
      35      40      45
His Val Phe Thr Ser His Pro Arg Met Leu Lys Arg Gln Pro Ala Ile
      50      55      60
Glu Leu Pro Leu Gly Gly Glu Tyr Ser Ser Asp Val Pro Arg Pro Leu
      65      70      75      80

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<400> 1599

```

Phe Arg Arg Arg Arg Arg Arg Arg Glu Arg Asp Cys Ala Ala Gln Gly
 1           5           10           15
Ala Arg Arg His Cys Arg His Leu Ala Glu Cys Lys Leu Val Ser Phe
      20           25           30
Pro Ile Gly Ile Tyr Lys Val Leu Arg Asn Val Ser Gly Gln Ile His
      35           40           45
Leu Ile Thr Leu Ala Asn Asn Glu Leu Lys Ser Leu Thr Ser Lys Phe
      50           55           60
Met Thr Thr Phe Ser Gln Leu Arg Glu Leu His Leu Glu Gly Asn Phe
      65           70           75           80
Leu His Arg Leu Pro Ser Glu Val Ser Ala Leu Gln His Leu Lys Ala
      85           90           95
Ile Asp Leu Ser Arg Asn Gln Phe Gln Asp Phe Pro Glu Gln Leu Thr
      100           105           110
Ala Leu Pro Ala Leu Glu Thr Ile Asn Leu Glu Glu Asn Glu Ile Val
      115           120           125
Asp Val Pro Val Glu Lys Leu Ala Ala Met Pro Ala Leu Arg Ser Ile
      130           135           140
Asn Leu
145 146

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<210> 1600

<211> 145

<212> PRT

<213> Homo sapiens

<400> 1600

```

Leu Leu Pro Gly Ser Leu Gly Val Pro Ile Leu His Ser Gln Pro Trp
 1           5           10           15
Asp Pro Ser Pro Gln Cys Pro His Arg Ala Pro Ser Thr Pro Arg Arg
      20           25           30
Leu Pro Pro Leu Gly Ala Leu Ser Gln Ala Leu Thr Phe Leu Ser Arg
      35           40           45
Ala Ala Lys Asn His Ser Gln Asp Pro Gly Lys Gly Thr Lys Pro Phe
      50           55           60
Pro Ala Ala Pro Ala Ala Pro Pro Pro Arg Ser Ser Leu Pro Ala Pro
      65           70           75           80
Leu Pro Met Gly Leu Lys Asp Lys Gly Pro Gln Pro Ala Pro Pro Thr
      85           90           95
Ile Phe Asn Ser Pro Trp His Pro Ala Thr Leu Pro Gly Ala Leu Gly
      100           105           110
Pro Gln Leu Ser Gln Ala Ala Pro Ser Pro Ile Pro Pro Pro Cys Leu
      115           120           125
Met Gly Ile Ser Ser Cys Pro Asp Leu Lys Leu Thr Lys Ser Ser Thr
      130           135           140
Pro
145

```

<210> 1601

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1601

```

Phe Val Phe Asp Leu Lys Leu Arg Val Pro Gly Phe Ala Ala Leu Leu
 1           5           10           15

```

```

Ile Lys Gly Ser Phe Lys Gln Thr Tyr Leu Val Cys Leu Cys Thr Ser
 65          70          75          80
Ser Pro Asn Gly Lys Leu Ile Glu Glu Val Ser Met Phe Ser Phe Ile
          85          90          95
Ser Asn Tyr Phe Leu Ser
          100          102

```

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<210> 1597
<211> 87
<212> PRT
<213> Homo sapiens

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<400> 1597
Asp Ala Trp Val Lys Asn Asp Ile Ile Phe Asn Gln Thr Glu Arg Lys
 1          5          10          15
Gln Lys Ile Ser Glu Asn Leu Lys His Leu Ala Ser Val Arg Val Val
          20          25          30
Gln Lys Asn Leu Val Phe Val Val Gly Leu Ser Gln Arg Leu Ala Asp
          35          40          45
Pro Glu Val Ser Pro Leu Val Phe Phe Val Ile Leu Ile Phe Phe Val
          50          55          60
Ser Leu Ser Tyr Leu Glu Ile Ile Phe Asp Pro Ala Gln Leu Cys Asp
          65          70          75          80
Ser Ser Glu His Ile Ile Ser
          85          87

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<210> 1598
<211> 134
<212> PRT
<213> Homo sapiens

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```

<400> 1598
Asp Phe Thr Thr Leu Ala Ala Met Met Arg Thr Leu Phe Ser Leu Phe
 1          5          10          15
Gly Asp Val Arg Ser Asp Val His Arg Phe Ser Val Thr Leu Phe Gly
          20          25          30
Ala Ala Ile Lys Ser Val Lys Asn Pro Asp Lys Lys Ser Ile Glu Asn
          35          40          45
Gln Val Leu Asp Ser Leu Val Pro Leu Leu Leu Tyr Ser Gln Asp Glu
          50          55          60
Asn Asp Ala Val Ala Glu Ser Arg Gln Val Leu Thr Ile Cys Ala
          65          70          75          80
Gln Phe Leu Lys Trp Lys Leu Pro Arg Glu Val Tyr Ser Lys Asp Pro
          85          90          95
Trp His Ile Lys Pro Thr Glu Ala Gly Thr Ile Cys Arg Phe Phe Glu
          100          105          110
Lys Lys Cys Lys Gly Lys Ile Asn Ile Leu Glu Gln Thr Leu Met Tyr
          115          120          125
Ser Lys Asn Pro Lys Leu
          130          134

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<210> 1599
<211> 146
<212> PRT
<213> Homo sapiens

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Asn Phe Ser Glu Val Lys Thr Glu Lys Lys Asn Ser Ser Pro Pro Ser
    275                280                285
Ser Asp Lys Thr Ile Ile Ala Pro Lys Val Lys Asp Arg Thr His Asn
    290                295                300
Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val Leu
    305                310                315                320
Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile Asn Lys Phe Thr Ile Leu
    325                330                335
His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu
    340                345                350
Val Ile Tyr Thr Ala Ile Phe Thr Pro Tyr Ser Ala Ala Phe Leu Leu
    355                360                365
Asn Asp Arg Glu Glu Gln Lys Arg Arg Glu Cys Gly Tyr Ser Cys Ser
    370                375                380
Pro Leu Asn Val Val Asp Leu Ile Val Asp Ile Met Phe Ile Ile Asp
    385                390                395                400
Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Gln Asn Glu Glu Val
    405                410                415
Val Ser Asp Pro Ala Ser Val
    420                423

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<210> 1595
<211> 127
<212> PRT
<213> Homo sapiens

```

```

<400> 1595
Asn Leu Thr Trp Trp Pro Leu Phe Arg Asp Val Ser Phe Tyr Ile Val
  1          5          10          15
Asp Leu Ile Met Leu Ile Ile Phe Phe Leu Asp Asn Val Ile Met Trp
    20          25          30
Trp Glu Ser Leu Leu Leu Leu Thr Ala Tyr Phe Cys Tyr Val Val Phe
    35          40          45
Met Lys Phe Asn Val Gln Val Glu Lys Trp Val Lys Gln Met Ile Asn
    50          55          60
Arg Asn Lys Val Val Lys Val Thr Ala Pro Glu Ala Gln Ala Lys Pro
    65          70          75          80
Ser Ala Ala Arg Asp Lys Asp Glu Pro Thr Leu Pro Ala Lys Pro Arg
    85          90          95
Leu Gln Arg Gly Gly Ser Ser Ala Ser Leu His Asn Ser Leu Met Arg
   100          105          110
Asn Ser Ile Phe Gln Asn Lys Ile His Thr Leu Asp Pro His Val
   115          120          125          127

```

```

<210> 1596
<211> 102
<212> PRT
<213> Homo sapiens

```

```

<400> 1596
Val Leu Val Leu Gln Met Asn Tyr Tyr Gln Met Leu Ile Ile Tyr Tyr
  1          5          10          15
Val Leu Phe Phe Lys Val Asn Glu Phe Leu Ala Phe Glu Gly Pro Ile
    20          25          30
Leu Leu Asp Met Arg Ile Lys His Leu Ile Lys Thr Asn Gln Leu Ser
    35          40          45
Gln Ala Thr Ala Leu Ala Lys Leu Cys Ser Asp His Pro Glu Ile Gly
    50          55          60

```

<400> 1593
 Cys Leu Ala Met Ile Lys Gly Ile Gln Ser Ser Gly Lys Ile Ile Tyr
 1 5 10 15
 Phe Ser Ser Leu Phe Pro Tyr Val Val Leu Ile Cys Phe Leu Ile Arg
 20 25 30
 Ala Phe Leu Leu Asn Gly Ser Ile Asp Gly Ile Arg His Met Phe Thr
 35 40 45
 Pro Lys Leu Glu Ile Met Leu Glu Pro Lys Val Trp Arg Glu Ala Ala
 50 55 60
 Thr Gln Val Phe Phe Ala Leu Gly Leu Gly Phe Gly Gly Val Ile Ala
 65 70 75 80
 Phe Ser Ser Tyr Asn Lys Arg Asp Asn Asn Cys His Phe Asp Ala Val
 85 90 95
 Leu Val Ser Phe Ile Asn Phe Phe Thr Ser Val Leu Ala Thr Leu Val
 100 105 110
 Val Phe Ala Val Leu Gly Phe Lys Ala Asn Val Ile Asn Glu Lys Cys
 115 120 125
 Ile Thr Gln Asn Ser Glu Thr Val
 130 135 136

<210> 1594
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 1594
 Met Thr Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg
 1 5 10 15
 Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala
 20 25 30
 Ala Val Leu Met Leu Leu Met Cys Ile Phe Ala Leu Ile Ala His Trp
 35 40 45
 Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu
 50 55 60
 Thr Asp Lys Ile Gly Trp Leu Asp Ser Leu Gly Gln Gln Ile Gly Lys
 65 70 75 80
 Arg Tyr Asn Asp Ser Asp Ser Ser Ser Gly Pro Ser Ile Lys Asp Lys
 85 90 95
 Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly
 100 105 110
 Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile Phe Ser Ile
 115 120 125
 Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn
 130 135 140
 Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His
 145 150 155 160
 Met Gln Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro
 165 170 175
 Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala Trp Thr
 180 185 190
 Tyr Thr Asn Gly Ile Asp Met Asn Met Val Thr Asn Gly Thr Cys Ser
 195 200 205
 Ser Cys Thr Ser Asp Asp Gly His Phe Ile Leu Val Ser Asn His His
 210 215 220
 Gln Gly Gly Leu Ile Tyr Ser Trp Asn Asp Ala Ala Ser Met Gln Arg
 225 230 235 240
 Pro Phe Asn His Ile Lys Ser Ser Leu Leu Gly Ser Thr Ser Asp Ser
 245 250 255
 Asn Leu Asn Lys Tyr Ser Thr Ile Asn Lys Ile Pro Gln Leu Thr Leu
 260 265 270

<210> 1591
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1591
 Ile Arg Leu Thr Ile Leu Arg Cys Val Phe Met Arg Leu Ala Thr Ile
 1 5 10 15
 Cys Val Leu Val Phe Thr Leu Gly Ser Lys Ile Thr Ser Cys Asp Asp
 20 25 30
 Asp Thr Cys Asp Leu Cys Gly Tyr Asn Gln Lys Leu Tyr Pro Cys Trp
 35 40 45
 Glu Thr Gln Val Gly Gln Glu Met Tyr Lys Leu Met Ile Phe Asp Phe
 50 55 60
 Ile Ile Ile Leu Ala Val Thr Leu Phe Val Asp Phe Pro Arg Lys Leu
 65 70 75 80
 Leu Val Thr Tyr Cys Ser Ser Cys Lys Leu Ile Gln Cys Trp Gly Gln
 85 90 95
 Gln Glu Phe Ala Ile Pro Asp Asn Val Leu Gly Ile Val Tyr Gly Gln
 100 105 110
 Thr Ile Cys Trp Ile Gly Ala Phe Phe Ser Pro Leu Leu Pro Ala Met
 115 120 125
 Tyr
 129

<210> 1592
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 1592
 Tyr Phe Lys Asn Thr Thr Leu Leu Leu Val Gly Val Ile Cys Val Ala
 1 5 10 15
 Ala Ala Val Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Arg Met
 20 25 30
 Val Leu Met Ala Gly Ala Lys Pro Gly Met Leu Leu Leu Cys Phe Met
 35 40 45
 Cys Cys Thr Thr Leu Leu Ser Met Trp Leu Ser Asn Thr Ser Thr Thr
 50 55 60
 Ala Met Val Met Pro Ile Val Glu Ala Val Leu Gln Glu Leu Val Ser
 65 70 75 80
 Ala Glu Asp Glu Gln Leu Val Ala Gly Asn Ser Asn Thr Glu Glu Ala
 85 90 95
 Glu Pro Ile Ser Leu Asp Val Lys Asn Ser Gln Pro Ser Val Glu Leu
 100 105 110
 Ile Phe Val Asn Glu Asp Ile Leu Asp Phe Leu Met Lys Ser Pro Leu
 115 120 125
 Met Ile Ser Gln Ala Cys Ile
 130 135

<210> 1593
 <211> 136
 <212> PRT
 <213> Homo sapiens

<211> 226
 <212> PRT
 <213> Homo sapiens

<400> 1589
 Met Lys Pro Asp Asn Ile Leu Leu Asp Glu His Gly His Val His Ile
 1 5 10 15
 Thr Asp Phe Asn Ile Ala Ala Met Leu Pro Arg Glu Thr Gln Ile Thr
 20 25 30
 Thr Met Ala Gly Thr Lys Pro Tyr Met Ala Pro Glu Met Phe Ser Ser
 35 40 45
 Arg Lys Gly Ala Gly Tyr Ser Phe Ala Val Asp Trp Trp Ser Leu Gly
 50 55 60
 Val Thr Ala Tyr Glu Leu Leu Arg Gly Arg Arg Pro Tyr His Ile Arg
 65 70 75 80
 Ser Ser Thr Ser Ser Lys Glu Ile Val His Thr Phe Glu Thr Thr Val
 85 90 95
 Val Thr Tyr Pro Ser Ala Trp Ser Gln Glu Met Val Ser Leu Leu Lys
 100 105 110
 Lys Leu Leu Glu Pro Asn Pro Asp Gln Arg Phe Ser Gln Leu Ser Asp
 115 120 125
 Val Gln Asn Phe Pro Tyr Met Asn Asp Ile Asn Trp Asp Ala Val Phe
 130 135 140
 Gln Lys Arg Leu Ile Pro Gly Phe Ile Pro Asn Lys Gly Arg Leu Asn
 145 150 155 160
 Cys Asp Pro Thr Phe Glu Leu Glu Glu Met Ile Leu Glu Ser Lys Pro
 165 170 175
 Leu His Lys Lys Lys Lys Arg Leu Ala Lys Lys Glu Lys Asp Met Arg
 180 185 190
 Lys Cys Asp Ser Ser Gln Thr Cys Leu Leu Gln Glu His Leu Asp Ser
 195 200 205
 Val Gln Lys Glu Phe Ile Ile Ile Asn Arg Glu Lys Val Asn Arg Asp
 210 215 220
 Cys Ile
 225 226

<210> 1590
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1590
 Glu Leu Leu Asp Pro Thr Thr Pro Met Arg Thr Lys Cys Ile Glu Leu
 1 5 10 15
 Leu Tyr Ala Ala Leu Thr Ser Ser Ser Thr Asp Gln Pro Lys Ala Asp
 20 25 30
 Leu Trp Gln Asn Phe Ala Arg Glu Ile Glu Glu His Val Phe Thr Leu
 35 40 45
 Tyr Ser Lys Asn Ile Lys Lys Tyr Lys Thr Cys Ile Arg Ser Lys Val
 50 55 60
 Ala Asn Leu Lys Asn Pro Arg Asn Ser His Leu Gln Gln Asn Leu Leu
 65 70 75 80
 Ser Gly Thr Thr Ser Pro Arg Glu Phe Ala Glu Met Thr Val Met Glu
 85 90 95
 Met Ala Asn Lys Glu Leu Lys Gln Leu Arg Ala Ser Tyr Thr Glu Ser
 100 105 110
 Cys Ile Gln Glu His Tyr Leu Pro Gln Val Ile Asp Gly Thr Leu Tyr
 115 120 125 128

Pro Pro Asn Val
130 132

<210> 1588
<211> 368
<212> PRT
<213> Homo sapiens

<400> 1588

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Trp Ser Pro Cys Ser Leu Thr Cys Gly Val Gly Leu Gln Thr Arg Asp
 1          5          10          15
Val Phe Cys Ser His Leu Leu Ser Arg Glu Met Asn Glu Thr Val Ile
          20          25          30
Leu Ala Asp Glu Leu Cys Arg Gln Pro Lys Pro Ser Thr Val Gln Ala
          35          40          45
Cys Asn Arg Phe Asn Cys Pro Pro Ala Trp Tyr Pro Ala Gln Trp Gln
          50          55          60
Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Gln Lys Arg Glu Val Leu
          65          70          75          80
Cys Lys Gln Arg Met Ala Asp Gly Ser Phe Leu Glu Leu Pro Glu Thr
          85          90          95
Phe Cys Ser Ala Ser Lys Pro Ala Cys Gln Gln Ala Cys Lys Lys Asp
          100          105          110
Asp Cys Pro Ser Glu Trp Leu Leu Ser Asp Trp Thr Glu Cys Ser Thr
          115          120          125
Ser Cys Gly Glu Gly Thr Gln Thr Arg Ser Ala Ile Cys Arg Lys Met
          130          135          140
Leu Lys Thr Gly Leu Ser Thr Val Val Asn Ser Thr Leu Cys Pro Pro
          145          150          155          160
Leu Pro Phe Ser Ser Ile Arg Pro Cys Met Leu Ala Thr Cys Ala
          165          170          175
Arg Pro Gly Arg Pro Ser Thr Lys His Ser Pro His Ile Ala Ala Ala
          180          185          190
Arg Lys Val Tyr Ile Gln Thr Arg Gln Arg Lys Leu His Phe Val
          195          200          205
Gly Gly Gly Phe Ala Tyr Leu Leu Pro Lys Thr Ala Val Val Leu Arg
          210          215          220
Cys Pro Ala Arg Arg Val Arg Lys Pro Leu Ile Thr Trp Glu Lys Asp
          225          230          235          240
Gly Gln His Leu Ile Ser Ser Thr His Val Thr Val Ala Pro Phe Gly
          245          250          255
Tyr Leu Lys Ile His Arg Leu Lys Pro Ser Asp Ala Gly Val Tyr Thr
          260          265          270
Cys Ser Ala Gly Pro Ala Arg Glu His Phe Val Ile Lys Leu Ile Gly
          275          280          285
Gly Asn Arg Lys Leu Val Ala Arg Pro Leu Ser Pro Arg Ser Glu Glu
          290          295          300
Glu Val Leu Ala Gly Arg Lys Gly Gly Pro Lys Glu Ala Leu Gln Thr
          305          310          315          320
His Lys His Gln Asn Gly Ile Phe Ser Asn Gly Ser Lys Ala Glu Lys
          325          330          335
Arg Gly Leu Ala Ala Asn Pro Gly Ser Arg Tyr Asp Asp Leu Val Ser
          340          345          350
Arg Leu Leu Glu Gln Gly Ala Pro Cys Ser Ser Ser Lys Lys Lys Asn
          355          360          365          368

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<210> 1589

Leu Gln Met Asn Glu Ala Met Val Ala Leu Val Thr Asp Arg Leu Gln
 225 230 235 240
 Gly Trp Asn Ser Gly Glu Gly Asn Trp Asp Arg Ala Asp Lys Phe Gly
 245 250 255
 Asp Leu Val Asp Tyr Leu Arg Val His Ser His Ser Ala Val Tyr Ala
 260 265 270
 Ser Ser Met Ser Pro Pro Ile Ala Glu Gln Ile Ile Arg Ser Leu Lys
 275 280 285
 Leu Ile Met Gly Leu Asp Gly Thr Thr Gln
 290 295 298

<210> 1586
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 1586
 Asn Thr Ser Ser Phe Pro Ala Gln Pro Ser Ser Pro Ala Arg Pro Ser
 1 5 10 15
 Leu Pro His Leu Ser Gln His Pro Ser Asn Pro Leu Leu Pro Leu Ala
 20 25 30
 Ser Ala Asp His Pro Gln Cys Gly Arg Phe Leu Pro Leu His Glu Pro
 35 40 45
 Glu Pro Leu Cys Pro Ser Pro Ser Leu Ser Tyr Pro Thr Leu Val Ser
 50 55 60
 Ser Trp Ser Ser Pro Phe Ser Ser His His Gly Cys Pro Pro Gly Leu
 65 70 75 80
 Tyr Pro Phe Pro Thr Ser Pro Lys Thr Ile Gln Pro Pro Gly Leu Ala
 85 90 95
 Gln Leu Lys Met Leu Cys Ile Pro Pro Gly Arg Gln Gln Leu Arg Gly
 100 105 110
 Ala Gln Ser Met Pro Gly His Gly Ala Leu Ser Pro Leu Leu Leu Pro
 115 120 125
 Pro Ala
 130

<210> 1587
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 1587
 Asp Leu Val Cys Lys Ile Ser Gly Phe Gly Arg Gly Pro Arg Asp Arg
 1 5 10 15
 Ser Glu Ala Val Tyr Thr Thr Met Ser Gly Arg Ser Pro Ala Leu Trp
 20 25 30
 Ala Ala Pro Glu Thr Leu Gln Phe Gly His Phe Ser Ser Ala Ser Asp
 35 40 45
 Val Trp Ser Phe Gly Ile Ile Met Trp Glu Val Met Ala Phe Gly Glu
 50 55 60
 Arg Pro Tyr Trp Asp Met Ser Gly Gln Asp Val Ile Lys Ala Val Glu
 65 70 75 80
 Asp Gly Phe Arg Leu Pro Pro Pro Arg Asn Cys Pro Asn Leu Met His
 85 90 95
 Arg Leu Met Leu Asp Cys Trp Gln Lys Asp Pro Gly Glu Arg Pro Arg
 100 105 110
 Phe Ser Gln Ile His Ser Ile Leu Ser Lys Met Val Gln Asp Pro Glu
 115 120 125

Asp Val Thr Ser Gly Leu Ile Gly Gly Glu Asp Gly Arg Val Tyr Val
 20 25 30
 Tyr Asn Gly Lys Glu Thr Thr Leu Gly Asp Met Thr Gly Lys Cys Lys
 35 40 45
 Ser Trp Ile Thr Pro Cys Pro Glu Glu Lys Val Asn Val Leu Gln Asn
 50 55 60
 Ser Ile Pro Tyr Trp Glu Arg Ile Thr
 65 70 73

<210> 1584
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 1584
 Pro Leu Thr Leu Cys Leu Pro Glu Asn Asn Lys Pro Pro Gln Ala Asp
 1 5 10 15
 Ala Val Pro Asp Lys Glu Leu Thr Leu Pro Val Asp Ser Thr Thr Leu
 20 25 30
 Asp Gly Ser Lys Ser Ser Asp Asp Gln Lys Ile Ile Ser Tyr Leu Trp
 35 40 45
 Glu Lys Thr Gln
 50 52

<210> 1585
 <211> 298
 <212> PRT
 <213> Homo sapiens

<400> 1585
 Asp Val Leu Glu Val Tyr Gly Thr Gly Val Ala Ser Thr Arg His Glu
 1 5 10 15
 Met Gly Thr Leu Asp Lys His Lys Glu Leu Glu Asp Leu Val Ala Lys
 20 25 30
 Phe Leu Asn Val Glu Ala Ala Met Val Phe Gly Met Gly Phe Ala Thr
 35 40 45
 Asn Ser Met Asn Ile Pro Ala Leu Val Gly Lys Gly Cys Leu Ile Leu
 50 55 60
 Arg Asp Glu Val Asn His Thr Ser Leu Val Leu Gly Ala Arg Leu Leu
 65 70 75 80
 Gly Ala Thr Ile Gly Ile Phe Lys His Asn Tyr Ala Gln Ser Leu Glu
 85 90 95
 Lys Leu Leu Arg Asp Ala Val Ile Tyr Gly Gln Pro Arg Thr Arg Arg
 100 105 110
 Ala Trp Lys Lys Ile Leu Ile Leu Val Glu Gly Val Tyr Ser Met Glu
 115 120 125
 Gly Ser Ile Val His Leu Pro Gln Ile Ile Ala Leu Lys Lys Lys Tyr
 130 135 140
 Lys Ala Tyr Leu Tyr Ile Asp Glu Ala His Ser Ile Gly Ala Val Gly
 145 150 155 160
 Pro Thr Gly Arg Gly Val Thr Glu Phe Phe Gly Leu Asp Pro His Glu
 165 170 175
 Val Asp Val Leu Met Gly Thr Phe Thr Lys Ser Phe Gly Ala Ser Gly
 180 185 190
 Gly Tyr Ile Ala Gly Arg Lys Ala Arg Ile Leu Ser Pro Pro Ala Cys
 195 200 205
 Leu Val Pro Asn Thr Gly Ser His Ser Leu His Arg Leu Thr Arg Asp
 210 215 220

Ala Val Thr Phe Ser Val Val Phe Ala Tyr Val Ala Asp Ile Thr Gln
 1 5 10 15
 Glu His Glu Arg Ser Met Ala Tyr Gly Leu Val Cys Met Phe Ile Leu
 20 25 30
 Tyr Leu Leu Tyr Leu Leu Arg Asn Ala Phe Phe Leu Arg
 35 40 45

<210> 1581
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 1581
 Ser Gly Pro Tyr Thr Asp Phe Thr Pro Trp Pro Thr Glu Glu Gln Lys
 1 5 10 15
 Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Pro Pro Glu Arg
 20 25 30
 Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Ala Cys
 35 40 45
 Ile Lys Arg Tyr Lys Val Ala Asp Leu Arg Ile Ser Lys
 50 55 60 61

<210> 1582
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 1582
 Ser Thr Val Thr Gly Gln Pro Arg Arg Leu Leu Asp Thr Ala Gly His
 1 5 10 15
 Gln Gln Pro Phe Leu Glu Leu Lys Ile Arg Ala Asn Glu Pro Gly Ala
 20 25 30
 Gly Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu
 35 40 45
 Cys Cys Arg Arg Asp His Tyr Val Asn Phe Gln Glu Leu Gly Trp Arg
 50 55 60
 Asp Trp Ile Leu Leu Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly
 65 70 75 80
 Gln Cys Pro Thr His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe
 85 90 95
 His Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Gly
 100 105 110
 Arg Thr Ser Trp Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu
 115 120 125
 Tyr Leu
 130

<210> 1583
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1583
 Leu Leu Phe Ser Asp Glu Ile Ile Met Ala Ala Pro Leu Arg Ile Ala
 1 5 10 15

<210> 1578
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1578
 Leu Pro Phe Leu Gly Leu Gly Ser Val Leu Pro Gln Gly Met Val Met
 1 5 10 15
 Ala Ser Pro Glu Met Asn Pro Thr Ile Cys Ser Val Phe Glu Ala His
 20 25 30
 Ile Val Leu Leu Phe His Ala Thr Thr Phe Arg Arg Gly Phe Gln Val
 35 40 45
 Thr Val Leu Val Gly Asn Val Arg Gln Thr Ala Val Val Glu Lys Ile
 50 55 60
 His Ala Lys Val Arg Gly Thr Trp Pro Phe Ile Ser Pro Glu Val Arg
 65 70 75 80
 Lys Glu Gly Gly Leu Pro Gln Thr Gly Arg Glu Leu Leu Asp Pro Thr
 85 90 95
 Met Gly Ile Lys Pro His Leu Trp Trp Val Ala Ala
 100 105 108

<210> 1579
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 1579
 Asp Asp Lys Asn Ala Gln Gly Ile Lys Arg His Val Lys Pro Thr Ser
 1 5 10 15
 Gly Asn Ala Phe Thr Ile Cys Lys Tyr Pro Cys Gly Lys Ser Arg Glu
 20 25 30
 Cys Val Ala Pro Asn Ile Cys Lys Cys Lys Pro Gly Tyr Ile Gly Ser
 35 40 45
 Asn Cys Gln Thr Ala Leu Cys Asp Pro Asp Cys Lys Asn His Gly Lys
 50 55 60
 Cys Ile Lys Pro Asn Ile Cys Gln Cys Leu Pro Gly His Gly Gly Ala
 65 70 75 80
 Thr Cys Asp Glu Glu His Cys Asn Pro Pro Cys Gln His Gly Gly Thr
 85 90 95
 Cys Leu Ala Gly Asn Leu Cys Thr Cys Pro Tyr Gly Phe Val Gly Pro
 100 105 110
 Arg Cys Glu Thr Met Val Cys Asn Arg His Cys Glu Asn Gly Gly Gln
 115 120 125
 Cys Leu Thr Pro Asp Ile Cys Gln Cys Lys Pro Gly Trp Tyr Gly Pro
 130 135 140
 Thr Cys Ser Thr Ala
 145 149

<210> 1580
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 1580

Arg Glu Lys Met Met Pro Ala Asp Ala Ile Val Asp His Ile Met Asp
 130 135 140
 Arg Ile Phe Ser
 145 148

<210> 1577
 <211> 397
 <212> PRT
 <213> Homo sapiens

<400> 1577
 Val Leu Ser Asp Leu Cys Leu Phe Tyr Tyr Arg Asp Glu Lys Glu Glu
 1 5 10 15
 Gly Ile Leu Gly Ser Ile Leu Leu Pro Ser Phe Gln Ile Ala Leu Leu
 20 25 30
 Thr Ser Glu Asp His Ile Asn Arg Lys Tyr Ala Phe Lys Ala Ala His
 35 40 45
 Pro Asn Met Arg Thr Tyr Tyr Phe Cys Thr Asp Thr Gly Lys Glu Met
 50 55 60
 Glu Leu Trp Met Lys Ala Met Leu Asp Ala Ala Leu Val Gln Thr Glu
 65 70 75 80
 Pro Val Lys Arg Val Asp Lys Ile Thr Ser Glu Asn Ala Pro Thr Lys
 85 90 95
 Glu Thr Asn Asn Ile Pro Asn His Arg Val Leu Ile Lys Pro Glu Ile
 100 105 110
 Gln Asn Asn Gln Lys Asn Lys Glu Met Ser Lys Ile Glu Glu Lys Lys
 115 120 125
 Ala Leu Glu Ala Glu Lys Tyr Gly Phe Gln Lys Asp Gly Gln Asp Arg
 130 135 140
 Pro Leu Thr Lys Ile Asn Ser Val Lys Leu Asn Ser Leu Pro Ser Glu
 145 150 155 160
 Tyr Glu Ser Gly Ser Ala Cys Pro Ala Gln Thr Val His Tyr Arg Pro
 165 170 175
 Ile Asn Leu Ser Ser Ser Glu Asn Lys Ile Val Asn Val Ser Leu Ala
 180 185 190
 Asp Leu Arg Gly Gly Asn Arg Pro Asn Thr Gly Pro Leu Tyr Thr Glu
 195 200 205
 Ala Asp Arg Val Ile Gln Arg Thr Asn Ser Met Gln Gln Leu Glu Gln
 210 215 220
 Trp Ile Lys Ile Gln Lys Gly Arg Gly His Glu Glu Glu Thr Arg Gly
 225 230 235 240
 Val Ile Ser Tyr Gln Thr Leu Pro Arg Asn Met Pro Ser His Arg Ala
 245 250 255
 Gln Ile Met Ala Arg Tyr Pro Glu Gly Tyr Arg Thr Leu Pro Arg Asn
 260 265 270
 Ser Lys Thr Arg Pro Glu Ser Ile Cys Ser Val Thr Pro Ser Thr His
 275 280 285
 Asp Lys Thr Leu Gly Pro Gly Ala Glu Glu Lys Arg Arg Ser Met Arg
 290 295 300
 Asp Asp Thr Met Trp Gln Leu Tyr Glu Trp Gln Gln Arg Gln Phe Tyr
 305 310 315 320
 Asn Lys Gln Ser Thr Leu Pro Arg His Ser Thr Leu Ser Ser Pro Lys
 325 330 335
 Thr Met Val Asn Ile Ser Asp Gln Thr Met His Ser Ile Pro Thr Ser
 340 345 350
 Pro Ser His Gly Ser Ile Ala Ala Tyr Gln Gly Tyr Ser Pro Gln Arg
 355 360 365
 Thr Tyr Arg Ser Glu Val Ser Ser Pro Ile Gln Arg Gly Asp Val Thr
 370 375 380
 Ile Asp Arg Arg His Arg Ala His His Pro Lys Val Lys
 385 390 395 397

<211> 241
 <212> PRT
 <213> Homo sapiens

<400> 1575
 Met Ser Ala Arg Lys Glu Arg Arg Glu Lys Gly Glu Glu Glu Gly Glu
 1 5 10 15
 Gly Glu Lys Asp Gly Asp Glu Asp Glu Lys Glu Glu Glu Lys Glu Gly
 20 25 30
 Leu Gly Glu Glu Glu Lys Glu Ala Gly Lys Lys Lys Lys Lys Gln
 35 40 45
 Glu Glu Lys Glu Lys Glu Lys Gly Ala Val Tyr Ser Arg Val Ala Arg
 50 55 60
 Ile Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys His
 65 70 75 80
 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
 85 90 95
 Ser Phe Phe Tyr Phe Asp Val Leu Gln Ser Ile Thr Asp Ile Ile Gln
 100 105 110
 Ile Asn Gly Ile Pro Thr Val Val Gly Val Phe Thr Thr Gln Leu Asn
 115 120 125
 Ser Ile Pro Gly Ser Ala Val Cys Ala Phe Ser Met Asp Asp Ile Glu
 130 135 140
 Lys Val Phe Lys Gly Arg Phe Lys Glu Gln Lys Thr Pro Asp Ser Val
 145 150 155 160
 Trp Thr Ala Val Pro Glu Asp Lys Val Pro Lys Pro Arg Pro Gly Cys
 165 170 175
 Cys Ala Lys His Gly Leu Ala Glu Ala Tyr Lys Thr Ser Ile Asp Phe
 180 185 190
 Pro Asp Glu Thr Leu Ser Phe Ile Lys Ser His Pro Leu Met Asp Ser
 195 200 205
 Ala Val Pro Pro Ile Ala Asp Glu Pro Trp Phe Thr Lys Thr Arg Val
 210 215 220
 Arg Tyr Arg Leu Thr Ala Ile Ser Val Asp His Ser Ala Gly Pro Tyr
 225 230 235 240
 His
 241

<210> 1576
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 1576
 Glu Gly Val Leu Phe Val Tyr Gly Asn Tyr Val Gly Asp Val Met Asn
 1 5 10 15
 Phe Glu Met Ala Ala Glu Met Ala Gln Glu Val Ala Ile Pro Thr Arg
 20 25 30
 Thr Val Leu Thr Thr Asp Asp Ile Ser Ser Ser Pro Ile Glu Asp Arg
 35 40 45
 Asp Gly Arg Arg Gly Val Ala Gly Asn Phe Phe Ile Phe Lys Val Ala
 50 55 60
 Gly Ala Ala Cys Asp Arg Gly Met Ser Leu Glu Ala Cys Glu Ala Val
 65 70 75 80
 Thr Arg Lys Ala Asn Arg Arg Thr Tyr Thr Met Gly Val Ala Leu Glu
 85 90 95
 Pro Cys Ser Leu Pro Gln Thr Arg Arg His Asn Phe Glu Ile Gly Ala
 100 105 110
 Glu Glu Met Glu Ile Gly Met Gly Ile His Gly Glu Arg Gly Val Ile
 115 120 125

Ser Ile Glu His Gln Gln Glu Ile Thr Lys Leu Lys Thr Asp Leu Glu
 115 120 125
 Lys Lys Ser
 130 131

<210> 1573
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 1573
 Asn Asp Pro Ala Ile Ile Ser Asn Phe Ser Ala Ala Val Val His Thr
 1 5 10 15
 Ile Val Asn Glu Thr Leu Glu Ser Met Thr Ser Leu Glu Val Thr Lys
 20 25 30
 Met Val Asp Glu Arg Thr Asp Tyr Leu Thr Lys Ser Leu Lys Glu Lys
 35 40 45
 Thr Pro Pro Phe Ser His Cys Asp Gln Ala Val Leu Gln Cys Ser Glu
 50 55 60
 Ala Ser Ser Asn Lys Asp Met Phe Ala Asp Arg Leu Ser Lys Ser Ile
 65 70 75 80
 Ile Lys His Ser Ile Asp Lys Ser Lys Ser Val Ile Pro Asn Ile Asp
 85 90 95
 Lys Asn Ala Val Tyr Lys Glu Ser Leu Pro Val Ser Gly Glu Glu Ser
 100 105 110
 Gln Leu Thr Pro Glu Lys Ser Pro Lys Phe Pro Asp Ser Gln Asn Gln
 115 120 125
 Leu Thr His Cys Ser Leu Ser Ala Ala
 130 135 137

<210> 1574
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 1574
 Gly Ala Ser Leu Cys Phe Ile Ser Thr Ala Phe Thr Val Leu Thr Phe
 1 5 10 15
 Leu Ile Asp Ser Cys Arg Phe Ser Tyr Pro Glu Arg Pro Ile Ile Phe
 20 25 30
 Leu Ser Met Cys Tyr Asn Ile Tyr Ser Ile Ala Tyr Ile Val Arg Leu
 35 40 45
 Thr Val Gly Arg Glu Arg Ile Ser Cys Asp Phe Glu Glu Ala Ala Glu
 50 55 60
 Pro Val Leu Ile Gln Glu Gly Leu Lys Asn Thr Gly Cys Ala Ile Ile
 65 70 75 80
 Phe Leu Leu Met Tyr Phe Phe Gly Met Ala Ser Ser Ile Trp Trp Val
 85 90 95
 Ile Leu Thr Leu Thr Trp Phe Leu Ala Ala Gly Leu Lys Trp Gly His
 100 105 110
 Glu Ala Ile Glu Met His Ser Ser Tyr Phe His Ile Ala Ala Trp Ala
 115 120 125
 Ile Pro Ala Val Lys
 130 133

<210> 1575

Gln Lys Ala Ser Ala Glu Ile Gln Arg Leu Arg Gly Asp Leu Glu Asn
 385 390 395 400
 Thr Lys Ala Leu Thr Met Glu Ile Gln Gln Glu Gln Ser Arg Leu Lys
 405 410 415
 Thr Leu His Val Val Ile Thr Ser Gln Glu Gln Leu Gln Arg Thr Gln
 420 425 430 432

<210> 1571
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 1571
 Arg Val Arg Leu Asn Asn Asp Gly Leu Ser Pro Leu Met Met Ala Ala
 1 5 10 15
 Lys Thr Gly Lys Ile Gly Ile Phe Gln His Ile Ile Arg Arg Glu Val
 20 25 30
 Thr Asp Glu Asp Thr Arg His Leu Ser Arg Lys Phe Lys Asp Trp Ala
 35 40 45
 Tyr Gly Pro Val Tyr Ser Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr
 50 55 60
 Cys Gly Glu Glu Ala Ser Val Leu Glu Ile Leu Val Tyr Asn Ser Lys
 65 70 75 80
 Ile Glu Asn Arg His Glu Met Leu Ala Val Glu Pro Ile Asn Glu Leu
 85 90 95
 Leu Arg Asp Lys Trp Arg Lys Phe Gly Ala Val Ser Phe Tyr Ile Asn
 100 105 110
 Val Val Ser Tyr Leu Cys Ala Met Val Ile Phe Thr Leu Thr Ala Tyr
 115 120 125
 Tyr Gln Pro Leu Glu Gly Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val
 130 135 140
 Asp Tyr Leu Arg Leu Ala Gly Glu Val Ile Thr Leu Phe Thr Gly Val
 145 150 155 160
 Leu Phe Phe Phe Thr Asn
 165 166

<210> 1572
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 1572
 Asp Ala His Cys Gln Arg Lys Leu Ala Met Gln Glu Phe Met Glu Ile
 1 5 10 15
 Asn Glu Arg Leu Thr Glu Leu His Thr Gln Lys Gln Lys Leu Ala Arg
 20 25 30
 His Val Arg Asp Lys Glu Glu Glu Val Asp Leu Val Met Gln Lys Val
 35 40 45
 Glu Ser Leu Arg Gln Glu Leu Arg Arg Thr Glu Arg Ala Lys Lys Glu
 50 55 60
 Leu Glu Val His Thr Glu Ala Leu Ala Ala Glu Ala Ser Lys Asp Arg
 65 70 75 80
 Lys Leu Arg Glu Gln Ser Glu His Tyr Ser Lys Gln Leu Glu Asn Glu
 85 90 95
 Leu Glu Gly Leu Lys Gln Lys Gln Ile Ser Tyr Ser Pro Gly Val Cys
 100 105 110

Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu
 100 105 110
 Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser
 115 120 125
 Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser
 130 135 140 142

<210> 1570

<211> 432

<212> PRT

<213> Homo sapiens

<400> 1570

Met Asp Gly Glu Ala Val Arg Phe Cys Thr Asp Asn Gln Cys Val Ser
 1 5 10 15
 Leu His Pro Gln Glu Val Asp Ser Val Ala Met Ala Pro Ala Ala Pro
 20 25 30
 Lys Ile Pro Arg Leu Val Gln Ala Thr Pro Ala Phe Met Ala Val Thr
 35 40 45
 Leu Val Phe Ser Leu Val Thr Leu Phe Val Val Asp His His His Phe
 50 55 60
 Gly Arg Glu Ala Glu Met Arg Glu Leu Ile Gln Thr Phe Lys Gly His
 65 70 75 80
 Met Glu Asn Ser Ser Ala Trp Val Val Glu Ile Gln Met Leu Lys Cys
 85 90 95
 Arg Val Asp Asn Val Asn Ser Gln Leu Gln Val Leu Gly Asp His Leu
 100 105 110
 Gly Asn Thr Asn Ala Asp Ile Gln Met Val Lys Gly Val Leu Lys Asp
 115 120 125
 Ala Thr Thr Leu Ser Leu Gln Thr Gln Met Leu Arg Ser Ser Leu Glu
 130 135 140
 Gly Thr Asn Ala Glu Ile Gln Arg Leu Lys Glu Asp Leu Glu Lys Ala
 145 150 155 160
 Asp Ala Leu Thr Phe Gln Thr Leu Asn Phe Leu Lys Ser Ser Leu Glu
 165 170 175
 Asn Thr Ser Ile Glu Leu His Val Leu Ser Arg Gly Leu Glu Asn Ala
 180 185 190
 Asn Ser Glu Ile Gln Met Leu Asn Ala Ser Leu Glu Thr Ala Asn Thr
 195 200 205
 Gln Ala Gln Leu Ala Asn Ser Ser Leu Lys Asn Ala Asn Ala Glu Ile
 210 215 220
 Tyr Val Leu Arg Gly His Leu Asp Ser Val Asn Asp Leu Arg Thr Gln
 225 230 235 240
 Asn Gln Val Leu Arg Asn Ser Leu Glu Gly Ala Asn Ala Glu Ile Gln
 245 250 255
 Gly Leu Lys Glu Asn Leu Gln Asn Thr Asn Ala Leu Asn Ser Gln Thr
 260 265 270
 Gln Ala Phe Ile Lys Ser Ser Phe Asp Asn Thr Ser Ala Glu Ile Gln
 275 280 285
 Phe Leu Arg Gly His Leu Glu Arg Ala Gly Asp Glu Ile His Val Leu
 290 295 300
 Lys Arg Asp Leu Lys Met Val Thr Ala Gln Thr Gln Lys Ala Asn Gly
 305 310 315 320
 Arg Leu Asp Gln Thr Asp Thr Gln Ile Gln Val Phe Lys Ser Glu Met
 325 330 335
 Glu Asn Val Asn Thr Leu Asn Ala Gln Ile Gln Val Leu Asn Gly His
 340 345 350
 Met Lys Asn Ala Ser Arg Glu Ile Gln Thr Leu Lys Gln Gly Met Lys
 355 360 365
 Asn Ala Ser Ala Leu Thr Ser Gln Thr Gln Met Leu Asp Ser Asn Leu
 370 375 380

Cys Arg Thr Leu Cys Glu Gly Pro Gln Arg Phe Glu Glu Tyr Glu Tyr
 1 5 10 15
 Leu Gly Tyr Lys Ala Gly Leu Tyr Glu Ala Ile Ala Asp His Tyr Met
 20 25 30
 Gln Val Leu Val Cys Gln His Glu Cys Val Arg Glu Leu Ala Thr Arg
 35 40 45
 Pro Gly Arg Leu Ser Pro Ile Glu Asn Phe Leu Pro Leu His Tyr Asp
 50 55 60
 Tyr Leu Gln Phe Ala Tyr Tyr Arg Val Gly Glu Tyr Val Lys Ala Leu
 65 70 75 80
 Glu Cys Ala Lys Ala Tyr Leu Leu Cys His Pro Asp Asp Glu Asp Val
 85 90 95
 Leu Asp Asn Val Asp Tyr Tyr Glu Ser Leu Leu Asp Asp Ser Ile Asp
 100 105 110
 Pro Ala Ser Ile Glu Ala Arg Glu Asp Leu Thr Met Phe Val Lys Arg
 115 120 125
 His Lys Leu Glu Ser Glu Leu Ile Lys Ser Ala Ala Glu Gly Leu Gly
 130 135 140
 Xaa Ser Tyr Thr Glu Pro Asn Tyr Trp
 145 150 153

<210> 1568
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 1568
 Ala Phe Ser Ser Pro His Pro Ser Pro Ala Pro Gln Phe Pro Glu Cys
 1 5 10 15
 Gly Phe Tyr Gly Leu Tyr Asp Lys Ile Leu Leu Phe Lys His Asp Pro
 20 25 30
 Thr Ser Ala Asn Leu Leu Gln Leu Val Arg Ser Ser Gly Asp Ile Gln
 35 40 45
 Glu Gly Asp Leu Val Glu Val Val Leu Ser Ala Ser Ala Thr Phe Glu
 50 55 60
 Asp Leu Gln Ile Arg Pro His Ala Leu Thr Val His Ser Tyr Arg Ala
 65 70 75 80
 Pro
 81

<210> 1569
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1569
 Ser Ser Arg Leu Val Leu Leu Ala Gly Ala Ala Ala Leu Ala Ser Gly
 1 5 10 15
 Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys Val Leu Gln Cys
 20 25 30
 Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His Phe Arg Ser Arg
 35 40 45
 Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys Arg Asp Asp Cys
 50 55 60
 Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr Leu Gln Glu Gly
 65 70 75 80
 His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe Ser Arg Phe Leu
 85 90 95

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Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His Ala Thr Val Pro
      820      825      830
Gly Val His Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala Val Ser
      835      840      845
Thr His Ser Thr Val Pro Gly Val Arg Ile Ser Ser Arg Thr Pro Asp
      850      855      860
Leu Thr Cys Ala Val Ser Ile His Ser Thr Val Pro Gly Val His Ile
      865      870      875      880
Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala Val Ser Thr His Ser Thr
      885      890      895
Val Pro Gly Val His Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala
      900      905      910
Val Ser Thr His Ser Thr Val Pro Gly Val His Ile Ser Ser Arg Thr
      915      920      925
Pro Asp Leu Thr Cys Ala Val Ser Ile His Ala Thr Val Pro Ser Val
      930      935      940
His Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His
      945      950      955      960
Ser Thr Val Pro Gly Leu Leu Thr Ser Val Ser Gln Thr Ser Thr Gly
      965      970      975 976

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<210> 1566
 <211> 138
 <212> PRT
 <213> Homo sapiens

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<400> 1566
Phe Arg Thr Lys Ser Tyr Arg Lys Gly Ser Tyr Arg Cys Ile Val Ser
. 1      5      10      15
Glu Trp Ile Ala Glu Gln Gly Asn Trp Gln Glu Ile Gln Glu Lys Ala
      20      25      30
Val Glu Val Ala Thr Val Val Ile Gln Pro Thr Val Leu Arg Ala Ala
      35      40      45
Val Pro Lys Asn Val Ser Val Ala Glu Gly Lys Glu Leu Asp Leu Thr
      50      55      60
Cys Asn Ile Thr Thr Asp Arg Ala Asp Asp Val Arg Pro Glu Val Thr
      65      70      75      80
Trp Ser Phe Ser Arg Met Pro Asp Ser Thr Leu Pro Gly Ser Arg Val
      85      90      95
Leu Ala Arg Leu Asp Arg Asp Phe Leu Val His Ser Ser Pro His Val
      100      105      110
Ala Leu Ser His Val Asp Ala Arg Ser Tyr His Leu Leu Val Arg Asp
      115      120      125
Val Ser Lys Glu Asn Ser Gly Tyr Tyr Tyr
      130      135      138

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<210> 1567
 <211> 153
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(153)
 <223> Xaa = any amino acid or nothing

<400> 1567

Gly Val Arg Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala Val Ser
 305 310 315 320
 Ile His Ala Thr Val Pro Gly Val Arg Ile Ser Ser Cys Thr Pro Asp
 325 330 335
 Leu Thr Cys Ala Val Ser Thr His Ser Thr Val Pro Gly Val Arg Ile
 340 345 350
 Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His Ala Thr
 355 360 365
 Val Pro Gly Val Arg Ile Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala
 370 375 380
 Val Ser Ile His Ala Thr Val Pro Gly Val Arg Ile Ser Ser Cys Thr
 385 390 395 400
 Pro Asp Leu Thr Cys Ala Val Ser Ile His Ala Thr Val Pro Gly Val
 405 410 415
 Arg Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His
 420 425 430
 Ala Thr Val Pro Gly Val Arg Ile Ser Ser Arg Thr Pro Asp Leu Thr
 435 440 445
 Cys Ala Val Ser Ile His Ala Thr Val Pro Gly Val Arg Ile Ser Ser
 450 455 460
 Cys Thr Pro Asp Leu Thr Cys Ala Val Ser Thr His Ser Thr Val Pro
 465 470 475 480
 Gly Val Arg Ile Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala Val Ser
 485 490 495
 Ile His Ala Thr Val Pro Gly Val Arg Ile Ser Ser Cys Thr Pro Asp
 500 505 510
 Leu Thr Cys Ala Val Ser Thr His Ser Thr Val Pro Gly Val Arg Ile
 515 520 525
 Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His Ala Thr
 530 535 540
 Val Pro Gly Val His Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala
 545 550 555 560
 Val Ser Thr His Ser Thr Val Pro Gly Val Arg Ile Ser Ser Arg Thr
 565 570 575
 Pro Asp Leu Thr Cys Ala Val Ser Ile His Ser Thr Val Pro Gly Val
 580 585 590
 Cys Ile Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His
 595 600 605
 Ser Thr Val Pro Ser Val His Ile Ser Ser Cys Thr Pro Asp Leu Thr
 610 615 620
 Cys Ala Val Ser Ile His Ser Thr Val Pro Gly Val Arg Ile Ser Ser
 625 630 635 640
 Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Thr His Ser Thr Val Pro
 645 650 655
 Gly Val His Ile Ser Ser Cys Thr Thr Asp Leu Thr Cys Ala Val Ser
 660 665 670
 Ile His Ala Thr Val Pro Gly Val His Ile Ser Ser Cys Thr Pro Asp
 675 680 685
 Leu Thr Cys Ala Val Ser Thr His Thr Thr Val Pro Gly Val Arg Ile
 690 695 700
 Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His Ser Thr
 705 710 715 720
 Val Pro Gly Val Arg Ile Ser Ser Cys Thr Pro Asp Leu Thr Cys Ala
 725 730 735
 Val Ser Thr His Ser Thr Val Pro Gly Val Arg Ile Ser Ser Arg Thr
 740 745 750
 Pro Asp Leu Thr Cys Ala Val Ser Thr His Leu Thr Val Pro Gly Val
 755 760 765
 Arg Ile Ser Ser Arg Thr Pro Asp Leu Thr Cys Ala Val Ser Ile His
 770 775 780
 Ala Thr Val Pro Gly Val His Ile Ser Ser Cys Thr Pro Asp Leu Thr
 785 790 795 800
 Cys Ala Val Ser Ile His Ala Thr Val Pro Gly Val Arg Ile Ser Ser
 805 810 815

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<210> 1565
<211> 976
<212> PRT
<213> Homo sapiens
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786

Asp Leu Glu Arg Glu Phe Asp Asp Pro Gly Gln Gln Val Pro Ala Ser
 85 90 95
 Pro Gln Gly Pro Ala Val Pro Trp Lys Asp Leu Thr Cys Leu Arg Ala
 100 105 110
 Ser Gln Glu Ser Thr Asp Ile His Leu Gln Pro Leu Lys Thr Gln Leu
 115 120 125
 Lys Ser Trp Lys Pro Cys Leu Ser Pro Lys Ser Asp Cys Glu Asn Ser
 130 135 140
 Glu Thr Ala Thr Lys Glu Gly Ile Ser Glu Glu Lys Ser Gln Gly Leu
 145 150 155 160
 Pro Gln Glu Pro Ser Phe Arg Gly Ile Ser Glu His Glu Ser Asn Leu
 165 170 175
 Val Trp Lys Gln Gly Ser Ala Thr Gly Glu Lys Leu Arg Ser Pro Ser
 180 185 190
 Gln Gly Gly Ser Phe Ser Gln Val Ile Phe Thr Asn Lys Ser Leu Gly
 195 200 205
 Lys Arg Asp Leu Tyr Asp Glu Ala Glu Arg Cys Leu Ile Leu Thr Thr
 210 215 220
 Asp Ser Ile Met Cys Gln Lys Val Pro Pro Glu Glu Arg Pro Tyr Arg
 225 230 235 240
 Cys Asp Val Cys Gly His Ser Phe Lys Gln His Ser Ser Leu Thr Gln
 245 250 255
 His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Gln Cys
 260 265 270
 Gly Lys Ala Phe Ser Leu Arg Ser Tyr Leu Ile Ile His Gln Arg Ile
 275 280 285
 His Ser Gly Glu Lys Ala Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe
 290 295 300
 Asn Gln Ser Ser Ala Leu Ile Arg His Arg Lys Ile His Thr Gly Glu
 305 310 315 320
 Lys Ala Cys Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Ser Ser
 325 330 335
 Tyr Leu Ile Ile His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu
 340 345 350
 Cys Asn Glu Cys Gly Lys Thr Phe Ser Gln Ser Ser Lys Leu Ile Arg
 355 360 365
 His Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Glu Cys Asn Glu Cys
 370 375 380
 Gly Lys Ala Phe Arg Gln Ser Ser Glu Leu Ile Thr His Gln Arg Ile
 385 390 395 400
 His Ser Gly Glu Lys Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe
 405 410 415
 Ser Leu Ser Ser Asn Leu Ile Arg His Gln Arg Ile His Ser Gly
 420 425 430 431

<210> 1564

<211> 205

<212> PRT

<213> Homo sapiens

<400> 1564

Gly Ile Pro Gly Ser Thr Ile Ser Ser Ser Arg Asn Ile Phe Leu Glu
 1 5 10 15
 Asp Asp Leu Ala Trp Gln Ser Leu Ile His Pro Asp Ser Ser Asn Thr
 20 25 30
 Pro Leu Ser Thr Arg Leu Val Ser Val Gln Glu Asp Ala Gly Lys Ser
 35 40 45
 Pro Ala Arg Asn Arg Ser Ala Ser Ile Thr Asn Leu Ser Leu Asp Arg
 50 55 60
 Ser Gly Ser Pro Met Val Pro Ser Tyr Glu Thr Ser Val Ser Pro Gln
 65 70 75 80

```

Gly Met Pro Leu Asp Ser Cys His Phe Arg Thr Lys Pro Ile His Arg
  130                      135                      140
Asn Thr Leu Asn Pro Met Trp Asn Glu Gln Phe Leu Phe His Val His
 145                      150                      155                      160
Phe Glu Asp Leu Val Phe Leu Arg Phe Ala Val Val Glu Asn Asn Ser
                      165                      170                      175
Ser Ala Val Thr Ala Gln Arg Ile Ile Pro Leu Lys Ala Leu Lys Arg
                      180                      185                      190
Gly Tyr Arg His Leu Gln Leu Arg Asn Leu His Asn Glu Val Leu Glu
                      195                      200                      205
Ile Ser Ser Leu Phe Ile Asn Ser Arg Arg Met Glu Glu Asn Ser Ser
                      210                      215                      220
Gly Asn Thr Met Ser Ala Ser Ser Met Phe Asn Thr Glu Glu Arg Lys
 225                      230                      235                      240
Cys Leu Gln Thr His Arg Val Thr Val His Gly Val Pro Gly
                      245                      250                      254

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<210> 1562
<211> 137
<212> PRT
<213> Homo sapiens

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<400> 1562
Gly Ile Arg Gly Thr Thr Gly His Leu Gly Cys Pro Ile Asn Asp Asp
  1                      5                      10                      15
Pro Ser Leu Thr Leu Thr Val Ser Trp Val Met Glu Asp Lys Pro Ile
                      20                      25                      30
Tyr Ile Gly Asn Gly Thr Lys Lys Glu Asp Asp Ser Leu Thr Ile Phe
                      35                      40                      45
Ala Val Ala Lys Arg Asp His Val Ser Asp Thr Cys Gly Ala Cys Thr
                      50                      55                      60
Asp Leu Asp His Asn Leu Asp Lys Gly Tyr Leu Thr Val Leu Gly Glu
 65                      70                      75                      80
Gln Ala Thr Pro Thr Asn Arg Leu Gly Ala Leu Pro Lys Gly Arg Ala
                      85                      90                      95
Asn Arg Thr Arg Asp Leu Glu Leu Thr Tyr Leu Ala Glu Arg Ile Val
                      100                      105                      110
Arg Leu Thr Trp Ile Pro Gly Asp Ala Asn Asn Arg Pro Ile Thr Asp
                      115                      120                      125
Tyr Asp Cys Gln Ile Glu Glu His Gln
 130                      135                      137

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<210> 1563
<211> 431
<212> PRT
<213> Homo sapiens

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<400> 1563
Met Ser Ser Ile Gly Cys Leu Trp Val Ser Arg Ser Ser Gln Ile Asp
  1                      5                      10                      15
Gly Leu Thr Ala Glu Lys Ser Gly Pro Glu Lys Pro His Gly Thr Trp
                      20                      25                      30
Leu Met Pro Glu Leu His Pro Lys Glu Gln Ile Leu Glu Leu Leu Val
                      35                      40                      45
Leu Glu Gln Phe Leu Ser Ile Leu Pro Glu Glu Leu Gln Ile Trp Val
                      50                      55                      60
Gln Gln His Asn Pro Glu Ser Gly Glu Glu Ser Val Thr Leu Leu Glu
 65                      70                      75                      80

```

Gly Leu His Asp Leu Gly Arg Ser Ser Ser Ser Leu Leu Ala Ser Pro
 225 230 235 240
 Gly His Ile Ser Val Lys Glu Pro Thr Pro Ser Ile Ala Ser Asp Ile
 245 250 255
 Ser Leu Pro Ile Ala Thr Gln Glu Leu Arg Gln Arg Leu Arg Gln Leu
 260 265 270
 Glu Asn Gly Thr Thr Leu Gly Gln Ser Pro Leu Gly Gln Ile Gln Leu
 275 280 285
 Thr Ile Pro
 290 291

<210> 1560
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 1560
 Arg Glu Phe Ala Ala Ser Asp Leu Glu Pro Phe Thr Pro Thr Asp Gln
 1 5 10 15
 Pro Ile Ser Pro Glu Ala Ile Thr Gln Pro Ser Cys Ile Lys Arg Gln
 20 25 30
 Arg Ala Ala Gly Asn Pro Gly Ser Leu Ala Ala Thr Ile Asp His Lys
 35 40 45
 Pro Cys Ser Ala Pro Leu Glu Pro Lys Ile Gln Ala Ser Arg Asn Gln
 50 55 60
 Arg Trp Gly Ala Val Arg Ala Ala Glu Ser Leu Thr Asp Ile Ala Glu
 65 70 75 80
 Pro Ala Ser Pro Gln Val His Glu Thr Pro Ile Asp Ala Ser Gln Thr
 85 90 95
 Gln Lys Val Glu Pro Ala Ser Lys Ser Arg Phe Thr Pro Glu Leu Gln
 100 105 110
 Ala Lys Val Ser His Ser Arg Glu Arg Ala Leu Ser Thr Met Asp Ala
 115 120 125
 Thr Pro His His Ala Gln Pro Gln Arg Gly Glu Gly
 130 135 140

<210> 1561
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 1561
 Arg Arg Tyr Ser Gln Lys Leu Ile Gln His Thr Ala Cys Gln Leu Leu
 1 5 10 15
 Arg Thr Tyr Pro Ala Ala Thr Arg Ile Asp Ser Ser Asn Pro Asn Pro
 20 25 30
 Leu Met Phe Trp Leu His Gly Ile Gln Leu Val Ala Leu Asn Tyr Gln
 35 40 45
 Thr Asp Asp Leu Pro Leu His Leu Asn Ala Ala Met Phe Glu Ala Asn
 50 55 60
 Gly Gly Cys Gly Tyr Val Leu Lys Pro Pro Val Leu Trp Asp Lys Asn
 65 70 75 80
 Cys Pro Met Tyr Gln Lys Phe Ser Pro Leu Glu Arg Asp Leu Asp Ser
 85 90 95
 Met Asp Pro Ala Val Tyr Ser Leu Thr Ile Val Ser Gly Gln Asn Val
 100 105 110
 Cys Pro Ser Asn Ser Met Gly Ser Pro Cys Ile Glu Val Asp Val Leu
 115 120 125

<213> Homo sapiens

<221> misc_feature

<222> (1)...(143)

<223> Xaa = any amino acid or nothing

<400> 1558

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Val Gln Gly Thr Gly Xaa Xaa Phe Ile Ala Phe Thr Glu Ala Met Thr
 1           5           10           15
His Phe Pro Ala Ser Pro Val Trp Ala Gly Met Phe Phe Leu Met Leu
           20           25           30
Ile Asn Leu Gly Leu Gly Ser Met Ile Gly Thr Met Ala Gly Ile Thr
           35           40           45
Thr Pro Ile Ile Asp Thr Phe Lys Val Pro Lys Glu Met Phe Thr Gly
           50           55           60
Gly Cys Cys Val Phe Ala Phe Leu Val Gly Leu Leu Phe Val Gln Arg
 65           70           75           80
Ser Gly Asn Tyr Phe Val Thr Met Phe Asp Asp Tyr Ser Ala Thr Leu
           85           90           95
Pro Leu Thr Leu Ile Val Ile Leu Glu Asn Ile Ala Val Ala Trp Ile
           100          105          110
Tyr Gly Thr Lys Lys Phe Met Gln Glu Leu Thr Glu Met Leu Gly Phe
           115          120          125
Arg Pro Tyr Arg Phe Tyr Phe Tyr Met Trp Lys Phe Val Ser Pro
 130          135          140          143

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<210> 1559

<211> 291

<212> PRT

<213> Homo sapiens

<400> 1559

```

Glu Lys Glu Arg Leu Leu Asp Glu Trp Phe Thr Leu Asp Glu Val Pro
 1           5           10           15
Lys Gly Lys Leu His Leu Arg Leu Glu Trp Leu Thr Leu Met Pro Asn
           20           25           30
Ala Ser Asn Leu Asp Lys Val Leu Thr Asp Ile Lys Ala Asp Lys Asp
           35           40           45
Gln Ala Asn Asp Gly Leu Ser Ser Ala Leu Leu Ile Leu Tyr Leu Asp
           50           55           60
Ser Ala Arg Asn Leu Pro Ile Arg Tyr Lys Thr Asn Glu Pro Val Trp
 65           70           75           80
Glu Glu Asn Phe Thr Phe Phe Ile His Asn Pro Lys Arg Gln Asp Leu
           85           90           95
Glu Val Glu Val Arg Asp Glu Gln His Gln Cys Pro Leu Gly Asn Leu
           100          105          110
Lys Val Pro Leu Ser Gln Leu Leu Thr Ser Glu Asp Met Thr Val Ser
           115          120          125
Gln Arg Phe Gln Leu Gly Asn Ser Gly Pro Asn Ser Thr Ile Lys Met
 130          135          140
Lys Ile Ala Leu Arg Val Leu His Leu Glu Lys Arg Glu Arg Pro Pro
 145          150          155          160
Asp His Gln His Ser Ala Gln Val Lys Arg Pro Ser Val Ser Lys Glu
           165          170          175
Gly Arg Lys Thr Ser Ile Lys Ser His Met Ser Gly Ser Pro Gly Pro
           180          185          190
Gly Gly Ser Asn Thr Ala Pro Ser Thr Pro Val Ile Gly Gly Ser Asp
           195          200          205
Lys Pro Gly Met Glu Glu Lys Ala Gln Pro Pro Glu Ala Gly Pro Gln
 210          215          220

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<211> 67
 <212> PRT
 <213> Homo sapiens

<400> 1555
 Ala Ala Val Ala Leu Arg Asp Ile Ser Trp Gln Gln Pro Tyr Pro Met
 1 5 10 15
 Asp Phe Tyr Ala Gly Ser Ser Leu Gly Pro Trp Thr Val Asn His Gly
 20 25 30
 Gln Asp Arg Arg Pro His Ala Pro Gly Arg Pro Ala Arg Gly Lys Val
 35 40 45
 Gln Glu Gly Ser Ala Arg Pro Pro Ser Ala Val Ala Cys Glu Asp Cys
 50 55 60
 Ser Cys Arg
 65 67

<210> 1556
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1556
 Asp Leu Ser Pro Asp Ser Arg Glu Asp His Pro Gln Gly His Arg Arg
 1 5 10 15
 Leu Leu Pro Lys Arg Pro Val Arg Gly Ser Leu Met Pro Gly His Thr
 20 25 30
 His His Pro Cys Pro Val Ser Ser Thr Thr Asn Asp Thr Pro Asp Gln
 35 40 45
 Ile Trp Val Ser Val Gly Ser Leu Arg Met Gly Thr Gly Gly Met Gly
 50 55 60
 Ala Asn Ala Ser Thr Ser Pro Arg Cys Trp Asp Leu Ser Ser Gly Asn
 65 70 75 80
 Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Glu Ser
 85 90 95
 Arg Gly Gly Leu Leu Ala Thr Gly Val Gly Gly Met Cys Ala Cys Val
 100 105 110
 Pro Arg Asn Gln Pro Leu Thr Gly Thr
 115 120 121

<210> 1557
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 1557
 Leu Trp Thr Leu Tyr Arg His Lys Gln Gln Val Gln His Asn His Ser
 1 5 10 15
 Asn Arg Leu Ser Cys Arg Pro Ser Gln Glu Asp Arg Ala Thr His Thr
 20 25 30
 Ile Met Val Leu Asp Lys Glu Asn Thr Leu Ser
 35 40 43

<210> 1558
 <211> 143
 <212> PRT

```

Ile Leu Val Ala Val Ser Ser Ser Gly Glu Lys Val Leu Leu Gln Pro
                245                250                255
Thr Glu Asp Cys Val Phe Thr Ala Leu Gly Ile Asn Ser His Leu Phe
                260                265                270
Ala Cys Thr Arg Asp Ser Tyr Glu Ala Leu Val Pro Leu Pro Glu Glu
                275                280                285
Ile Gln Val Ser Pro Gly Asp Thr Glu Ile His Arg Val Glu Pro Glu
                290                295                300
Asp Val Ala Asn His Leu Thr Ala Phe His Trp Glu Leu Phe Arg Cys
305                310                315                320
Val His Glu Leu Glu Phe Val Asp Tyr Val Phe His Gly Glu
                325                330                334

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<210> 1553
 <211> 134
 <212> PRT
 <213> Homo sapiens

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<400> 1553
Asn Asn Leu Asn Cys Ala Glu Pro Leu Phe Glu Gln Asn Asn Ser Leu
 1                5                10                15
Asn Val Asn Phe Asn Thr Gln Lys Lys Thr Val Trp Leu Ile His Gly
                20                25                30
Tyr Arg Pro Val Gly Ser Ile Pro Leu Trp Leu Gln Asn Phe Val Arg
                35                40                45
Ile Leu Leu Asn Glu Glu Asp Met Asn Val Ile Val Val Asp Trp Ser
 50                55                60
Arg Gly Ala Thr Thr Phe Ile Tyr Asn Arg Ala Val Lys Asn Thr Arg
 65                70                75                80
Lys Val Ala Val Ser Leu Ser Val His Ile Lys Asn Leu Leu Lys His
                85                90                95
Gly Ala Ser Leu Asp Asn Phe His Phe Ile Gly Gly Ser Leu Gly Ala
                100                105                110
His Ile Ser Gly Phe Val Gly Lys Ile Phe His Gly Gln Leu Gly Arg
                115                120                125
Ile Thr Gly Leu Asp Pro
130                134

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<210> 1554
 <211> 65
 <212> PRT
 <213> Homo sapiens

```

<400> 1554
Ser Pro Ser Leu Leu Pro Gln Cys Leu Met Ser Leu Ser Asp Leu Ser
 1                5                10                15
Leu Ser Pro Ala Pro Pro Ser His Leu Ser Pro Arg Cys Pro Ser Pro
                20                25                30
Gln Ala Gly Ser Arg Leu Gly Ala Met Arg Arg Cys Ala Arg Glu Met
                35                40                45
Asp Ala Thr Pro Met Pro Pro Ala Pro Ser Cys Pro Ser Glu Arg Val
 50                55                60
Thr
65

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<210> 1555

<400> 1551

```

Ile Ser Trp Glu Ala Gln Ile Ala Glu Ile Ile Gln Trp Val Ser Asp
 1           5           10           15
Glu Lys Asp Ala Arg Gly Tyr Leu Gln Ala Leu Ala Ser Lys Met Thr
      20           25           30
Glu Glu Leu Glu Ala Leu Arg Ser Ser Ser Leu Gly Ser Arg Thr Leu
      35           40           45
Asp Pro Leu Trp Lys Val Arg Arg Ser Gln Lys Leu Asp Met Ser Ala
      50           55           60
Arg Leu Glu Leu Gln Ser Ala Leu Glu Ala Glu Ile Arg Ala Lys Gln
      65           70           75           80
Leu Val Gln Glu Glu Leu Arg Lys Val Lys Asp Ala Asn Leu Thr Leu
      85           90           95
Glu Ser Lys Leu Lys Asp Ser Glu Ala Lys Asn Arg Glu Leu Leu Glu
      100          105          110
Glu Met Glu Ile Leu Lys Lys Lys Met Glu Glu Lys Phe Arg Ala Asp
      115          120          125
Thr Gly Lys Leu Met Leu Cys Asp Ser Ala Leu Phe Glu Tyr Lys Tyr
      130          135          140
Phe Ser Asn Glu Cys Phe Tyr Phe Leu Phe Asp Leu Ile Val Thr Leu
      145          150          155          160
Glu Ala Pro Thr Glu Phe Gln Ile Gln Tyr
      165          170

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<210> 1552

<211> 334

<212> PRT

<213> Homo sapiens

<400> 1552

```

Pro Ser Ser Tyr Ser Ser Asp Glu Leu Ser Pro Gly Glu Pro Leu Thr
 1           5           10           15
Ser Pro Pro Trp Ala Pro Leu Gly Ala Pro Glu Arg Pro Glu His Leu
      20           25           30
Leu Asn Arg Val Leu Glu Arg Leu Ala Gly Gly Ala Thr Arg Asp Ser
      35           40           45
Ala Ala Ser Asp Ile Leu Leu Asp Asp Ile Val Leu Thr His Ser Leu
      50           55           60
Phe Leu Pro Thr Glu Lys Phe Leu Gln Glu Leu His Gln Tyr Phe Val
      65           70           75           80
Arg Ala Gly Gly Met Glu Gly Pro Glu Gly Leu Gly Arg Lys Gln Ala
      85           90           95
Cys Leu Ala Met Leu Leu His Phe Leu Asp Thr Tyr Gln Gly Leu Leu
      100          105          110
Gln Glu Glu Glu Gly Ala Gly His Ile Ile Lys Asp Leu Tyr Leu Leu
      115          120          125
Ile Met Lys Asp Glu Ser Leu Tyr Gln Gly Leu Arg Glu Asp Thr Leu
      130          135          140
Arg Leu His Gln Leu Val Glu Thr Val Glu Leu Lys Ile Pro Glu Glu
      145          150          155          160
Asn Gln Pro Pro Ser Lys Gln Val Lys Pro Leu Phe Arg His Phe Arg
      165          170          175
Arg Ile Asp Ser Cys Leu Gln Thr Arg Val Ala Phe Arg Gly Ser Asp
      180          185          190
Glu Ile Phe Cys Arg Val Tyr Met Pro Asp His Ser Tyr Val Thr Ile
      195          200          205
Arg Ser Arg Leu Ser Ala Ser Val Gln Asp Ile Leu Gly Ser Val Thr
      210          215          220
Glu Lys Leu Gln Tyr Ser Glu Glu Pro Ala Gly Arg Glu Asp Ser Leu
      225          230          235          240

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<210> 1549
 <211> 125
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(125)
 <223> Xaa = any amino acid or nothing

<400> 1549
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 1 5 10 15
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 20 25 30
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
 35 40 45
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 50 55 60
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 65 70 75 80
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
 85 90 95
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Xaa
 100 105 110
 Asp Arg Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile
 115 120 125

<210> 1550
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 1550
 Pro Arg Val Arg Pro Gln Gln Arg Lys Met Ser Phe Phe Phe Lys Thr
 1 5 10 15
 Glu Leu Gly Glu Lys Leu Val Thr Lys Phe Leu Phe Glu Thr Asp Phe
 20 25 30
 Ser Asp Asp Pro Met Leu Pro Ser Pro Asp Gln Leu Lys Lys Lys Ala
 35 40 45
 Pro Phe Thr Asn Lys Lys Leu Lys Ala His Gln Thr Pro Val Asp Ile
 50 55 60
 Leu Lys Gln Lys Ala His Gln Leu Ala Ser Met Gln Val Gln Ala Tyr
 65 70 75 80
 Asn Gly Gly Asn Ala Asn Pro Arg Pro Ala Asn Asn Glu Glu Glu Glu
 85 90 95
 Asp Glu Glu Asp Glu Tyr Asp Tyr Asp Tyr Glu Ser Leu Ser Asp Asp
 100 105 110
 Asn Ile Leu Glu Asp Arg Pro Glu Asn Lys Ser Cys His Asp Gln Leu
 115 120 125
 Gln Phe Glu Tyr Lys Glu Glu Met
 130 135 136

<210> 1551
 <211> 170
 <212> PRT
 <213> Homo sapiens

<210> 1547
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 1547
 Gln Leu Ala Ile Glu Ile Gly Val Arg Ala Leu Leu Phe Gly Val Phe
 1 5 10 15
 Val Phe Thr Glu Phe Leu Asp Pro Phe Gln Arg Val Ile Gln Pro Glu
 20 25 30
 Glu Ile Trp Leu Tyr Lys Asn Pro Leu Gly Gln Ser Asp Asn Ile Pro
 35 40 45
 Thr Arg Leu Met Phe Ala Ile Ser Phe Leu Thr Pro Leu Ala Val Ile
 50 55 60
 Cys Val Val Lys Ile Ile Arg Arg Thr Asp Lys Thr Glu Ile Lys Glu
 65 70 75 80
 Ala Phe Leu Ala Val Ser Leu Ala Leu Ala Leu Asn Gly Val Cys Thr
 85 90 95
 Asn Thr Ile Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr
 100 105 110
 Arg Cys Phe Pro Asp Gly Val Met Asn Ser Glu Met His Cys Thr Gly
 115 120 125
 Asp Pro Asp Leu Val Ser Glu Gly Arg Lys Ser Phe Pro Ser Ile His
 130 135 140
 Ser Ser Phe Ala Phe Ser Gly Leu Gly Phe Thr Thr Phe Tyr Leu Ala
 145 150 155 160
 Gly Lys Leu His Cys Phe Thr Glu Ser Gly Arg Gly Lys Ser Trp Arg
 165 170 175
 Leu Cys Ala Ala Ile Leu Pro Leu
 180 184

<210> 1548
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1548
 Thr Cys Thr Thr Val Val Val Ile Pro Arg Met Leu Val Asp Phe Leu
 1 5 10 15
 Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu Cys Ala Thr Gln Met Phe
 20 25 30
 Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys Phe Ile Met Ala Ala Met
 35 40 45
 Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn Pro Leu Gln Tyr His Thr
 50 55 60
 Leu Met Thr Arg Lys Ile Cys Leu Gln Met Met Met Ala Ser Trp Met
 65 70 75 80
 Val Gly Phe Leu Phe Ser Leu Cys Ile Ile Val Thr Val Phe Asn Leu
 85 90 95
 Ser Leu Cys Asp Leu Asn Thr Ile Gln His Tyr Phe Cys Asp Ile Ser
 100 105 110
 Pro Val Val Ser Leu Ala Cys Asn Tyr Thr Phe Tyr His Glu Met Ala
 115 120 125
 Ile Phe Val Leu Ser Ala
 130 134

<211> 224
 <212> PRT
 <213> Homo sapiens

<400> 1545
 Met Gly Val Ala Ser Asp Trp Thr Lys Arg Ile Glu Tyr Gln Pro Gly
 1 5 10 15
 Ser Gly Ser Met Pro Leu Phe Pro Ser Ile His Leu Glu Thr Cys Asp
 20 25 30
 Gly Ala Val Ser Ser Leu Gln Ile Val Thr Glu Leu Gln Thr Asn Tyr
 35 40 45
 Ile Gly Lys Gly Cys Asp Arg Glu Thr Tyr Ser Glu Lys Ser Leu Gln
 50 55 60
 Lys Leu Cys Gly Ala Ser Ser Gly Ile Ile Asp Leu Leu Pro Ser Pro
 65 70 75 80
 Ser Ala Ala Thr Asn Trp Thr Ala Gly Leu Leu Val Asp Ser Ser Glu
 85 90 95
 Met Ile Phe Lys Phe Asp Gly Arg Gln Gly Ala Lys Ile Pro Asp Gly
 100 105 110
 Ile Val Pro Lys Asn Leu Thr Asp Gln Phe Thr Ile Thr Met Trp Met
 115 120 125
 Lys His Gly Pro Ser Pro Gly Val Arg Ala Glu Lys Glu Thr Ile Leu
 130 135 140
 Cys Tyr Ser Asp Lys Thr Glu Met Asn Arg His His Tyr Ala Leu Tyr
 145 150 155 160
 Val His Asn Cys Arg Leu Val Phe Leu Leu Arg Lys Asp Phe Asp Gln
 165 170 175
 Ala Asp Thr Phe Arg Pro Ala Glu Phe His Trp Lys Leu Asp Gln Gln
 180 185 190
 Ala Leu Ala Lys Val Asp Gly Gln Pro Gly Lys Ser Ile Thr Arg Gln
 195 200 205
 Leu Gln Glu Met Pro Val Thr Ile Gln Gly Ile Ser Leu Lys Pro Ser
 210 215 220 224

<210> 1546
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 1546
 Phe Arg Gly Thr Pro Val Ser Gly Leu Thr Asn Arg Asp Thr Leu Ala
 1 5 10 15
 Val Ile Arg His Phe Arg Glu Pro Ile Arg Leu Lys Thr Val Lys Pro
 20 25 30
 Gly Lys Val Ile Asn Lys Asp Leu Arg His Tyr Leu Ser Leu Gln Phe
 35 40 45
 Gln Lys Gly Ser Ile Asp His Lys Leu Gln Gln Val Ile Arg Asp Asn
 50 55 60
 Leu Tyr Leu Arg Thr Ile Pro Cys Thr Thr Arg Ala Pro Arg Asp Gly
 65 70 75 80
 Glu Val Pro Gly Val Asp Tyr Asn Phe Ile Ser Val Glu Gln Phe Lys
 85 90 95
 Ala Leu Glu Glu Ser Gly Ala Leu Leu Glu Ser Gly Thr Tyr Asp Gly
 100 105 110
 Asn Phe Tyr Gly Thr Pro Lys Pro Pro Ala Glu Pro Ser Pro Phe Gln
 115 120 125
 Pro Asp Pro Val
 130 132

<223> Xaa = any amino acid or nothing

<400> 1542

```

Pro Ser Lys Xaa Gly Gly Ile Arg Leu Leu Leu Thr Gly Thr Gln Leu
 1           5           10           15
Tyr Gly Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Arg
          20           25           30
Asp Gly Tyr Asn Gly Glu Gly Arg Glu Glu Pro Tyr
      35           40           44

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<210> 1543

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1543

```

Glu Tyr Phe Pro Asn Ser Ile Trp Arg Ser Leu Phe Ser Thr Met Asp
 1           5           10           15
Leu Gly Asp Ile Gly Phe Tyr Thr Tyr Arg Ile Leu Gln Ala Leu Ser
          20           25           30
Tyr Thr His Ser Lys Gly Ile Met His Arg Asp Val Lys Pro Leu Asn
      35           40           45
Ile Leu Cys Asn Ser Pro Arg Asn Lys Val Ile Leu Ala Asp Trp Gly
      50           55           60
Leu Ala Glu Phe Tyr His Pro Met Arg Lys Tyr Ser Val His Val Ala
      65           70           75           80
Thr Arg Tyr Tyr Lys Ser Pro Glu Ile Leu Leu Asp Tyr Glu Tyr Tyr
          85           90           95
Asp Tyr Ser Leu Asp Ile Trp Ala Val Gly Val Ile Leu Leu Glu Leu
          100           105           110
Leu Thr Leu Lys Leu His Val Phe Glu Gly Gly Asp Asn Glu Gln
      115           120           125           127

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<210> 1544

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1544

```

Arg Lys Gly Val Gly Lys Met Pro Thr Ser Glu Gly Arg Pro Gly Gln
 1           5           10           15
Glu Arg Ser Asp Trp Val Thr Ser Tyr Lys Val Met Gly Ser Asn Asp
          20           25           30
Ser His Thr Trp Val Thr Val Lys Asn Gly Ser Gly Asp Met Ile Phe
      35           40           45
Glu Gly Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val
      50           55           60
Pro Met Gly Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp
      65           70           75           80
Asn Gly Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro
          85           90           95
Asp Pro Asn Asn Tyr
      100 101

```

<210> 1545

<213> Homo sapiens

<221> misc_feature

<222> (1)...(112)

<223> Xaa = any amino acid or nothing

<400> 1540

```

Met Arg Leu Asn Gln Asn Thr Leu Leu Leu Glu Ser Phe Gly Xaa Xaa
 1           5           10           15
Arg Pro Tyr Thr Ser Glu His Ala Pro Thr Tyr His Gln Trp Met Lys
          20          25          30
Ala Asp Glu Leu Leu Arg Trp Thr Thr Ser Glu Pro Leu Thr Leu Glu
          35          40          45
His Glu Tyr Ala Met Gln Arg Thr Trp Leu Glu Asp Ala Tyr Glu Cys
          50          55          60
Thr Phe Ile Val Leu Asp Ala Glu Lys Arg His Ala Gln Pro Gly Ala
          65          70          75          80
Thr Glu Glu Ser Cys Met Val Gly Asp Val Asn Leu Phe Leu Thr Asp
          85          90          95
Leu Glu Asp Leu Thr Leu Gly Glu Ile Glu Val Leu Ile Ala Glu Pro
          100          105          110          112

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<210> 1541

<211> 156

<212> PRT

<213> Homo sapiens

<400> 1541

```

Cys Leu Asp Arg Ala Ala Gly Ile Arg His Glu Arg Asn Val Ile Tyr
 1           5           10           15
Ile Asn Glu Thr His Thr Arg His Arg Gly Trp Leu Ala Arg Arg Leu
          20          25          30
Ser Tyr Val Leu Phe Ile Gln Glu Arg Asp Val His Lys Gly Met Phe
          35          40          45
Ala Thr Asn Val Thr Glu Asn Val Leu Asn Ser Ser Arg Val Gln Glu
          50          55          60
Ala Ile Ala Glu Val Ala Ala Glu Leu Asn Pro Asp Gly Ser Ala Gln
          65          70          75          80
Gln Gln Ser Lys Ala Val Asn Lys Val Lys Lys Lys Ala Lys Arg Ile
          85          90          95
Leu Gln Glu Met Val Ala Thr Val Ser Pro Ala Met Ile Arg Leu Thr
          100          105          110
Gly Trp Val Leu Leu Lys Leu Phe Asn Ser Phe Phe Trp Asn Ile Gln
          115          120          125
Ile His Lys Gly Gln Leu Glu Met Val Lys Ala Ala Thr Glu Thr Asn
          130          135          140
Leu Pro Leu Leu Phe Leu Pro Val His Arg Ser His
          145          150          155          156

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<210> 1542

<211> 44

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(44)

<210> 1538
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 1538
 Ala His Leu Gly Gly Ala Trp Leu Thr Gln Arg Ser Leu Gly Ser Trp
 1 5 10 15
 Ala Ala Pro Gly Pro Ala Arg Ala Ala Lys Glu Val Val Ala Cys Ile
 20 25 30
 Pro Gln Asn Gln Lys Met Asn Ile Trp Arg Met Lys Thr Ser Lys His
 35 40 45
 Leu Gln Leu Leu Ser Phe Val Leu Gly Ala Val Ser Pro Ala Val Val
 50 55 60
 Val Pro Tyr Met Met Val Leu Gln Glu Asn Gly Tyr Gly Val Glu Glu
 65 70 75 80
 Gly Ile Pro Thr Leu Leu Met Ala Ala Ser Ser Met Asp Asp Ile Leu
 85 90 95
 Ala Ile Thr Gly Phe Asn Thr Cys Leu Ser Ile Val Phe Ser Ser Gly
 100 105 110
 Cys Ala Arg Ser Ser Gly Ser Arg Asn Ser Lys Ser Leu Arg Thr Pro
 115 120 125
 Leu Gly Thr Ile Cys Glu Gly Cys Asp Asp Ser Ser Ile Phe Ser His
 130 135 140
 Leu Asp His Ser Ser Lys Trp Ser Ser Thr Tyr Gly His Ser Gly Ala
 145 150 155 160

<210> 1539
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 1539
 Glu Phe Leu Ser Ser Asn Gln Ile Thr Gln Leu Pro Asn Thr Thr Phe
 1 5 10 15
 Arg Pro Met Pro Asn Leu Arg Ser Val Asp Leu Ser Tyr Asn Lys Leu
 20 25 30
 Gln Ala Leu Ala Pro Asp Leu Phe His Gly Leu Arg Lys Leu Thr Thr
 35 40 45
 Leu His Met Arg Ala Asn Ala Ile Gln Phe Val Pro Val Arg Ile Phe
 50 55 60
 Gln Asp Cys Arg Ser Leu Lys Phe Leu Asp Ile Gly Tyr Asn Gln Leu
 65 70 75 80
 Lys Ser Leu Ala Arg Asn Ser Phe Ala Gly Leu Phe Lys Leu Thr Glu
 85 90 95
 Leu His Leu Glu His Asn Asp Leu Val Lys Val Asn Phe Ala His Phe
 100 105 110
 Pro Arg Leu Ile Ser Leu His Ser Leu Cys Leu Arg Arg Asn Lys Val
 115 120 125
 Ala Ile Val Val Ser Ser Leu Asp Trp
 130 135 137

<210> 1540
 <211> 112
 <212> PRT

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Phe His Ser Thr Thr Ala Val Ser Glu Lys Lys Ile Leu Leu Glu Ala
      115      120      125
Leu Thr Cys Ser Asp Asp Arg Asn Leu Leu Asn Arg Leu Leu Asn Leu
      130      135      140
Ser Leu Asn Ser Glu Val Val Leu Asp Gln Asp Ala Ile Asp Val Ile
145      150      155      160
Ile His Val Ala Arg Asn Pro His Gly Arg Asp Leu Ala Trp Lys Phe
      165      170      175
Phe Arg Asp Lys Trp Lys Ile Leu Asn Thr Arg Ile Arg Gln Lys Thr
      180      185      190
Leu Glu Phe Asp Phe Ala Glu Pro Leu Ile Leu Ala Phe Pro Ile Ile
      195      200      205
Leu Tyr Thr Ala Ile Asp Asn Pro Pro Leu Val Arg Glu His Glu
210      215      220      223

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<210> 1536
<211> 133
<212> PRT
<213> Homo sapiens

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<400> 1536
Gly Pro Met Cys Asp Lys His Ser Ala Phe Ala Glu Lys Phe His Ala
 1      5      10      15
Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp Ala His
      20      25      30
Leu Ala Leu Pro Asp Ala Gln Asp Ile Leu Tyr Thr Leu Glu Asp Asn
      35      40      45
Arg Asn Trp Val Asp Ser Met Ile Pro Gln Ser Pro Ser Pro Pro Leu
      50      55      60
Asp Glu Gln Asn Arg Asp Trp Gln Gly Leu Leu Glu Asn Leu His Val
      65      70      75      80
Glu Leu Thr Leu Asp Glu Glu Asp Ser Glu Gly Pro Glu Lys Glu Gly
      85      90      95
Glu Gly Gln Thr Tyr Phe Thr Ser Ser Lys Thr Leu Cys Gly Ile Val
      100      105      110
Pro Gln Asn Thr Asp Ser Leu Gly Glu Thr Gly Ile His Ile Cys Ala
      115      120      125
His Asp Lys Ser Pro
130      133

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<210> 1537
<211> 71
<212> PRT
<213> Homo sapiens

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<400> 1537
Phe Asn Cys Phe Arg Val Ala Ser Asp Ser Phe Leu Glu Asn Ser Ser
 1      5      10      15
Leu Leu Ile Met Ile Leu Pro Leu Arg Asn Ala Thr Gln Glu Phe Ile
      20      25      30
Ile Arg Pro Gly Ala Val Ala Tyr Thr Cys Asn Pro Ser Thr Leu Gly
      35      40      45
Gly Trp Gly Gly Trp Ile Thr Arg Ser Gly Val Arg Asp Gln Pro Gly
      50      55      60
Gln His Gly Gly Thr Pro Ser
65      70      71

```

Val Phe Ala Ile Leu Pro Val Pro Val Ala Phe Ile Gly Arg Arg Phe
 145 150 155 160
 Ser Leu Ile Asp Asp Gly Ala Gly Pro Phe Cys Ser Ala Ala Tyr Thr
 165 170 175
 Thr Thr Gly Cys Arg Thr Pro Tyr Leu
 180 185

<210> 1534
 <211> 178
 <212> PRT
 <213> Homo sapiens

<400> 1534
 His Glu Leu Thr Val Ala Ala Ala Asp Arg Gly Gln Pro Pro Gln Ser
 1 5 10 15
 Ser Val Val Pro Val Thr Val Thr Val Leu Asp Val Asn Asp Asn Pro
 20 25 30
 Pro Val Phe Thr Arg Ala Ser Tyr Arg Val Thr Val Pro Glu Asp Thr
 35 40 45
 Pro Val Gly Ala Glu Leu Leu His Val Glu Ala Ser Asp Ala Asp Pro
 50 55 60
 Gly Pro His Gly Leu Val Arg Phe Thr Val Ser Ser Gly Asp Pro Ser
 65 70 75 80
 Gly Leu Phe Glu Leu Asp Glu Ser Ser Gly Thr Leu Arg Leu Ala His
 85 90 95
 Ala Leu Asp Cys Glu Thr Gln Ala Arg His Gln Leu Val Val Gln Ala
 100 105 110
 Ala Asp Pro Ala Gly Ala His Phe Ala Leu Ala Pro Val Thr Ile Glu
 115 120 125
 Val Gln Asp Val Asn Asp His Gly Pro Ala Phe Pro Leu Asn Leu Leu
 130 135 140
 Ser Thr Ser Val Ala Glu Asn Gln Pro Pro Gly Thr Leu Val Thr Thr
 145 150 155 160
 Leu His Ala Ile Asp Gly Asp Ala Gly Ala Phe Gly Arg Leu Arg Tyr
 165 170 175
 His Leu
 178

<210> 1535
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 1535
 Leu Asp Lys Leu Leu Asp Arg Met Glu Asn Tyr Asn Ile Phe Asn Glu
 1 5 10 15
 Tyr Ile Leu Lys Gln Val Ala Ala Thr Tyr Ile Lys Leu Gly Trp Pro
 20 25 30
 Lys Asn Asn Phe Asn Gly Ser Leu Val Gln Ala Ser Tyr Gln His Glu
 35 40 45
 Glu Leu Arg Arg Glu Val Ile Met Leu Ala Cys Ser Phe Gly Asn Lys
 50 55 60
 His Cys His Gln Gln Ala Ser Thr Leu Ile Ser Asp Trp Ile Ser Ser
 65 70 75 80
 Asn Arg Asn Arg Ile Pro Leu Asn Val Arg Asp Ile Val Tyr Cys Thr
 85 90 95
 Gly Val Ser Leu Leu Asp Glu Asp Val Trp Glu Phe Ile Trp Met Lys
 100 105 110

Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp Asn Gly Ser Ile Cys Ile
 115 120 125 128

<210> 1532
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 1532
 Arg Thr Lys Thr Asp Val Tyr Ile Leu Asn Leu Ala Val Ala Asp Leu
 1 5 10 15
 Leu Leu Leu Phe Thr Leu Pro Phe Trp Ala Val Asn Ala Val His Gly
 20 25 30
 Trp Val Leu Gly Lys Ile Met Cys Lys Ile Thr Ser Ala Leu Tyr Thr
 35 40 45
 Leu Asn Phe Val Ser Gly Met Gln Phe Leu Ala Cys Ile Ser Ile Asp
 50 55 60
 Arg Tyr Val Ala Val Thr Lys Val Pro Ser Gln Ser Gly Val Gly Lys
 65 70 75 80
 Pro Cys Trp Ile Ile Cys Phe Cys Val Trp Met Ala Ala Ile Leu Leu
 85 90 95
 Ser Ile Pro Gln Leu Val Phe Tyr Thr Val Asn Asp Asn Ala Arg Cys
 100 105 110
 Ile Pro Ile Phe Pro Arg Tyr Leu Gly Thr Ser Met Lys Ala Leu Ile
 115 120 125
 Gln Met Leu Glu Ile Cys Ile Gly Phe Val Val Pro Phe Leu Ile Met
 130 135 140
 Gly Val Cys Tyr Phe Ile Thr Ala Arg Thr Leu Met Lys Met Pro Asn
 145 150 155 160
 Ile Lys Ile Ser
 164

<210> 1533
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 1533
 Arg Gln Ala Trp His Glu Ala Phe Lys Val Arg Lys Glu Ile Leu Thr
 1 5 10 15
 Val Ile Cys Cys Leu Leu Ala Phe Cys Ile Gly Leu Ile Phe Val Gln
 20 25 30
 Arg Ser Gly Asn Tyr Phe Val Thr Met Phe Asp Asp Tyr Ser Ala Thr
 35 40 45
 Leu Pro Leu Leu Ile Val Val Ile Leu Glu Asn Ile Ala Val Cys Phe
 50 55 60
 Val Tyr Gly Ile Asp Lys Phe Met Glu Asp Leu Lys Asp Met Leu Gly
 65 70 75 80
 Phe Ala Pro Ser Arg Tyr Tyr Tyr Tyr Met Trp Lys Tyr Ile Ser Pro
 85 90 95
 Leu Met Leu Leu Ser Leu Leu Ile Ala Ser Val Val Asn Met Gly Leu
 100 105 110
 Ser Pro Pro Gly Tyr Asn Ala Trp Ile Glu Asp Lys Ala Ser Glu Glu
 115 120 125
 Phe Leu Ser Tyr Pro Thr Trp Gly Leu Ala Val Cys Ala Ser Leu Asp
 130 135 140

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Pro Thr Arg Ser Ser Thr Arg Pro Pro Ser Leu Phe Val His Ala Ser
 1           5           10           15
Ala Lys Gly Gly Glu Lys Glu Glu Gly Asp Asp Gly His Tyr Leu Met
          20           25           30
Arg Thr Glu Ser His Thr Gly Leu Lys Lys Gly Gly Asn Ala Asn Leu
      35           40           45
Val Phe Met Leu Lys Arg Asn Thr Glu Pro Lys Lys Gly Ser Tyr His
      50           55           60
Phe Asp Leu Glu Arg Leu Arg Ala Ala His Ile Leu Phe Glu Arg Glu
65           70           75           80
Gln Glu His Leu Ala Pro Gly Gly Ile Ser Met Pro Leu Pro Pro Pro
          85           90           95
Leu Pro Leu Pro Ala Cys Leu Gly
          100           104

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<210> 1530
 <211> 120
 <212> PRT
 <213> Homo sapiens

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<400> 1530
Thr Ser Ile Lys Arg Ala Ile Glu Thr Thr Asp Val Thr Arg Ser Phe
 1           5           10           15
Gly Trp Asp Ser Ser Glu Ala Trp Gln Gln His Asp Val Gln Glu Leu
          20           25           30
Cys Arg Val Met Phe Asp Ala Leu Glu Gln Lys Trp Lys Gln Thr Glu
      35           40           45
Gln Ala Asp Leu Ile Asn Glu Leu Tyr Gln Gly Lys Leu Lys Asp Tyr
      50           55           60
Val Arg Ser Leu Glu Cys Gly Tyr Glu Gly Trp Arg Ile Asp Thr Tyr
65           70           75           80
Leu Asp Ile Pro Leu Val Ile Arg Pro Tyr Gly Ser Ser Gln Ala Phe
          85           90           95
Ala Ser Val Val Cys Thr Phe His Leu Thr Ala Cys Val Ser Leu His
          100           105           110
Arg Ile His Asn Ser Thr Val Val
          115           120

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<210> 1531
 <211> 128
 <212> PRT
 <213> Homo sapiens

```

<400> 1531
Tyr Gly Leu Gly Ala His Phe Gly Arg Leu Phe Ile Gln Ala Gly Ile
 1           5           10           15
Asn Glu Asn Asp Phe Tyr Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp
          20           25           30
Leu Gln Gln Trp Ile Glu Val Asp Ala Arg Arg Leu Thr Arg Phe Thr
      35           40           45
Gly Val Ile Thr Gln Gly Arg Asn Ser Leu Trp Leu Ser Asp Trp Val
      50           55           60
Thr Ser Tyr Lys Val Met Val Ser Asn Asp Ser His Thr Trp Val Thr
65           70           75           80
Gly Lys Asn Gly Ser Gly Asp Met Ile Phe Glu Gly Asn Ser Glu Lys
          85           90           95
Glu Ile Pro Val Leu Asn Glu Leu Pro Val Pro Met Val Ala Arg Tyr
          100           105           110

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<210> 1527
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1527
 Gly Lys Gly Gln Val Ser Leu Glu Gly Arg Pro His Arg Gly Pro Leu
 1 5 10 15
 Cys Leu Gly Ser Trp Trp Pro Gly Ser Arg Val Pro Gly Cys Cys Asp
 20 25 30
 Gly Ala Trp Leu Ala Trp Ala Cys Trp Val Phe Gly Asn Asp Phe Pro
 35 40 45
 Ser Pro Ala Ser Ala Ala Cys Ser Ala Leu Leu Gly Cys Ser Val Ser
 50 55 60
 Thr Ala Cys Leu Cys Val Pro Leu Cys Ser Gly Ser Pro Leu Ala Pro
 65 70 75 80
 Phe Arg Arg Thr Ala Ala Leu Gln Glu Gly Leu Arg Arg Ala Val Ser
 85 90 95
 Val Pro Leu Thr Leu Ala Glu Thr Val Ala Ser Leu Trp Pro Ala Leu
 100 105 110
 Gln Glu Leu Ala Arg Cys Gly Asn Leu Ala Cys Arg Ser Asp Leu Gln
 115 120 125 128

<210> 1528
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 1528
 Ala Leu Gln Ser Thr Leu Gly Ala Val Trp Leu Gly Leu Leu Leu Asn
 1 5 10 15
 Ser Leu Trp Lys Val Ala Glu Ser Lys Asp Gln Val Phe Gln Pro Ser
 20 25 30
 Thr Ala Ala Ser Ser Glu Gly Ala Val Val Glu Ile Phe Cys Asn His
 35 40 45
 Ser Val Ser Asn Ala Tyr Asn Phe Phe Trp Tyr Leu His Phe Pro Gly
 50 55 60
 Cys Ala Pro Arg Leu Leu Val Lys Gly Ser Lys Pro Ser Gln Gln Gly
 65 70 75 80
 Arg Tyr Asn Met Thr Tyr Glu Arg Phe Ser Ser Ser Leu Leu Ile Leu
 85 90 95
 Gln Val Arg Glu Ala Asp Ala Ala Val Tyr Tyr Cys Ala Val Glu Val
 100 105 110
 Pro Asn Thr Asp Lys Leu Ile Phe Gly Thr Gly Thr Arg Leu Gln Val
 115 120 125
 Phe Pro Asn Ile Gln Asn Pro Asp
 130 135 136

<210> 1529
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1529

<210> 1525
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 1525
 Ala Ala Leu Thr Trp Ser Gln Pro Gln Glu Phe Trp Pro Met Glu Met
 1 5 10 15
 Gln Pro Ile Val Thr Asp Met Val Thr Val His Trp Val Ala Glu Ser
 20 25 30
 Ser Thr Val Gly Trp Leu Cys Ala Leu Phe Arg Val Thr His Val Gly
 35 40 45
 Val Gly Ala Thr Gly His Gly Val Val Cys Gly Arg Arg Val Leu Cys
 50 55 60
 Gly Leu Pro Leu Pro Ser Pro Ala Pro Met Pro Ile Met Ser Leu Pro
 65 70 75 80
 Glu Gly Glu Ser Arg Lys Glu Arg Glu Val Gln Arg Leu Gln Phe Pro
 85 90 95
 Tyr Leu Glu Pro Gly His Glu Leu Pro Ala Thr Thr Leu Leu Ala Phe
 100 105 110
 Leu Ala Ala Val
 115 116

<210> 1526
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 1526
 Glu Gly Ser Val Asn Phe Lys Phe Gly Val Leu Phe Ala Lys Asp Gly
 1 5 10 15
 Gln Leu Thr Asp Asp Glu Met Phe Ser Asn Glu Ile Gly Ser Glu Pro
 20 25 30
 Phe Gln Lys Phe Leu Asn Leu Leu Gly Asp Thr Ile Thr Leu Lys Gly
 35 40 45
 Trp Thr Gly Tyr Arg Gly Gly Leu Asp Thr Lys Asn Asp Thr Thr Gly
 50 55 60
 Ile His Ser Val Tyr Thr Val Tyr Gln Gly His Glu Ile Met Phe His
 65 70 75 80
 Val Ser Thr Met Leu Pro Tyr Ser Lys Glu Asn Lys Gln Gln Val Glu
 85 90 95
 Arg Lys Arg His Ile Gly Asn Asp Ile Val Thr Ile Val Phe Gln Glu
 100 105 110
 Gly Glu Glu Ser Ser Pro Ala Phe Lys Pro Ser Met Ile Arg Ser His
 115 120 125
 Phe Thr His Ile Phe Ala Leu Val Arg Tyr Asn Gln Gln Asn Asp Asn
 130 135 140
 Tyr Arg Leu Lys Ile Phe Ser Glu Glu Ser Val Pro Leu Phe Gly Pro
 145 150 155 160
 Pro Leu Pro Thr Pro Pro Val Phe Thr Asp His Gln Glu Phe Arg Asp
 165 170 175
 Phe Leu Leu Val Lys Leu Ile Asn Gly Glu Lys Ala Thr Leu Glu Thr
 180 185 190
 Pro Cys Ile
 195

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Arg Pro Val Arg Asp Arg Ile Leu Lys Glu Arg Ala Leu Lys Ile Lys
  50          55          60
Glu Glu Arg Ser Gly Leu Thr Thr Asp Asp Asp Thr Met Ser Glu Met
  65          70          75          80
Lys Met Gly Arg Tyr Trp Ser Lys Glu Glu Arg Lys Gln His Leu Val
          85          90          95
Arg Gly Lys Glu Gln Arg Arg Arg Arg Glu Phe Met Met Arg Ile Arg
          100          105          110
Leu Lys Cys Leu Lys Glu Ser
          115          119

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<210> 1523
<211> 129
<212> PRT
<213> Homo sapiens

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<400> 1523
Gly Thr Arg Ile Leu Ser Met Gln Ile Pro Phe Val Gly Phe Gln Pro
  1          5          10          15
Ile Arg Thr Ser Glu His Met Ala Ala Ala Gly Val Phe Ala Leu Leu
          20          25          30
Gln Ala Tyr Ala Phe Leu Gln Tyr Leu Arg Asp Arg Leu Thr Lys Gln
          35          40          45
Glu Phe Gln Thr Leu Phe Phe Leu Gly Val Ser Leu Ala Ala Gly Ala
          50          55          60
Val Phe Leu Ser Val Ile Tyr Leu Thr Tyr Thr Gly Tyr Ile Ala Pro
          65          70          75          80
Trp Ser Gly Arg Phe Tyr Ser Leu Trp Asp Thr Gly Tyr Ala Lys Ile
          85          90          95
His Ile Pro Ile Ile Ala Ser Val Ser Glu His Gln Pro Thr Thr Trp
          100          105          110
Val Ser Phe Phe Phe Asp Leu His Ile Leu Gly Cys Thr Phe Pro Ala
          115          120          125
Gly
129

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<210> 1524
<211> 123
<212> PRT
<213> Homo sapiens

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<400> 1524
Leu Leu Met Gly Pro Lys Ala Lys Lys Ser Gly Ser Lys Lys Lys Lys
  1          5          10          15
Val Thr Lys Ala Glu Arg Leu Lys Leu Leu Gln Glu Glu Glu Glu Arg
          20          25          30
Arg Leu Lys Glu Glu Glu Glu Ala Arg Leu Lys Tyr Glu Lys Glu Glu
          35          40          45
Met Glu Arg Leu Glu Ile Gln Arg Ile Glu Lys Glu Lys Trp His Arg
          50          55          60
Leu Glu Ala Lys Asp Leu Glu Arg Arg Asn Glu Glu Leu Glu Glu Leu
          65          70          75          80
Tyr Leu Leu Glu Arg Cys Phe Pro Glu Ala Glu Lys Leu Lys Gln Glu
          85          90          95
Thr Lys Leu Leu Ser Gln Trp Lys His Tyr Ile Gln Cys Asp Gly Ser
          100          105          110
Pro Asp Pro Ser Val Ala Gln Glu Met Asn Thr
          115          120          123

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Val Val Ile Ser Ser Ala Lys Thr Leu Cys Glu Thr Val Lys Asp Phe
      20      25      30
Val Ala Lys Val Glu Lys Thr Tyr Asp Lys Thr Leu Glu Asn Ala Val
      35      40      45
Val Ala Asp Ala Val Ala Ser Lys Cys Ser Val Leu Asn Glu Lys Leu
      50      55      60
Glu Gln Leu Leu Gln Ala Leu His Thr Asp Ser Gln Ala Ala Pro Val
      65      70      75      80
Leu Pro Gly Leu Ser Pro Leu Ile Val Glu Glu Asp Ala Val Glu Ser
      85      90      95
Ser Ser Glu Glu Ser Leu Gly Glu Ser Lys Glu Gln Leu Gly Asp Asp
      100      105      110
Val Thr Lys Pro Ser Ser Gln Lys Ala
      115      120 121

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<210> 1521
<211> 179
<212> PRT
<213> Homo sapiens

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<400> 1521
Ile Pro Ser Arg Pro Trp Leu Gly Arg Ile Thr Gly Leu Asp Pro Ala
  1      5      10      15
Gly Pro Leu Phe Asn Gly Lys Pro His Gln Asp Arg Leu Asp Pro Ser
      20      25      30
Asp Ala Gln Phe Val Asp Val Ile His Ser Asp Thr Asp Ala Leu Gly
      35      40      45
Tyr Lys Glu Pro Leu Gly Asn Ile Asp Phe Tyr Pro Asn Gly Gly Leu
      50      55      60
Asp Gln Pro Gly Cys Pro Lys Thr Ile Leu Gly Gly Phe Gln Tyr Phe
      65      70      75      80
Lys Cys Asp His Gln Arg Ser Val Tyr Leu Tyr Leu Ser Ser Leu Arg
      85      90      95
Glu Ser Cys Thr Ile Thr Ala Tyr Pro Cys Asp Ser Tyr Gln Asp Tyr
      100      105      110
Arg Asn Gly Lys Cys Val Ser Cys Gly Thr Ser Gln Lys Glu Ser Cys
      115      120      125
Pro Leu Leu Gly Tyr Tyr Ala Asp Asn Trp Lys Asp His Leu Arg Gly
      130      135      140
Lys Asp Pro Pro Met Thr Lys Ala Phe Phe Asp Thr Ala Glu Glu Ser
      145      150      155      160
Pro Phe Cys Met Tyr His Tyr Phe Val Asp Ile Ile Thr Trp Asn Lys
      165      170      175
Asn Val Arg
      179

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<210> 1522
<211> 119
<212> PRT
<213> Homo sapiens

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<400> 1522
Leu Ile Gln His Lys Ser Ala Val Glu Tyr Ala Gln Ser His Leu Ser
  1      5      10      15
Leu Val Ser Met Cys Lys Glu Ser His Lys Cys Ser Glu Pro Lys Met
      20      25      30
Glu Trp Lys Val Lys Ile Arg Ser Asp Gly Thr Arg Tyr Ile Thr Lys
      35      40      45

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Phe Gln Gly Gln Asp Gln Val Leu Arg
 115 120 121

<210> 1519
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 1519
 Gln Asn Leu Glu Asp Arg Glu Val Leu Asn Gly Val Gln Thr Glu Leu
 1 5 10 15
 Leu Thr Ser Pro Arg Thr Lys Asp Thr Leu Ser Asp Met Thr Arg Thr
 20 25 30
 Val Glu Ile Ser Gly Glu Gly Gly Pro Leu Gly Ile His Val Val Pro
 35 40 45
 Phe Phe Ser Ser Leu Ser Gly Arg Ile Leu Gly Leu Phe Ile Arg Gly
 50 55 60
 Ile Glu Asp Asn Ser Arg Ser Lys Arg Glu Gly Leu Phe His Glu Asn
 65 70 75 80
 Glu Cys Ile Val Lys Ile Asn Asn Val Asp Leu Val Asp Lys Thr Phe
 85 90 95
 Ala Gln Ala Gln Asp Val Phe Arg Gln Ala Met Lys Ser Pro Ser Val
 100 105 110
 Leu Leu His Val Leu Pro Pro Gln Asn Arg Glu Gln Tyr Glu Lys Ser
 115 120 125
 Val Ile Gly Ser Leu Asn Ile Phe Gly Asn Asn Asp Gly Val Leu Lys
 130 135 140
 Thr Lys Val Pro Pro Pro Val His Gly Lys Ser Gly Leu Lys Thr Ala
 145 150 155 160
 Asn Leu Thr Gly Thr Asp Ser Pro Glu Thr Asp Ala Ser Ala Ser Leu
 165 170 175
 Gln Gln Asn Lys Ser Pro Arg Val Pro Arg Leu Gly Gly Lys Pro Ser
 180 185 190
 Ser Pro Ser Leu Ser Pro Leu Met Gly Phe Gly Ser Asn Lys Asn Ala
 195 200 205
 Lys Lys Ile Lys Ile Asp Leu Lys Lys Gly Pro Glu Gly Leu Gly Phe
 210 215 220
 Thr Val Val Thr Arg Asp Ser Ser Ile His Gly Pro Gly Pro Ile Phe
 225 230 235 240
 Val Lys Asn Ile Leu Pro Lys Gly Ala Ala Ile Lys Asp Gly Arg Leu
 245 250 255
 Gln Ser Gly Asp Arg Ile Leu Glu Val Asn Gly Arg Asp Val Thr Gly
 260 265 270
 Arg Thr Gln Glu Glu Leu Val Ala Met Leu Arg Ser Thr Lys Gln Gly
 275 280 285
 Glu Thr Ala Ser Leu Val Ile Ala Arg Gln Glu Gly His Phe Leu Pro
 290 295 300
 Arg Glu Leu Val Met Phe Arg Ser Gln Ser His
 305 310 315

<210> 1520
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1520
 Pro Val Ala Thr His Leu Thr Lys Ile Leu Asn Ser Asp Glu His Ala
 1 5 10 15

Thr Asp Leu Pro
305 308

<210> 1517
<211> 208
<212> PRT
<213> Homo sapiens

<400> 1517
Ala Ala Ala Ser Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg Leu
1 5 10 15
Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly Ala
20 25 30
Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr Ser
35 40 45
Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro Trp
50 55 60
Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His Ala
65 70 75 80
Glu Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr Gly
85 90 95
Arg Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val Thr
100 105 110
Ser Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly
115 120 125
Glu Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe
130 135 140
Thr Leu Leu Gly Lys Pro Leu Leu Gly Lys Asp Leu Val Arg Val Glu
145 150 155 160
Ala Thr Val Ile Glu Lys Thr Glu Ser Trp Pro Arg Ile Ile Met Arg
165 170 175
Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ile Val Thr Thr Pro
180 185 190
Gln Thr Val Leu Arg Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu Leu
195 200 205 208

<210> 1518
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1518
His Leu Gln Val Ala Ala Arg Val Phe Met Pro Leu Gln Ala Val Asp
1 5 10 15
Ser Ala Pro Lys Pro Leu Lys Gly Gln Ala Gln Ala Pro Gln Arg Leu
20 25 30
Gln Gly Ala Ala Arg Val Phe Met Pro Leu Gln Ala Gln Val Lys Ala
35 40 45
Lys Ala Ser Lys Pro Leu Gln Met Gln Ile Lys Ala Pro Pro Arg Leu
50 55 60
Arg Arg Ala Ala Arg Val Leu Met Pro Leu Gln Ala Gln Val Arg Ala
65 70 75 80
Pro Arg Leu Leu Gln Val Gln Ser Gln Val Ser Lys Lys Gln Gln Ala
85 90 95
Gln Thr Gln Thr Ser Glu Pro Gln Asp Leu Asp Gln Val Pro Glu Glu
100 105 110

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Phe Ser Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro Ala Asn
      20      25      30
Tyr Asn Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala Ala Phe
      35      40      45
Ala Ile Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala Met Met
      50      55      60
Gly Asp Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu Trp Arg
      65      70      75      80
Ala Gln Ile Val Ala Thr Thr Val Met Leu Glu Arg Lys Leu Pro Arg
      85      90      95
Cys Leu Trp Pro Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly
      100      105      110
Asp Arg Trp Ile Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln
      115      120      125
Arg Ile Gln Arg Tyr Ala
      130      134

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<210> 1516
<211> 308
<212> PRT
<213> Homo sapiens

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<400> 1516
Cys Cys Gln Arg Glu Gly Leu Gly Leu Lys Ala Val Val Gln Ile Leu
 1      5      10      15
Leu Ser His Gly Arg Asn Gly Leu Pro Gly Glu Pro Ala Ser Ser Gln
      20      25      30
Gly Leu Ser Ala Ala Ser Ser Thr Pro Val Phe His Leu Ala Leu Gln
      35      40      45
Ile Asp Ser Ala Pro Asp Asn Ile Asp Trp Val Glu Met Leu Phe Asn
      50      55      60
Lys Asn Met Val Thr Glu Arg Leu Gln Asn Val Met Val Leu Glu Gln
      65      70      75      80
Cys Phe Ser Asp Ser Ser Ser Leu Tyr Arg Phe Leu Thr Tyr Ser Tyr
      85      90      95
Leu Leu Ala Phe Asn Val Trp Leu Leu Leu Ala Pro Val Thr Leu Cys
      100      105      110
Tyr Asp Trp Gln Val Gly Ser Ile Pro Leu Val Glu Thr Ile Trp Asp
      115      120      125
Met Arg Asn Leu Ala Thr Ile Phe Leu Ala Val Val Met Ala Leu Leu
      130      135      140
Ser Leu His Cys Leu Ala Ala Phe Lys Arg Leu Glu His Lys Glu Val
      145      150      155      160
Leu Val Gly Leu Leu Phe Leu Val Phe Pro Phe Ile Pro Ala Ser Asn
      165      170      175
Leu Phe Phe Arg Val Gly Phe Val Val Ala Glu Arg Val Leu Tyr Met
      180      185      190
Pro Ser Met Gly Tyr Cys Ile Leu Phe Val His Gly Leu Ser Lys Leu
      195      200      205
Cys Thr Trp Leu Asn Arg Cys Gly Ala Thr Thr Leu Ile Val Ser Thr
      210      215      220
Val Leu Leu Leu Leu Leu Phe Ser Trp Lys Thr Val Lys Gln Asn Glu
      225      230      235      240
Ile Trp Leu Ser Arg Glu Ser Leu Phe Arg Ser Gly Val Gln Thr Leu
      245      250      255
Pro His Asn Ala Lys Val His Tyr Asn Tyr Ala Asn Phe Leu Lys Asp
      260      265      270
Gln Gly Arg Asn Lys Glu Ala Ile Tyr His Tyr Arg Thr Ala Leu Asn
      275      280      285
Asn Asn Lys Ala Trp Asp Tyr Leu Cys Trp Arg Phe Arg Lys Thr Leu
      290      295      300

```

Ser Phe Ser Gly Ser Ser Asn Phe Gly Glu Gly Ser Gly Pro Ile Trp
 65 70 75 80
 Phe Asp Asp Leu Ile Cys Asn Gly Asn Glu Ser Ala Leu Trp Asn Cys
 85 90 95
 Lys His Gln Gly Trp Gly Lys His Asn Cys Asp His Ala Glu Asp Ala
 100 105 110
 Gly Val Ile Cys Ser Ser Lys Asp
 115 120

<210> 1513
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 1513
 Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr Thr
 1 5 10 15
 Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly Asp
 20 25 30
 Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg Cys
 35 40 45
 Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu Phe
 50 55 60
 Gly Asp Ile Ile Asn Leu Ser Thr Phe Val Val His Ser
 65 70 75 77

<210> 1514
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1514
 Ser Leu Leu Cys Leu Phe Pro Gly Thr Ser Thr Val Val Cys Lys Pro
 1 5 10 15
 Ile Val Ile Glu Thr Gln Leu Tyr Val Ile Val Ala Gln Leu Phe Gly
 20 25 30
 Gly Ser His Ile Tyr Lys Arg Asp Ser Phe Ala Asn Lys Phe Ile Lys
 35 40 45
 Ile Gln Ala Ile Glu Ile Leu Lys Ile Arg Lys Pro Asn Asp Ile Glu
 50 55 60
 Thr Phe Lys Ile Glu Asn Asn Trp Tyr Phe Val Val Ala Asp Ser Ser
 65 70 75 80
 Lys Ala Gly Phe Thr Thr Ile Tyr Lys Trp Glu Arg Glu Thr Gly Phe
 85 90 95
 Tyr Ser His Gln Ser Phe Thr Arg
 100 104

<210> 1515
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1515
 Glu Asp Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met Ala Leu
 1 5 10 15

Ala Tyr Glu Ala Met Lys Asn Val Ala Cys Leu Ile Asn Glu Arg Lys
 115 120 125
 Arg Lys Leu Glu Ser Ile Asp Lys Ile Ala
 130 135 138

<210> 1511
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 1511
 Arg Glu Thr Gly Ser Val Ser Leu Ser Pro Ser Gly Leu Glu Gly Ala
 1 5 10 15
 Glu Ser Tyr Ala Val Ser Pro Ile Leu Tyr Ser Ser Pro Asp Val Lys
 20 25 30
 Glu Leu Trp Leu Glu Thr Leu Gln Gly Gln Arg His Ser His Thr Gly
 35 40 45
 Val Lys Ser Thr Pro Gly Gln Ser Ala Ala Ile Leu Met Lys Leu Arg
 50 55 60
 Ser Ser His Asn Ala Ser Lys Thr Leu Asn Ala Asn Asn Met Glu Thr
 65 70 75 80
 Leu Ile Glu Cys Gln Ser Glu Gly Asp Ile Lys Glu His Pro Leu Leu
 85 90 95
 Ala Ser Cys Glu Ser Glu Asp Ser Ile Cys Gln Leu Ile Glu Val Lys
 100 105 110
 Lys Arg Lys Lys Val Leu Ser Trp Pro Phe Leu Met Arg Arg Leu Ser
 115 120 125
 Pro Ala Ser Asp Phe Ser Gly Ala Leu Glu Thr Asp Leu Lys Ala Ser
 130 135 140
 Leu Phe Asp Gln Pro Leu Ser Ile Ile Cys Gly Asp Ser Asp Thr Leu
 145 150 155 160
 Pro Arg Pro Ile Gln Asp Ile Leu Thr Ile Leu Cys Leu Lys Gly Pro
 165 170 175
 Ser Thr Glu Gly Ile Phe Arg Arg Ala Ala Asn Glu Lys Ala Arg Lys
 180 185 190
 Glu Leu Lys Glu Glu Leu Asn Ser Gly Asp Ala Val Asp Leu Glu Arg
 195 200 205
 Leu Pro Val His Leu Leu Ala Val Val Phe Lys Asp Phe Leu Arg Ser
 210 215 220
 Ile Pro Arg Lys Leu Leu Ser Ser Asp Leu Phe Glu Glu Trp Met Gly
 225 230 235 240
 Ala Leu Glu Met Gln Asp Glu Glu Asp Arg Ile Glu Ala Leu Lys
 245 250 255

<210> 1512
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1512
 Leu Leu Asn Ser Gly Leu Phe Ser Ala Pro Asp Gly Ser Asn Leu Glu
 1 5 10 15
 Met Arg Leu Thr Arg Gly Gly Asn Met Cys Ser Gly Arg Ile Glu Ile
 20 25 30
 Lys Phe Gln Gly Arg Trp Gly Thr Val Cys Asp Asp Asn Phe Asn Ile
 35 40 45
 Asp His Ala Ser Val Ile Cys Arg Gln Leu Glu Cys Gly Ser Ala Val
 50 55 60

Cys Leu Val Tyr Gly Phe Leu Pro Tyr Gly Ser Leu Glu Asp Arg Leu
 50 55 60
 His Cys Gln Thr Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu
 65 70 75 80
 Asp Ile Leu Leu Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp
 85 90 95
 Ser Pro Ser Leu Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu
 100 105 110
 Asp Glu Arg Leu Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe
 115 120 125
 Ser Arg Phe Ala Gly Ser Ser Pro Ile Gln Ser Ser Met
 130 135 140 141

<210> 1509
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 1509
 His Thr Ser Thr Ala Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu
 1 5 10 15
 Ala Val Thr Ser Asp Gly Tyr Thr Ala Leu His Leu Ala Ala Arg Asn
 20 25 30
 Gly His Leu Ala Thr Val Lys Leu Leu Val Glu Glu Lys Ala Asp Val
 35 40 45
 Leu Ala Arg Gly Pro Leu Asn Gln Thr Ala Leu His Leu Ala Ala Ala
 50 55 60
 His Gly His Ser Glu Val Val Glu Glu Leu Val Ser Ala Asp Val Ile
 65 70 75 80
 Asp Leu Phe Asp Glu Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln
 85 90 95
 Gly Arg His Ala Gln Thr Val Glu Thr Leu Leu Arg His Gly Ala His
 100 105 110
 Ile Asn Leu Gln Ser Leu Lys Phe Gln Gly Gly His Gly Pro Ala Ala
 115 120 125
 Thr Leu Leu Arg
 130 132

<210> 1510
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 1510
 Lys Phe Leu Lys Asp Leu Glu Lys Gln Tyr Asn Lys Glu Glu Pro His
 1 5 10 15
 Leu Ser Glu Ile Gly Ser Cys Phe Leu Gln Asn Gln Glu Gly Phe Ala
 20 25 30
 Ile Tyr Ser Glu Tyr Cys Asn Asn His Pro Gly Ala Cys Leu Glu Leu
 35 40 45
 Ala Asn Leu Met Lys Gln Gly Lys Tyr Arg His Phe Phe Glu Ala Cys
 50 55 60
 Arg Leu Leu Gln Gln Met Ile Asp Ile Ala Ile Asp Gly Phe Leu Leu
 65 70 75 80
 Thr Pro Val Gln Lys Ile Cys Lys Tyr Pro Leu Gln Leu Ala Glu Leu
 85 90 95
 Leu Lys Tyr Thr Thr Gln Glu His Gly Asp Tyr Ser Asn Ile Lys Ala
 100 105 110

Tyr Ile Ile Arg Thr Tyr Arg Leu Ile Glu Asp Asp Arg Ile Asn Ile
 100 105 110
 Gln Ile Ser Gly His Trp Gln Glu Ser Pro
 115 120 122

<210> 1506
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 1506
 Val Thr Arg Lys Leu Pro Ile Phe Ile Val Asp Ala Phe Thr Ala Arg
 1 5 10 15
 Ala Phe Arg Gly Ser Pro Ala Ala Asp Cys Leu Leu Glu Asn Glu Leu
 20 25 30
 Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser Glu
 35 40 45
 Thr Ala Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln Arg
 50 55 60
 Ser Cys Phe Gly Leu Ile Trp Phe Thr Pro Thr Thr Asp Leu Gln Ile
 65 70 75 80
 Leu Thr Ser Ser Ile Leu Pro Ser Ile Leu
 85 90

<210> 1507
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 1507
 Glu Ser Lys Val Asn Asn Glu Lys Phe Arg Thr Lys Ser Pro Lys Pro
 1 5 10 15
 Ala Glu Ser Pro Gln Ser Ala Thr Lys Gln Leu Asp Gln Pro Thr Ala
 20 25 30
 Ala Tyr Glu Tyr Tyr Asp Ala Gly Asn His Trp Cys Lys Asp Cys Asn
 35 40 45
 Thr Ile Cys Gly Thr Met Phe Asp Phe Phe Thr His Met His Asn Lys
 50 55 60
 Lys His Thr Gln Gly Gln Phe Gln Lys Ser Ser Asp Phe Gln Lys Glu
 65 70 75 80
 Glu Leu Gln Gln Thr Phe Leu Pro Pro Glu Arg Gln Gly
 85 90 93

<210> 1508
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 1508
 Thr Thr His Arg Leu Asn Val Thr Ala Glu Pro Pro Cys Thr Ser Met
 1 5 10 15
 Pro Ile Tyr Trp Met Pro Asp Val Pro His Arg Cys Thr Thr Ala Asn
 20 25 30
 Thr Cys Pro Val Asp Leu Thr Asp Tyr Cys Ala Gln Asn Gly Phe Tyr
 35 40 45

<211> 79
 <212> PRT
 <213> Homo sapiens

<400> 1503
 Ala Tyr Gln Ser Leu Arg Leu Glu Tyr Leu Gln Ile Pro Pro Val Ser
 1 5 10 15
 Arg Ala Tyr Thr Thr Ala Cys Val Leu Thr Ser Ala Ala Val Gln Leu
 20 25 30
 Glu Leu Ile Thr Pro Phe Gln Leu Tyr Phe Ile Pro Glu Leu Ile Phe
 35 40 45
 Lys His Phe Gln Ile Trp Arg Leu Ile Thr Asn Phe Leu Phe Phe Val
 50 55 60
 Pro Phe Gly Phe Asn Phe Leu Leu Tyr Met Ile Phe Leu Tyr Thr
 65 70 75 79

<210> 1504
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1504
 Glu Met Val Glu Gly Gly Glu Gly Lys Met Cys Ile Asn Thr Glu Trp
 1 5 10 15
 Gly Gly Phe Gly Asp Asn Gly Cys Ile Asp Asp Ile Arg Thr Arg Tyr
 20 25 30
 Asp Thr Glu Val Asp Glu Gly Ser Leu Asn Pro Gly Lys Gln Arg Tyr
 35 40 45
 Glu Lys Met Thr Ser Gly Met Tyr Leu Gly Glu Ile Val Arg Gln Ile
 50 55 60
 Leu Ile Asp Leu Thr Lys Gln Gly Leu Leu Phe Arg Gly Gln Ile Ser
 65 70 75 80
 Glu Arg Leu Arg Thr Arg Gly Ile Phe Glu Thr Lys Phe Leu Ser Gln
 85 90 95
 Ile Glu Ser Asp Arg Leu Ala Leu Leu Gln Val Arg Arg Ile Leu Gln
 100 105 110
 Gln Leu Gly Leu Asp
 115 117

<210> 1505
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1505
 Thr Glu Ile Ala Lys Ile Lys Met Glu Ala Lys Lys Lys Tyr Glu Lys
 1 5 10 15
 Glu Leu Thr Met Phe Gln Asn Asp Phe Glu Lys Ala Cys Gln Ala Lys
 20 25 30
 Ser Glu Ala Leu Val Leu Arg Glu Lys Ser Thr Leu Glu Arg Ile His
 35 40 45
 Lys His Gln Glu Ile Glu Thr Lys Glu Ile Tyr Ala Gln Arg Gln Leu
 50 55 60
 Leu Leu Lys Asp Met Asp Leu Leu Arg Gly Arg Glu Ala Glu Leu Lys
 65 70 75 80
 Gln Arg Val Glu Ala Phe Glu Ser Tyr Gln Leu Glu Leu Lys Asp Asp
 85 90 95

<211> 214
 <212> PRT
 <213> Homo sapiens

<400> 1501

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Gly Lys Thr Ile Gln Ile Gln Thr Thr Met Gln Asn Lys Tyr Lys Thr
 1           5           10           15
Val Gln Lys Gln Tyr Lys Thr Ile Pro Lys Asn Lys Lys Ala Met Glu
      20           25           30
Met Gln Ile Lys Lys Gln Phe Gln Asp Thr Cys Lys Val Gln Thr Lys
      35           40           45
Gln Tyr Lys Ala Leu Lys Asn His Gln Leu Glu Val Thr Pro Lys Asn
      50           55           60
Glu His Lys Thr Ile Leu Lys Thr Leu Lys Asp Glu Gln Thr Arg Lys
      65           70           75           80
Leu Ala Ile Leu Ala Glu Gln Tyr Glu Gln Ser Ile Asn Glu Met Met
      85           90           95
Ala Ser Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln
      100          105          110
Ala Leu Arg Leu Gln Leu Gln Gln Glu Met Glu Leu Leu Asn Ala Tyr
      115          120          125
Gln Ser Lys Ile Lys Met Gln Thr Glu Ala Gln His Glu Arg Glu Leu
      130          135          140
Gln Lys Leu Glu Gln Arg Val Ser Leu Arg Arg Ala His Leu Glu Gln
      145          150          155          160
Lys Ile Glu Glu Glu Leu Ala Ala Leu Gln Lys Glu Arg Ser Glu Arg
      165          170          175
Ile Lys Asn Leu Leu Glu Arg Gln Glu Arg Glu Ile Glu Thr Phe Asp
      180          185          190
Met Glu Ser Leu Arg Met Gly Phe Gly Asn Leu Val Thr Leu Asp Phe
      195          200          205
Pro Lys Glu Asp Tyr Arg
      210          214

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<210> 1502
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1502

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Leu Val Arg Leu Leu Asp Thr Gln Arg Asp Gly Leu Gln Asn Tyr Glu
 1           5           10           15
Ala Leu Leu Gly Leu Thr Asn Leu Ser Gly Arg Ser Asp Lys Leu Arg
      20           25           30
Gln Lys Ile Phe Lys Glu Arg Ala Leu Pro Asp Ile Glu Asn Tyr Met
      35           40           45
Phe Glu Asn His Asp Gln Leu Arg Gln Ala Ala Thr Glu Cys Met Cys
      50           55           60
Asn Met Val Leu His Lys Glu Val Gln Glu Arg Phe Leu Ala Asp Gly
      65           70           75           80
Asn Asp Arg Leu Lys Leu Val Val Leu Leu Cys Gly Glu Asp Asp Asp
      85           90           95
Lys Val Gln Asn Ala Ala Ala Gly Ala Leu Ala Met Leu Thr Ala Ala
      100          105          110
His Lys Lys Leu Cys Leu Lys Met Thr Gln Val Thr Thr
      115          120          125

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<210> 1503

Gln Val Ile Ser Gly Glu Glu Glu Ala Arg Leu Ile Tyr Gln Gly Val
 65 70 75 80
 Ala His Thr Thr Gly Gly Ala Asp Gln Arg Leu Val Val Asp Ile Gly
 85 90 95
 Gly Ala Ser Thr Glu Leu Val Thr Gly Thr Gly Ala Gln Thr Thr Xaa
 100 105 110
 Leu Phe Ser Leu Ser Met Gly Cys Val Thr Trp Leu Glu Arg Tyr Phe
 115 120 125
 Ala Asp Arg Asn Leu Gly Gln Glu Asn Phe Asp Ala Ala Gln Lys Ala
 130 135 140
 Ala Arg Glu Val Leu Arg Pro Val Ala Asp Glu Leu Arg Tyr His Ser
 145 150 155 160
 Trp Lys Glu Val Arg Gly Ala Ser Val Thr Val Gln Ala Leu Gln Glu
 165 170 175
 Ile Met Met Ala Gln Gly Met Asp Glu Arg Ile Thr Met Glu Ile Trp
 180 185 190
 Pro Val Asp
 195

<210> 1500
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 1500
 Gly Arg Val Asp Phe Phe His Thr Asp Tyr Arg Pro Leu Ile Arg Asp
 1 5 10 15
 Ser Asn Asn Tyr Val Leu Asp Glu Gln Thr Gln Gln Ala Pro His Leu
 20 25 30
 Met Pro Pro Pro Phe Leu Val Asp Val Asp Gly Asn Pro His Pro Thr
 35 40 45
 Lys Tyr Gln Arg Leu Val Pro Gly Arg Glu Asn Ser Ala Asp Glu His
 50 55 60
 Leu Ile Pro Gln Leu Gly Tyr Val Ala Thr Ser Asp Gly Glu Val Ile
 65 70 75 80
 Glu Gln Ile Ile Ser Leu Gln Thr Asn Asp Asn Asp Glu Arg Ser Pro
 85 90 95
 Glu Ser Ser Ile Leu Asp Gly Met Ile Arg Gln Leu Gln Gln Gln
 100 105 110
 Asp Gln Arg Met Gly Ala Asp Gln Asp Thr Ile Pro Arg Gly Leu Ser
 115 120 125
 Asn Gly Glu Glu Thr Pro Arg Arg Gly Phe Arg Arg Leu Ser Leu Asp
 130 135 140
 Ile Gln Ser Pro Pro Asn Ile Gly Leu Arg Arg Ser Gly Gln Val Glu
 145 150 155 160
 Gly Val Arg Gln Met His Gln Asn Ala Pro Arg Ser Gln Ile Ala Thr
 165 170 175
 Glu Arg Asp Leu Gln Ala Trp Lys Arg Arg Val Val Val Pro Glu Val
 180 185 190
 Pro Leu Gly Ile Phe Arg Lys Leu Glu Asp Phe Arg Leu Glu Lys Gly
 195 200 205
 Glu Glu Glu Arg Asn Leu Tyr Ile Ile Gly Arg Lys Arg Lys Thr Leu
 210 215 220
 Gln Leu Ser His Lys Ser Asp Ser Val Gly Leu Val Ser Gln Ser Arg
 225 230 235 240
 Pro Arg Thr Cys Arg Arg Lys Tyr Pro
 245 249

<210> 1501

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Leu Leu Arg Ser Asp Thr Val Arg Lys Phe Met Val Gly Ser Gln Met
      100      105      110
Leu Ala Gln Ala Gln Arg Asp Leu Thr Pro Glu Gln
      115      120      124

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<210> 1498
<211> 187
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(187)
<223> Xaa = any amino acid or nothing

```

```

<400> 1498
Leu Leu Ser Ala Leu Asp Asp Lys Gly Gly Thr Gln Pro Ser Ala Ser
 1      5      10      15
Phe Ser Asn Ala Pro Thr Ile Val Cys Val Thr Ala Cys Pro Ala Gly
      20      25      30
Ile Ala His Thr Tyr Met Ala Ala Glu Tyr Leu Glu Lys Ala Gly Arg
      35      40      45
Lys Leu Gly Val Asn Val Tyr Val Glu Lys Gln Gly Ala Asn Gly Ile
      50      55      60
Glu Gly Arg Leu Thr Ala Asp Gln Leu Asn Ser Ala Thr Ala Cys Ile
      65      70      75      80
Phe Ala Ala Glu Val Ala Ile Lys Glu Ser Glu Arg Phe Asn Gly Ile
      85      90      95
Pro Ala Leu Ser Val Pro Val Ala Glu Pro Ile Arg His Ala Glu Ala
      100      105      110
Leu Met Gln Gln Ala Leu Thr Leu Lys Arg Ser Asp Glu Thr Arg Thr
      115      120      125
Val Gln Gln Asp Thr Gln Pro Val Lys Ser Val Lys Thr Glu Leu Lys
      130      135      140
Gln Ala Leu Leu Ser Gly Ile Ser Phe Ala Val Pro Leu Ile Val Ala
      145      150      155      160
Gly Gly Thr Gln Val Ala Xaa Ala Val Xaa Arg Gln Gly Ile Ser Ser
      165      170      175
Leu His Asp Val Gln Val Arg Thr Trp Asn Ser
      180      185      187

```

```

<210> 1499
<211> 195
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(195)
<223> Xaa = any amino acid or nothing

```

```

<400> 1499
Gly Leu Asn Ser Glu Asn Ala Leu Ser Asn Glu Ala Met Glu Arg Gly
 1      5      10      15
Trp Gln Cys Leu Arg Leu Phe Ala Glu Arg Leu Gln Asp Ile Pro Pro
      20      25      30
Ser Gln Ile Arg Val Val Ala Thr Ala Thr Leu Arg Leu Ala Val Asn
      35      40      45
Ala Gly Asp Phe Ile Ala Lys Ala Gln Glu Ile Leu Gly Cys Pro Val
      50      55      60

```

```

Gly Leu Thr Trp Ala Glu Lys Phe Gln Cys Glu Gly Ser Glu Thr His
  50          55          60
Leu Ala Leu Cys Pro Ile Val Gln His Pro Glu Asp Thr Cys Ile His
  65          70          75          80
Ser Arg Glu Val Gly Val Val Cys Ser Arg Tyr Thr Asp Val Arg Leu
          85          90          95
Val Asn Gly Lys Ser Gln Cys Asp Gly Gln Val Glu Ile Asn Val Leu
          100          105          110
Gly His Trp Gly Ser Leu Cys Asp Thr His Trp Asp Pro Glu Asp Ala
          115          120          125
Arg Val Leu Cys Arg Gln Leu Asn Cys Gly Thr Ala Leu
          130          135          140 141

```

```

<210> 1496
<211> 80
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(80)
<223> Xaa = any amino acid or nothing

```

```

<400> 1496
Gln His Glu Gly Gly Asp Leu Arg Arg Arg Gln Leu Gly Glu Ile Gln
  1          5          10          15
Leu Thr Val Arg Tyr Val Cys Leu Arg Ala Ala Ser Ala Cys Xaa Ser
          20          25          30
Met Ala Ala Glu Thr Xaa His His Val Pro Ala Ser Gly Ala Asp Pro
          35          40          45
Tyr Val Arg Val Tyr Leu Leu Pro Glu Arg Lys Trp Ala Cys Arg Lys
          50          55          60
Lys Thr Ser Val Lys Arg Lys Thr Leu Glu Pro Leu Phe Asp Glu Thr
          65          70          75          80

```

```

<210> 1497
<211> 124
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(124)
<223> Xaa = any amino acid or nothing

```

```

<400> 1497
Glu Arg Leu Val Leu Thr Ser Glu His Cys Leu Val Leu Thr Leu Phe
  1          5          10          15
Trp Pro Ser Trp Thr Tyr His Thr Leu Leu Ser Arg Gln His Val
          20          25          30
Arg Arg Leu Pro Lys Leu Thr His Ala Glu His Asp His Leu Ala Ser
          35          40          45
Ile Met Asn Lys Leu Leu Thr Asn Tyr Asp Asn Leu Phe Glu Thr Ser
          50          55          60
Val Thr Tyr Ser Met Gly Xaa His Gly Ala Pro Thr Gly Ser Glu Ala
          65          70          75          80
Gly Ala Asn Trp Asn His Xaa Xaa Leu His Ala His Tyr Tyr Pro Pro
          85          90          95

```

```

Asn Glu Leu Cys Glu Val Asn Arg Lys Gly Cys Thr Ser Gly Asp Pro
65          70          75          80
Cys Leu Pro Tyr Phe Cys Val Gln Gly Cys Lys Leu Gly Gln Ala Ser
85          90          95
Asp Phe Ile Ala Arg Gln Gly Thr Leu Ile Gln Val Pro Ser Ser Ala
100        105        110
Gly Glu Val Glu Cys Tyr Lys Ile Cys Ser Cys Gly Gln Ser Gly Leu
115        120        125
Leu Glu Asn Cys Met Glu Met His Cys Met Asp Leu Pro Thr Asp Thr
130        135        140
Ser Ala Leu Val Arg
145          149

```

```

<210> 1494
<211> 134
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(134)
<223> Xaa = any amino acid or nothing

```

```

<400> 1494
Pro Gly Arg Arg Phe Arg Pro Arg Leu Ser Gln Ala Gly Thr Asp Ser
1      5      10      15
Gly Ser Xaa Val Phe Pro Asp Ser Phe Pro Ser Ala Pro Ala Glu Pro
20     25     30
Leu Pro Tyr Phe Leu Gln Glu Pro Gln Asp Ala Tyr Ile Val Lys Asn
35     40     45
Lys Pro Val Glu Leu Arg Cys Arg Ala Phe Pro Ala Thr Gln Ile Tyr
50     55     60
Phe Lys Cys Asn Gly Glu Trp Val Ser Gln Asn Asp His Val Thr Gln
65     70     75     80
Glu Gly Leu Asp Glu Ala Thr Gly Leu Arg Val Arg Glu Val His Ile
85     90     95
Glu Val Ser Arg Gln Gln Val Glu Glu Leu Phe Gly Leu Glu Asp Tyr
100    105    110
Trp Cys Gln Cys Val Ala Trp Ser Ser Ala Gly Thr Thr Lys Ser Arg
115    120    125
Arg Ala Tyr Val Arg Ile
130          134

```

```

<210> 1495
<211> 141
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(141)
<223> Xaa = any amino acid or nothing

```

```

<400> 1495
Xaa Val Glu Glu Lys His Ala Asp Thr Trp Arg Ser Xaa Cys Leu Ser
1      5      10      15
Asp Phe Phe Phe His Ala Ala Lys Xaa Leu Cys Xaa Glu Xaa Asn Cys
20     25     30
Gly Asp Ala Ile Ser Leu Ser Val Gly Asp His Phe Gly Lys Gly Asn
35     40     45

```

```

Thr Ser Phe Leu Gly Thr Ala Ser Ala Phe Arg Phe His Tyr Met Ala
  50      55      60
Ala Leu Xaa Thr Glu Leu Ser Gly Arg Leu Arg Ser Ser Lys Ser Asn
  65      70      75      80
Gly Trp Asn Gly Asp Asn Ser Thr Gly Tyr Leu Thr Val Pro Leu Arg
      85      90      95
Pro Leu Thr Ile Val Lys Glu Val Thr Met Asp Val Pro Ala Pro Asn
      100      105      110
Val Arg Gly Leu Asn Trp Met Gly
      115      120

```

```

<210> 1492
<211> 135
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(135)
<223> Xaa = any amino acid or nothing

```

```

<400> 1492
Asn Asn Pro Ser Thr Leu Pro Arg Gly Ser Xaa Pro Met Ser Pro Arg
  1      5      10      15
Thr Thr Met Gly Arg Arg Arg Gln Arg Arg Arg Glu His Lys Ser Ser
      20      25      30
Leu Ser Leu Ala Ser Ser Thr Val Gly Pro Gly Gly Gln Ile Val His
      35      40      45
Thr Glu Thr Thr Glu Val Val Leu Cys Gly Asp Pro Leu Ser Gly Phe
      50      55      60
Gly Leu Gln Leu Gln Gly Gly Ile Phe Ala Thr Glu Thr Leu Ser Ser
      65      70      75      80
Pro Pro Leu Val Cys Phe Ile Glu Pro Asp Ser Pro Ala Glu Arg Cys
      85      90      95
Gly Leu Leu Gln Val Gly Asp Arg Val Leu Ser Ile Asn Gly Ile Ala
      100      105      110
Thr Glu Asp Gly Thr Met Glu Glu Ala Asn Gln Leu Leu Arg Asp Ala
      115      120      125
Ala Leu Ala His Lys Val Val
      130      135

```

```

<210> 1493
<211> 149
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(149)
<223> Xaa = any amino acid or nothing

```

```

<400> 1493
Gln Met Leu Arg Asn Gly Gly Asp Gln Asn Thr Val Pro Asp Tyr His
  1      5      10      15
Phe Ala Asp Arg Ile Arg Glu Leu Leu Xaa Pro Thr Glu Asp Gln Lys
      20      25      30
Asn Cys Ile Pro Xaa Asp Thr Tyr Leu Arg Pro Ser Ala Leu Gly Asn
      35      40      45
Ile Val Glu Glu Val Thr His Pro Cys Ser Pro Gly Pro Cys Pro Ala
      50      55      60

```

```

Thr Glu Ser Xaa Ile Arg Gln Ala Gly His Leu Leu Gly Arg Asn Glu
      20      25      30
Phe Ile Glu Thr Lys Ala Leu Gly Cys Ala Trp Phe Ser Leu Cys Tyr
      35      40      45
Tyr Leu Val Leu Tyr Phe Glu Ser Ser His Lys Val Asp Phe Val Phe
      50      55      60
Ile Val Xaa Cys Phe Ser Thr Pro Pro Gly Ala Gln Met Thr Ile Met
      65      70      75      80
Ser Gln Ala Cys Ala Glu Arg Cys Asn Ile Met Arg Leu Val Asp Arg
      85      90      95
Arg Trp Ala Gly Ile Ala Lys Gly Val Gly Thr Gln Lys Ile Ile Gly
      100      105      110
Arg Val His Leu Gly Glu Gln Lys Ala Leu Gly Leu
      115      120      124

```

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<210> 1490
<211> 124
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(124)
<223> Xaa = any amino acid or nothing

```

```

<400> 1490
Glu Arg Thr Asn Lys Phe Ile Lys Glu Leu Ile Met Asp Gly Lys Asn
 1      5      10      15
Leu Ile Ala Ala Thr Lys Ser Leu Ser Val Ala Gln Arg Lys Phe Ala
      20      25      30
His Ser Leu Arg Asp Phe Lys Phe Glu Phe Ile Gly Asp Ala Val Thr
      35      40      45
Asp Asp Glu Arg Cys Ile Asp Ala Ser Leu Arg Glu Phe Ser Asn Phe
      50      55      60
Leu Lys Asn Leu Glu Glu Gln Arg Glu Ile Met Val Ser Xaa Glu Gly
      65      70      75      80
Cys Lys Leu Ile Ser Gln Leu Ser Arg Gly Lys Lys Ile Trp Ile Trp
      85      90      95
Lys Leu Val Leu Val Glu Val Val Lys His Leu Ser Leu Gly Thr Val
      100      105      110
Val His Cys Asn Gly Lys Met Arg Phe Pro Glu Pro
      115      120      124

```

```

<210> 1491
<211> 120
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(120)
<223> Xaa = any amino acid or nothing

```

```

<400> 1491
Leu Ile Thr Asn Lys Val Phe Val Ala Arg Glu Leu Ser Cys Leu Asp
 1      5      10      15
Val His Leu Asp Ser Thr Gly Ser Thr Ala Val Val Ala Asp Gln Asp
      20      25      30
Lys Leu Glu Leu Glu Leu Val Leu Lys Gly Ser Tyr Glu Asp Thr Gln
      35      40      45

```


Ala Arg Ser Ser Ala Gly Thr Pro Ala Arg Ala Tyr Leu Asp Ile Pro
 915 920 925
 Asn Pro Arg Tyr Leu Gly Pro Ala Ile Ser Ser Gly Ala Ile Tyr Leu
 930 935 940
 Ala Ser Ser Tyr Gln Asp Lys Leu Arg Val Ile Cys Cys Lys Gly Asn
 945 950 955 960
 Leu Val Lys Glu Ser Gly Thr Glu His His Arg Gly Pro Ser Thr Ser
 965 970 975
 Arg Arg Xaa Pro Ala Ser Pro Leu Pro Gln Tyr Gln Gly Gln Arg Ala
 980 985 990
 Phe Leu Gln Gly Arg Arg Lys
 995 999

<210> 1488
 <211> 175
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(175)
 <223> Xaa = any amino acid or nothing

<400> 1488
 Gly Arg Pro Gln Gly Pro Ala Pro Gly Ala Gly Ser Pro Pro Glu Ser
 1 5 10 15
 Gly Pro Gly Leu Trp Ala Ala Leu Gly Cys Ser Leu Val Trp Val Pro
 20 25 30
 Leu Cys Cys Leu Gly Gly Ala Ala Gly Arg Leu Xaa Ala Arg Ser Gly
 35 40 45
 Lys Ser Gly Leu Arg Arg Arg Ala His Ala Gly Pro Pro Pro Gly
 50 55 60
 Gly Pro Cys Asn Ser Cys Pro Xaa Cys Ser Ala Pro Glu Ser Gly Gly
 65 70 75 80
 Arg Gly Pro Leu Pro Gly Pro Gly Thr Gly Gly Val Cys Ser Cys Trp
 85 90 95
 Thr Arg Gly Cys Gln Thr Thr Ala Arg Thr Ala Ala Ala Ala Ala
 100 105 110
 Pro Gly Pro Ala Gly Arg Arg Pro Pro Gly Gly Ala Pro Gln Asn Gly
 115 120 125
 Ser Cys Ala Ala Ser Ala Ser Gln Glu Ala Ala Ala Pro Pro Pro Met
 130 135 140
 Cys Pro Pro Gly Arg Arg Trp Ala Val Ala Ser Pro Pro Glu Thr Arg
 145 150 155 160
 Cys Pro Ala Ala Pro Gly Thr Arg Cys Arg Arg Leu Glu Ala Ala
 165 170 175

<210> 1489
 <211> 124
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(124)
 <223> Xaa = any amino acid or nothing

<400> 1489
 Leu Pro Ser Met Ser Asn Cys Thr Ser Cys Phe Arg Leu Gln Ser Arg
 1 5 10 15

Glu Ser Ser Thr Pro Glu Glu Phe Ser Arg Arg Leu Lys Glu Arg Met
 405 410 415
 His His Asn Ile Pro His Arg Phe Asn Val Gly Leu Asn Met Arg Ala
 420 425 430
 Thr Lys Cys Ala Val Cys Leu Asp Thr Val His Phe Gly Arg Gln Ala
 435 440 445
 Ser Lys Cys Leu Glu Cys Gln Val Met Cys His Pro Lys Cys Ser Thr
 450 455 460
 Cys Leu Pro Ala Thr Cys Gly Leu Pro Ala Glu Tyr Val Thr His Phe
 465 470 475 480
 Thr Glu Ala Phe Cys Arg Asp Lys Met Asn Ser Pro Gly Leu Gln Thr
 485 490 495
 Lys Glu Pro Ser Ser Ser Leu His Leu Glu Gly Trp Met Lys Val Pro
 500 505 510
 Arg Asn Asn Lys Arg Gly Gln Gln Gly Trp Asp Arg Lys Tyr Ile Val
 515 520 525
 Leu Glu Gly Ser Lys Val Leu Ile Tyr Asp Asn Glu Ala Arg Glu Ala
 530 535 540
 Gly Gln Arg Pro Val Glu Glu Phe Glu Leu Cys Leu Pro Asp Gly Asp
 545 550 555 560
 Val Ser Ile His Gly Ala Val Gly Ala Ser Glu Leu Ala Asn Thr Ala
 565 570 575
 Lys Ala Asp Val Pro Tyr Ile Leu Lys Met Glu Ser His Pro His Thr
 580 585 590
 Thr Cys Trp Pro Gly Arg Thr Leu Tyr Leu Leu Ala Pro Ser Phe Pro
 595 600 605
 Asp Lys Gln Arg Trp Val Thr Ala Leu Glu Ser Val Val Ala Gly Gly
 610 615 620
 Arg Val Ser Arg Glu Lys Ala Glu Ala Asp Ala Lys Leu Leu Gly Asn
 625 630 635 640
 Ser Leu Leu Lys Leu Glu Gly Asp Asp Arg Leu Asp Met Asn Cys Thr
 645 650 655
 Leu Pro Phe Ser Asp Gln Val Val Leu Val Gly Thr Glu Glu Gly Leu
 660 665 670
 Tyr Ala Leu Asn Val Leu Lys Asn Ser Leu Thr His Val Pro Gly Ile
 675 680 685
 Gly Ala Val Phe Gln Ile Tyr Ile Ile Lys Asp Leu Glu Lys Leu Leu
 690 695 700
 Met Ile Ala Gly Glu Glu Arg Ala Leu Cys Leu Val Asp Val Lys Lys
 705 710 715 720
 Val Lys Gln Ser Leu Ala Gln Ser His Leu Pro Ala Gln Pro Asp Ile
 725 730 735
 Ser Pro Asn Ile Phe Glu Ala Val Lys Gly Cys His Leu Phe Gly Ala
 740 745 750
 Gly Lys Ile Glu Asn Gly Leu Cys Ile Cys Ala Ala Met Pro Ser Lys
 755 760 765
 Val Val Ile Leu Arg Tyr Asn Glu Asn Leu Ser Lys Tyr Cys Ile Arg
 770 775 780
 Lys Glu Ile Glu Thr Ser Glu Pro Cys Ser Cys Ile His Phe Thr Asn
 785 790 795 800
 Tyr Ser Ile Leu Ile Gly Thr Asn Lys Phe Tyr Glu Ile Asp Met Lys
 805 810 815
 Gln Tyr Thr Leu Glu Glu Phe Leu Asp Lys Asn Asp His Ser Leu Ala
 820 825 830
 Pro Ala Val Phe Ala Ala Ser Ser Asn Ser Phe Pro Val Ser Ile Val
 835 840 845
 Gln Val Asn Ser Ala Gly Gln Arg Glu Glu Tyr Leu Leu Cys Phe His
 850 855 860
 Glu Phe Gly Val Phe Val Asp Ser Tyr Gly Arg Arg Ser Arg Thr Asp
 865 870 875 880
 Asp Leu Lys Trp Ser Arg Leu Pro Leu Ala Phe Ala Tyr Arg Glu Pro
 885 890 895
 Tyr Leu Phe Val Thr His Phe Asn Ser Leu Glu Val Ile Glu Ile Gln
 900 905 910

<210> 1487
 <211> 999
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(999)
 <223> Xaa = any amino acid or nothing

<400> 1487
 Ala His Arg Asp Glu Ile Gln Arg Lys Phe Asp Ala Leu Arg Asn Ser
 1 5 10 15
 Cys Thr Val Ile Thr Asp Leu Glu Glu Gln Leu Asn Gln Leu Thr Glu
 20 25 30
 Asp Asn Ala Glu Leu Asn Asn Gln Asn Phe Tyr Leu Ser Lys Gln Leu
 35 40 45
 Asp Glu Ala Ser Gly Ala Asn Asp Glu Ile Val Gln Leu Arg Ser Glu
 50 55 60
 Val Asp His Leu Arg Arg Glu Ile Thr Glu Arg Glu Met Gln Leu Thr
 65 70 75 80
 Ser Gln Lys Gln Thr Met Glu Ala Leu Lys Thr Thr Cys Thr Met Leu
 85 90 95
 Glu Glu Gln Val Met Asp Leu Glu Ala Leu Asn Asp Glu Leu Leu Glu
 100 105 110
 Lys Glu Arg Gln Trp Glu Ala Trp Arg Ser Val Leu Gly Asp Glu Lys
 115 120 125
 Ser Gln Phe Glu Cys Arg Val Arg Glu Leu Gln Arg Met Leu Asp Thr
 130 135 140
 Glu Lys Gln Ser Arg Ala Arg Ala Asp Gln Arg Ile Thr Glu Ser Arg
 145 150 155 160
 Gln Val Val Glu Leu Ala Val Lys Glu His Lys Ala Glu Ile Leu Ala
 165 170 175
 Leu Gln Gln Ala Leu Lys Glu Gln Lys Leu Lys Ala Glu Ser Leu Ser
 180 185 190
 Asp Lys Leu Asn Asp Leu Glu Lys Lys His Ala Met Leu Glu Met Asn
 195 200 205
 Ala Arg Ser Leu Gln Gln Lys Leu Glu Thr Glu Arg Glu Leu Lys Gln
 210 215 220
 Arg Leu Leu Glu Glu Gln Ala Lys Leu Gln Gln Gln Met Asp Leu Gln
 225 230 235 240
 Lys Asn His Ile Phe Arg Leu Thr Gln Gly Leu Gln Glu Ala Leu Asp
 245 250 255
 Arg Ala Asp Leu Leu Lys Thr Glu Arg Ser Asp Leu Glu Tyr Gln Leu
 260 265 270
 Glu Asn Ile Gln Val Leu Tyr Ser His Glu Lys Val Lys Met Glu Gly
 275 280 285
 Thr Ile Ser Gln Gln Thr Lys Leu Ile Asp Phe Leu Gln Ala Lys Met
 290 295 300
 Asp Gln Pro Ala Lys Lys Lys Lys Val Pro Leu Gln Tyr Asn Glu Leu
 305 310 315 320
 Lys Leu Ala Leu Glu Lys Glu Lys Ala Arg Cys Ala Glu Leu Glu Glu
 325 330 335
 Ala Leu Gln Lys Thr Arg Ile Glu Leu Arg Ser Ala Arg Glu Glu Ala
 340 345 350
 Ala His Arg Lys Ala Thr Asp His Pro His Pro Ser Thr Pro Ala Thr
 355 360 365
 Ala Arg Gln Gln Ile Ala Met Ser Ala Ile Val Arg Ser Pro Glu His
 370 375 380
 Gln Pro Ser Ala Met Ser Leu Leu Ala Pro Pro Ser Ser Arg Arg Lys
 385 390 395 400

<211> 139
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(139)
 <223> Xaa = any amino acid or nothing

<400> 1485
 Pro Thr Arg Pro Val Asn Ser Ser Gln Ala Phe Ala Leu Val Tyr Tyr
 1 5 10 15
 Thr Leu Gly Ala Leu Gly Gly Asn Leu Ile Ala His Met Gly Leu Gly
 20 25 30
 Tyr Arg Tyr Trp Ala Gly Ile Gly Val Leu Gln Ser Cys Glu Ser Ala
 35 40 45
 Leu Thr His Tyr Arg Leu Val Ala Asn His Val Ala Ser Asp Ile Ser
 50 55 60
 Leu Thr Gly Gly Ser Val Val Gln Arg Ile Arg Leu Pro Asp Glu Val
 65 70 75 80
 Glu Asn Pro Gly Met Asn Ser Gly Met Leu Gln Glu Asp Leu Ile Gln
 85 90 95
 Tyr Tyr Gln Phe Leu Ala Glu Lys Gly Asp Val Gln Ala Gln Val Gly
 100 105 110
 Leu Gly Gln Leu His Leu His Gly Gly Arg Gly Val Xaa Gln Asn His
 115 120 125
 Gln Arg Ala Phe Asp Tyr Phe Asn Leu Ala Ala
 130 135 139

<210> 1486
 <211> 171
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(171)
 <223> Xaa = any amino acid or nothing

<400> 1486
 Ala Asn Thr Ser Leu Ser Ser Ala Ala Val Ser Ala Val Ser Pro Pro
 1 5 10 15
 Pro Cys Arg Thr Ser Thr Ala Thr Thr Leu Pro Pro Pro Met Pro Ser
 20 25 30
 Phe Phe Cys Val Phe Pro Ser Pro Ser Met Ser Pro Ser Pro Ser Glu
 35 40 45
 Phe Leu Ser Cys Ile Ala Ser Val Ser Arg Val His Ser Leu Ser Ser
 50 55 60
 Ser Ser Ser Gly Ser Ser Thr Ala Ser Ser Leu Asn Phe Ser Ala
 65 70 75 80
 Ile Met Gly Ser Ser Ser Ala Thr Ala Ser Trp Val Leu Ser Thr Ala
 85 90 95
 Ser Thr Pro Pro Cys Pro Ser Ala Leu Pro Ser Ser Pro Ala Gln Glu
 100 105 110
 Ser Xaa Ser Leu Ala Ala Ser Ser Ala Trp Pro Val Ala Gly Ile
 115 120 125
 Ser Pro Ser Gly Ala Cys Thr Phe Pro Ala Gly Ser Ala Ser Gly Ala
 130 135 140
 Ala Lys Ala Pro Ser Pro Ser Trp Arg Cys Pro Ser Phe Arg Ala Leu
 145 150 155 160
 Phe Ser Leu Leu Asp Ser Ser Ser Leu Ser Leu
 165 170 171

```

Ile Thr Glu Ala Xaa Ser Lys Asp Lys Ser Pro Met Glu Glu Glu Lys
  50          55          60
Thr Glu Met Ile Arg Ser Tyr Ile Gln Glu Val Gly Arg Tyr Ile Lys
  65          70          75          80
Arg Leu Glu Glu Ala Gln Ser Lys Arg Leu Glu Lys Leu Arg Glu Lys
          85          90          95
His Lys Glu Ile Arg Gln Pro Ile Leu Asp Glu Lys Pro Lys Gly Glu
          100          105          110
Gly Ser Ser Ser Phe Leu Ser Glu Thr Cys His Glu Asp Thr Ser Trp
          115          120          125
Phe Pro Asn Phe Thr Pro
          130          134

```

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<210> 1484
<211> 270
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(270)
<223> Xaa = any amino acid or nothing

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```

<400> 1484
Pro Gly Ser Thr His Ala Ser Ala Arg Ile Thr Ile Tyr Xaa Leu Xaa
  1          5          10          15
Ile Ile Leu Ser Asn Ala Thr Glu Val Asp Asn Asn Phe Ser Lys Pro
          20          25          30
Pro Pro Phe Phe Pro Ala Gly Ala Pro Pro Ala Ser Ser Ser Ser
          35          40          45
Ser Ser Ser Ser Ser Pro Pro Thr Val Ser Thr Ala Pro Pro Leu Ile
          50          55          60
Pro Pro Pro Gly Phe Pro Pro Pro Pro Gly Ala Pro Pro Pro Ser Leu
          65          70          75          80
Ile Pro Thr Ile Glu Ser Gly His Ser Ser Gly Tyr Asp Ser Arg Ser
          85          90          95
Ala Arg Ala Phe Pro Tyr Gly Asn Val Ala Phe Pro His Leu Pro Gly
          100          105          110
Ser Ala Pro Ser Trp Pro Ser Leu Val Asp Thr Ser Lys Gln Trp Asp
          115          120          125
Tyr Tyr Ala Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
          130          135          140
Ser Ser Ser Pro Arg Asp Arg Asp Arg Glu Arg Xaa Arg Thr Arg Glu
          145          150          155          160
Arg Glu Arg Glu Arg Asp His Ser Pro Thr Pro Ser Val Phe Asn Ser
          165          170          175
Asp Glu Glu Arg Tyr Arg Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr Glu
          180          185          190
Arg His Arg Ala Ser Arg Glu Lys Glu Glu Arg His Arg Glu Arg Arg
          195          200          205
His Arg Glu Lys Glu Glu Thr Arg His Lys Ser Ser Arg Ser Asn Ser
          210          215          220
Arg Arg Arg His Glu Ser Glu Glu Gly Asp Ser His Arg Arg His Lys
          225          230          235          240
His Lys Lys Ser Lys Arg Ser Lys Glu Gly Lys Glu Ala Gly Ser Glu
          245          250          255
Pro Ala Pro Glu Gln Glu Ser Thr Glu Ala Thr Pro Ala Glu
          260          265          270

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<210> 1485

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Glu Asn Ala Leu Leu Gln Gly Phe Asn Leu Lys Leu Thr Asp Phe Gly
  50                      55                      60
Phe Ala Lys Val Leu Pro Lys Ser His Arg Glu Leu Ser Gln Thr Phe
  65                      70                      75                      80
Cys Gly Ser Thr Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro
                      85                      90                      95
His Asp Ser Lys Lys Gly Asp Val Trp Ser Met Gly Val Val Leu Tyr
                      100                    105                    110
Val Met Leu Cys Ala Ser Leu Pro Phe Asp Asp Thr Asp Ile Pro Lys
                      115                    120                    125
Met Leu Trp Gln Gln Gln Lys Gly Val Ser Phe Pro Thr His Leu Ser
  130                      135                      140
Ile Ser Ala Asp Cys Gln Asp Leu Leu Lys Arg Leu Leu Glu Pro Asp
  145                      150                      155                      160
Met Ile Leu Arg Pro Ser Ile Glu Glu Val Ser Trp His Pro Trp Leu
                      165                    170                    175
Ala Ser Thr Xaa Xaa Lys Gln Trp Gln Val Leu Ser Asn Lys Val Gly
                      180                    185                    190
Gly Glu Ser Lys Pro Lys Lys Lys Lys
                      195                    200 201

```

```

<210> 1482
<211> 67
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(67)
<223> Xaa = any amino acid or nothing

```

```

<400> 1482
Leu Val Ala Lys Ser Leu Leu Tyr Cys Gly Cys Leu Phe Phe Leu Leu
  1                      5                      10                      15
Gln Leu Ala Lys Asn Val Gly Asn Asn Ser Phe Asn Asp Ile Met Glu
                      20                      25                      30
Ala Asn Leu Thr Ser Pro Ser Pro Lys Pro Thr Pro Ser Ser Asp Met
                      35                      40                      45
Xaa Val Phe Leu Ile Tyr Xaa Thr Tyr Phe Gly Ala Trp His Val Val
  50                      55                      60
Asp Ala Gln
  65                      67

```

```

<210> 1483
<211> 134
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(134)
<223> Xaa = any amino acid or nothing

```

```

<400> 1483
Arg Lys His Ile Lys Leu Leu Ile Gln Lys Leu Ser Asp Val Pro Xaa
  1                      5                      10                      15
Glu Cys Gln Asn Asn Gln Leu Xaa Lys Leu Thr Glu Ile Cys Glu Lys
                      20                      25                      30
Glu Lys Lys Glu Phe Lys Lys Lys Met Asp Asp Gln Arg Pro Glu Lys
                      35                      40                      45

```

```

Leu Cys Val Trp Ala Leu Ser Leu Val Ile Tyr Ile Gly Pro Leu Leu
 65          70          75          80
Gly Trp Arg His Pro Ala Pro Glu Asp Glu Thr Ile Cys Gln Ile Asn
          85          90          95
Glu Glu Pro Gly Tyr Val Leu Phe Ser Thr Pro Gly Ser Phe Tyr Leu
          100          105          110
Pro Leu Ala Ile Met Leu Val Met Asn Xaa Arg Val Tyr Arg Val Ala
          115          120          125
Lys Thr Glu
          130 131

```

```

<210> 1480
<211> 154
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(154)
<223> Xaa = any amino acid or nothing

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```

<400> 1480
Asp Pro Arg Val Arg Thr Lys Ile Val Asn Arg Lys Thr Thr Ile Tyr
 1          5          10          15
Glu Ile Gln Asp Lys Thr Gly Ser Met Ala Val Val Gly Lys Gly Glu
          20          25          30
Cys His Asn Ile Pro Cys Glu Lys Gly Asp Lys Leu Arg Leu Phe Cys
          35          40          45
Phe Arg Leu Arg Lys Arg Glu Asn Met Ser Lys Leu Met Ser Glu Met
          50          55          60
His Ser Phe Ile Gln Ile Gln Lys Asn Thr Asn Gln Arg Ser His Asp
          65          70          75          80
Ser Arg Ser Met Ala Leu Pro Gln Glu Gln Ser Gln His Pro Lys Pro
          85          90          95
Ser Glu Ala Ser Thr Thr Leu Pro Glu Ser His Leu Lys Thr Pro Gln
          100          105          110
Met Pro Pro Thr Thr Pro Ser Ser Ser Phe Thr Lys Val Thr Lys
          115          120          125
Asp Lys Asp Ile Lys Xaa Leu Leu Phe Asn Leu Tyr Ser Ser Val Glu
          130          135          140
Ile Leu Pro Glu Val Leu His Leu Lys Thr
          145          150          154

```

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<210> 1481
<211> 201
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(201)
<223> Xaa = any amino acid or nothing

```

```

<400> 1481
Leu Ala Glu Gly Gly Asp Val Phe Asp Cys Val Leu Asn Gly Gly Pro
 1          5          10          15
Leu Pro Glu Ser Arg Ala Lys Ala Leu Phe Arg Gln Met Val Glu Ala
          20          25          30
Ile Arg Tyr Cys His Gly Cys Gly Val Ala His Arg Asp Leu Lys Cys
          35          40          45

```

```

Thr Glu Ser Pro Leu Leu Val Arg Pro Tyr Leu Pro Tyr Ile Thr Lys
 1          5          10          15
Ser Glu Leu His Ala Ile Met Thr Ala Gly Phe Ser Thr Ile Ala Gly
          20          25          30
Ser Val Leu Gly Ala Tyr Ile Ser Phe Gly Val Pro Ser Ser His Leu
          35          40          45
Leu Thr Ala Ser Val Met Ser Ala Pro Ala Ser Leu Ala Ala Lys
          50          55          60
Leu Phe Trp Pro Glu Thr Glu Lys Pro Lys Ile Thr Leu Lys Asn Ala
65          70          75          80
Met Lys Met Glu Ser Gly Asp Ser Gly Asn Leu Leu Xaa Ala Ala Thr
          85          90          95
Gln Gly Ala Ser Ser Ser Ile Ser Leu Val Ala Asn Ile Ala Val Asn
          100          105          110
Leu Ile Ala Phe Leu Ala Leu Leu Ser Phe Met Asn Ser Ala Leu Ala
          115          120          125
Trp Val Gly Asn Met Phe Asp Tyr Pro Gln Leu Ser Phe Glu Leu Ile
          130          135          140
Cys Ser Tyr Ile Phe Met Pro Phe Ser Phe Met Met Gly Val Glu Trp
145          150          155          160
Pro Asp Ser Phe Met
          165

```

```

<210> 1478
<211> 67
<212> PRT
<213> Homo sapiens

```

```

<400> 1478
Cys Cys Met Asn Ser Lys Ala Gln Glu Ser Val Phe Lys Asn Val Leu
 1          5          10          15
Cys Asn Pro Pro Ala Leu Ser Glu Met Pro Asp Val Lys Ala Glu Asp
          20          25          30
Glu Val Asp Phe Arg Ala Ser Ser Ile Ser Glu Glu Val Ala Val Gly
          35          40          45
Ser Ile Ala Ala Thr Leu Lys Met Lys Gln Gly Pro Met Thr Gln Ala
          50          55          60
Ile Asn Arg
65          67

```

```

<210> 1479
<211> 131
<212> PRT
<213> Homo sapiens

```

```

<221> misc_feature
<222> (1)...(131)
<223> Xaa = any amino acid or nothing

```

```

<400> 1479
Pro Thr Arg Gly Ala Leu Arg Tyr Trp Ile Phe Gly Arg Phe Leu Cys
 1          5          10          15
Asn Ile Trp Ala Ala Val Asp Val Arg Cys Cys Thr Ala Thr Ile Met
          20          25          30
Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Val Gly Val Ser Tyr Pro
          35          40          45
Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Leu Met Ala Leu
          50          55          60

```


<213> Homo sapiens

<221> misc_feature

<222> (1)...(151)

<223> Xaa = any amino acid or nothing

<400> 1475

```

Gly Gly Pro Ala Pro Asn Ser Arg Tyr Ala Glu Pro Xaa Lys Asn Ser
 1           5           10           15
Leu Ala Met Thr Xaa Ala His Ala Asp Cys Glu Asn Tyr Val Ala Cys
      20           25           30
Gly Gly Leu Asp Asn Ile Cys Ser Ile Tyr Asn Leu Lys Thr Arg Glu
      35           40           45
Gly Asn Val Arg Val Ser Arg Glu Leu Pro Gly His Thr Gly Tyr Leu
      50           55           60
Ser Cys Cys Arg Phe Leu Asp Asp Ser Gln Ile Val Thr Ser Ser Gly
      65           70           75           80
Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Ala Gln Gln Thr Thr
      85           90           95
Thr Phe Thr Gly His Ser Gly Asp Val Met Ser Leu Ser Leu Ser Pro
      100          105          110
Asp Met Arg Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ser Lys Leu
      115          120          125
Trp Asp Ile Arg Asp Gly Met Cys Arg Gln Ser Phe Thr Gly His Val
      130          135          140
Ser Asp Ile Asn Ala Val Ser
145           150 151

```

<210> 1476

<211> 58

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(58)

<223> Xaa = any amino acid or nothing

<400> 1476

```

Lys Ser Glu Lys Ser Cys Val Ser Ser Leu Ala His Phe Gly Thr Ser
 1           5           10           15
Cys Gln Arg Asp Tyr Asp Ala Met Val Lys Leu Val Glu Thr Leu Glu
      20           25           30
Met Leu Pro Thr Cys Asp Leu Ala Asp Gln His Asn Ile Lys Phe His
      35           40           45
Tyr Ala Phe Ala Leu Asn Arg Xaa Glu Arg
      50           55           58

```

<210> 1477

<211> 165

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(165)

<223> Xaa = any amino acid or nothing

<400> 1477

Lys Ser His Leu Trp Arg Gly Ile Val Ser Ile Thr Leu Ile Glu Gly
 35 40 45
 Arg Asp Leu Lys Ala Met Asp Ser Asn Gly Leu Ser Asp Pro Tyr Val
 50 55 60
 Lys Phe Arg Leu Gly His Gln Lys Tyr Lys Ser Lys Ile Met Pro Lys
 65 70 75 80
 Thr Leu Asn Pro Gln Trp Arg Glu Gln Phe Asp Phe His Leu Tyr Glu
 85 90 95
 Glu Arg Gly Gly Val Ile Asp Ile Thr Ala Trp Asp Lys Asp Ala Gly
 100 105 110
 Lys Arg Asp Asp Phe Ile Gly Arg Cys Gln Val Asp Leu Ser Ala Leu
 115 120 125
 Ser Arg Glu Gln Thr His Lys Lys Leu Glu Leu Gln Leu Glu Gly Glu
 130 135 140
 Gly His Leu Val Leu Leu Val Thr Leu Thr Ala Ser Ala Thr Val Ser
 145 150 155 160
 Ile Ser Asp Leu Ser Val Asn Ser Leu Glu Asp Gln Lys Glu Arg Glu
 165 170 175
 Glu Ile Leu Lys Arg Tyr Ser Pro Leu Arg Ile Phe His Asn Leu Lys
 180 185 190
 Asp Val Gly Phe Leu Gln Val Lys Val Ile Arg Ala Glu Gly Leu Met
 195 200 205
 Ala Ala Asp Val Thr Gly Lys Ser Asp Pro Phe Cys Val Val Glu Leu
 210 215 220
 Asn Asn Asp Arg Leu Leu Thr His Thr Val Tyr Lys Asn Leu Asn Pro
 225 230 235 240
 Glu Trp Asn Lys Val Phe Thr Leu Xaa Val Ala Leu Val Trp Lys Lys
 245 250 255
 Phe Gln Thr Gln Ser Leu Arg Leu Ser Asp Leu His Arg Lys Ser His
 260 265 270
 Leu Trp Arg Gly Ile Val Ser Ile Thr Leu Ile Glu Gly Arg Asp Leu
 275 280 285
 Lys Ala Met Asp Ser Asn Gly Leu Ser Asp Pro Tyr Val Lys Phe Arg
 290 295 300
 Leu Gly His Gln Lys Tyr Lys Ser Lys Ile Met Pro Lys Thr Leu Asn
 305 310 315 320
 Pro Gln Trp Arg Glu Gln Phe Asp Phe His Leu Tyr Glu Glu Arg Gly
 325 330 335
 Gly Val Ile Asp Ile Thr Ala Trp Asp Lys Asp Ala Gly Lys Arg Asp
 340 345 350
 Asp Phe Ile Gly Arg Cys Gln Val Asp Leu Ser Ala Leu Ser Arg Glu
 355 360 365
 Gln Thr His Lys Leu Glu Leu Gln Leu Glu Glu Gly Glu Gly His Leu
 370 375 380
 Val Leu Leu Val Thr Leu Thr Ala Ser Ala Thr Val Ser Ile Ser Asp
 385 390 395 400
 Leu Ser Val Asn Ser Leu Glu Asp Gln Lys Glu Arg Glu Glu Ile Leu
 405 410 415
 Lys Arg Tyr Ser Pro Leu Arg Ile Phe His Asn Leu Lys Asp Val Gly
 420 425 430
 Phe Leu Gln Val Lys Val Ile Arg Ala Glu Gly Leu Met Ala Ala Asp
 435 440 445
 Val Thr Gly Lys Ser Asp Pro Phe Cys Val Val Glu Leu Asn Asn Asp
 450 455 460
 Arg Leu Leu Thr His Thr Val Tyr Lys Asn Leu Asn Pro Glu Trp Asn
 465 470 475 480
 Lys Val Phe Thr Leu
 485

<210> 1475

<211> 151

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(69)

<223> Xaa = any amino acid or nothing

<400> 1472

```

Leu Gly Leu Phe Ser Phe Val Trp Thr Glu Val Leu Glu Glu Pro Lys
 1               5               10               15
Asp Phe Ser Cys Glu Thr Glu Asp Phe Lys Thr Leu His Cys Thr Trp
      20               25               30
Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser Gln
      35               40               45
Ser Tyr Thr Leu Phe Glu Ser Xaa Val Gly Ser Gly Tyr Ile Ile Asp
      50               55               60
Asn Phe Phe Leu Ala
 65               69

```

<210> 1473

<211> 99

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(99)

<223> Xaa = any amino acid or nothing

<400> 1473

```

Asp Ala Arg Thr Thr Trp Lys Pro Arg Asn Gly Ser Ser Gly Ile Trp
 1               5               10               15
Pro Gly Asp Gly Ala Lys Xaa Pro Pro Ala Val Glu Gln Ala Glu Arg
      20               25               30
Gly His Val Glu Met Ile Glu Lys Leu Thr Phe Leu Asn Leu His Thr
      35               40               45
Ser Glu Lys Asp Lys Gly Gly Asn Thr Ala Leu His Leu Ala Ala Lys
      50               55               60
His Gly His Ser Pro Ala Val Gln Val Leu Leu Ala Gln Trp Gln Asp
      65               70               75               80
Ile Asn Glu Met Asn Glu Lys Gln Gln Thr Pro Leu His Val Ala Ala
      85               90               95
Asp Arg Gly
      99

```

<210> 1474

<211> 485

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(485)

<223> Xaa = any amino acid or nothing

<400> 1474

```

Met Thr Phe Asp Asp Asp Asp Lys Asn Thr Tyr Gly Val Ala Leu Val
 1               5               10               15
Trp Lys Lys Phe Gln Thr Gln Ser Leu Arg Leu Ser Asp Leu His Arg
      20               25               30

```

```

Arg Leu Asp Ala Gln Gly Ala Arg Trp Met Glu Lys His Gly Phe Glu
      100      105      110
Arg Pro Lys Tyr Phe Val Pro Pro Asp Lys Asp Leu Leu Ala Leu Glu
      115      120      125
Gln Ser Lys Thr Phe Tyr Lys Pro Asp Trp Phe Asp Ile Val Glu Ser
      130      135      140
Glu Val Lys Cys Cys Lys Glu Ala Val Cys Val Ile Asp Met Ser Ser
      145      150      155      160
Phe Thr Glu Phe Glu Ile Thr Ser Thr Gly Asp Gln Ala Leu Glu Val
      165      170      175
Leu Gln Tyr Leu Phe Ser Asn Asp Leu Asp Val Pro Val Gly His Ile
      180      185      190
Val His Thr Gly Met Leu Asn Glu Gly Gly Gly Tyr Glu Asn Asp Cys
      195      200      205
Ser Ile Ala Arg Leu Asn Lys Arg Ser Phe Phe Met Ile Ser Pro Thr
      210      215      220
Asp Gln Gln Val His Cys Trp Ala Trp Leu Lys Lys His Met Pro Lys
      225      230      235      240
Asp Ser Asn Leu Leu Leu Glu Asp Val Thr Trp Lys Tyr Thr Ala Leu
      245      250      255
Asn Leu Ile Gly Pro Arg Ala Val Asp Val Leu Ser Glu Leu Ser Tyr
      260      265      270
Ala Pro Met Thr Pro Asp His Phe Pro Ser Leu Phe Cys Lys Glu Met
      275      280      285
Ser Val Gly Tyr Ala Asn Gly Ile Arg Val Met Ser Met Thr His Thr
      290      295      300
Gly Glu Pro Gly Phe Met Leu Tyr Ile Pro Ile Glu Tyr Arg Trp Gly
      305      310      315      320
Phe Thr Met Leu Ser Thr Leu Val Ser Asn Ser
      325      330 331

```

<210> 1471

<211> 101

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(101)

<223> Xaa = any amino acid or nothing

<400> 1471

```

Ala Gln Phe Leu Leu Val Gly Trp Asp His Ile Leu Xaa Leu Ile Val
  1          5          10          15
Leu Xaa Thr Asn Leu Thr Glu Leu Gly Arg Thr Thr Cys Asp Gln Asn
      20      25      30
Trp Pro Asn Ser Pro Asp Val Leu Asn His Gly Cys Phe Tyr Met Gln
      35      40      45
Cys Leu Ser Lys Asp Cys Thr Ile Gly Tyr Val Ser Arg Glu Met Leu
      50      55      60
Val Ala His Thr His Thr Val Glu Glu His Thr Gly Thr His Leu Gln
      65      70      75      80
Tyr Val Ser Trp Pro Asp His Ser Val Pro Asp Asp Ser Ser Asp Phe
      85      90      95
Val Glu Phe Glu Asn
      100 101

```

<210> 1472

<211> 69

<212> PRT

```

Gln Ala Ala Ser Glu Pro Ile Asn Asn Asn Phe Ala Glu Ser Lys Arg
      85          90          95
Asn Leu Ala Phe Leu Ala Thr Gly Val Val Arg His Met Arg Lys Leu
      100        105        110
Phe Met Gly Ala Asn Leu Glu Gly Pro Gly Pro Thr Val Ser His
      115        120        125        127

```

<210> 1469

<211> 132

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(132)

<223> Xaa = any amino acid or nothing

<400> 1469

```

Gly Thr Thr Ser Lys His His Xaa Leu Ala Arg Ser Leu Ile Arg Gly
  1          5          10          15
Pro Phe Asp His Asp Leu Lys Pro Asn Ala Ala Thr Arg Asp Gln Leu
      20        25        30
Asn Ile Ile Val Ser Tyr Pro Pro Thr Lys Gln Leu Thr Tyr Glu Glu
      35        40        45
Gln Asp Leu Gly Trp Lys Phe Arg Tyr Tyr Leu Thr Asn Gln Glu Lys
      50        55        60
Ala Leu Thr Lys Phe Leu Lys Trp Val Asn Trp Asp Leu Pro Gln Glu
      65        70        75        80
Ala Lys Gln Ala Leu Glu Leu Leu Gly Lys Trp Lys Pro Met Asp Val
      85        90        95
Lys Asp Ser Leu Glu Leu Leu Ser Ser His Tyr Thr Asn Pro Thr Val
      100       105       110
Arg Arg Tyr Ala Val Ala Arg Leu Arg Gln Ala Asp Asp Glu Asp Leu
      115       120       125
Leu Met Tyr Leu
      130       132

```

<210> 1470

<211> 331

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(331)

<223> Xaa = any amino acid or nothing

<400> 1470

```

Met Gly Glu Ser Pro Ala Val Xaa Gly Tyr Phe Val Leu Ala Gly Met
  1          5          10          15
Asn Ser Ala Gly Leu Ser Phe Gly Gly Gly Ala Gly Lys Tyr Leu Ala
      20        25        30
Glu Trp Met Val His Gly Tyr Pro Ser Glu Asn Val Trp Glu Leu Asp
      35        40        45
Leu Lys Arg Phe Gly Ala Leu Gln Ser Ser Arg Thr Phe Leu Arg His
      50        55        60
Arg Val Met Glu Val Met Pro Leu Met Tyr Asp Leu Lys Val Pro His
      65        70        75        80
Trp Asp Phe Gln Thr Gly Arg Gln Leu Arg Thr Ser Pro Leu Tyr Asp
      85        90        95

```

```

Tyr Trp Thr Lys Tyr Gln Val Trp Glu Trp Leu Gln His Phe Leu Asp
    35          40          45
Thr Asn Gln Leu Asp Ala Asn Cys Ile Pro Phe Gln Glu Phe Asp Ile
    50          55          60
Asn Gly Glu His Leu Cys Ser Met Ser Leu Gln Glu Phe Thr Arg Ala
    65          70          75          80
Ala Gly Thr Ala Gly Gln Leu Leu Tyr Ser Asn Leu Gln His Leu Lys
    85          90          95
Trp Asn Gly Asp Ser Leu Phe Leu Cys Leu Ser Leu Pro Cys
    100          105          110

```

```

<210> 1467
<211> 127
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(127)
<223> Xaa = any amino acid or nothing

```

```

<400> 1467
Gly Thr Ser Gly Gly Pro Lys Arg Val Leu Val Thr Glu Arg Phe Pro
 1      5      10      15
Trp Gln Asn Pro Leu Pro Val Asn Arg Gly Gln Ala Gln Arg Val Leu
    20      25      30
Gly Pro Ser Asn Ser Phe Gln Arg Val Pro Leu Gln Ala Gln Lys Leu
    35      40      45
Val Ser Ser His Lys Pro Gly Gln Asn Gln Lys His Lys Gln Leu Gln
    50      55      60
Ala Thr Ser Val Pro His Pro Val Cys Met Pro Leu Asn Asn Thr Gln
    65      70      75      80
Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu
    85      90      95
Glu Leu Ala Ser Asp Pro Asn Asn Glu Glu Ser Leu Xaa Arg Pro Trp
    100      105      110
Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly Lys Gly Lys
    115      120      125      127

```

```

<210> 1468.
<211> 127
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(127)
<223> Xaa = any amino acid or nothing

```

```

<400> 1468
Thr Tyr Leu Trp Leu Xaa Gly Asn Pro Pro Phe Tyr Glu Lys Asn Asp
 1      5      10      15
Gly Gly Leu Phe Glu Leu Ile Leu Arg Ala Lys Asp Glu Phe Asn Ser
    20      25      30
Pro Tyr Trp Asp Asp Met Ser Asp Ser Ala Lys His Phe Ile Arg Pro
    35      40      45
Leu Thr Gly Arg Asp Pro Xaa Lys Pro Phe Pro Cys Asp Gln Pro Leu
    50      55      60
Gln His Pro Trp Ile Glu Gly His Thr Cys Leu Asp Asn Asn Ile His
    65      70      75      80

```

```

Lys Gln Gln Ala Val Pro Glu Pro His Ser Ser Thr Thr Thr Pro Gln
 1           5           10           15
Glu Gln Glu Gln Asn Trp Tyr Gly Gln Asp Leu Leu Asn Leu Gln Gln
      20           25           30
Arg Thr Lys Val His Leu Pro Gly His Lys Thr Gly Pro Ala Val Ala
 35           40           45
Lys Asp Thr Pro Glu Pro Val Lys Lys Glu Phe Thr Val Pro Ala Thr
 50           55           60
Ser Gln Gly Pro Xaa Ser Pro Phe Ser Glu Glu Pro Pro Leu Pro Pro
 65           70           75           80
Ser Asn Glu Glu Val Pro Pro Thr Leu Pro Pro Xaa Glu Pro Gln Ser
      85           90           95
Glu Asp Pro Xaa Lys Asn Ala Xaa Leu Lys Gln Met His Ala Ala Thr
      100           105           110
Thr His Trp Gln Gln His Gln Gln His Gln Val Gly Cys Gln Tyr His
      115           120           125
Gly Ile Met Gln
      130           132

```

```

<210> 1465
<211> 96
<212> PRT
<213> Homo sapiens
/
<221> misc_feature
<222> (1)...(96)
<223> Xaa = any amino acid or nothing

```

```

<400> 1465
Ala Gly Ser Tyr Pro Ser Met Val Trp Ser Cys His Trp Gly Val Thr
 1           5           10           15
Gln Lys Arg Arg Ala Leu Xaa Val Tyr Ser Phe Glu Glu Gly Gly Arg
      20           25           30
Arg Lys Cys Gly Gln Tyr Trp Pro Leu Glu Lys Asp Ser Arg Ile Arg
 35           40           45
Phe Gly Phe Leu Thr Val Ser Asn Leu Gly Val Glu Asn Met Asn His
 50           55           60
Tyr Lys Lys Ser Thr Leu Glu Ile Leu Asn Pro Glu Val Asn Pro Gly
 65           70           75           80
Phe Phe Phe Leu Thr Leu Trp Lys Gln Gly Glu Asn Asn Tyr Cys Asn
      85           90           95           96

```

```

<210> 1466
<211> 110
<212> PRT
<213> Homo sapiens
/
<221> misc_feature
<222> (1)...(110)
<223> Xaa = any amino acid or nothing

```

```

<400> 1466
Leu Pro Pro Gln Arg Pro Ala Xaa Thr Asp Ser Tyr Ser Thr Cys Asn
 1           5           10           15
Val Ser Ser Gly Phe Leu Ala Gly Gln Ser His Asn Ile His Leu Gln
      20           25           30

```

<213> Homo sapiens

<221> misc_feature

<222> (1)...(109)

<223> Xaa = any amino acid or nothing

<400> 1462

```

Thr Thr Ser Trp Thr Thr Ser Cys Thr Arg Ser Cys Thr Xaa Ser Gly
 1          5          10          15
Ala Ser Ser Gly Pro Gly Trp Thr Pro Arg Thr Thr Trp Trp Arg Ser
          20          25          30
Arg Arg Ser Ser Gln Arg Thr Cys Ser Arg Ala Cys Ser Gly Ala Trp
          35          40          45
Ser Arg Thr Trp Xaa Arg Ser Ser Xaa Thr Ser Ser Ser Ser Cys Ser
          50          55          60
Thr Ser Cys Ser Ser Ser Ser Ser Arg Ser Cys Gly Arg Pro Gly Gly
          65          70          75          80
Pro Leu Gly Ala Arg Gly Val His Ile Thr Ser Cys Leu Asn Ser Cys
          85          90          95
Met Ser Ser Ser Thr Thr Ser Ser Thr Thr Ser Thr Phe
          100          105          109

```

<210> 1463

<211> 96

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(96)

<223> Xaa = any amino acid or nothing

<400> 1463

```

His Glu Asp Ile Met Thr His Tyr Asp Arg Leu Val Asp Glu Xaa Ala
 1          5          10          15
Leu Asn Ala Gly Lys Gln Arg Tyr Glu Lys Met Ile Ser Gly Met Tyr
          20          25          30
Leu Gly Glu Ile Val Arg Asn Ile Leu Ile Asp Phe Thr Lys Lys Gly
          35          40          45
Phe Leu Leu Arg Gly Gln Ile Ser Glu Met Leu Lys Thr Arg Gly Ile
          50          55          60
Phe Leu Thr Phe Leu Leu Ser Asn Phe Leu Ile Val Cys Val Leu Leu
          65          70          75          80
Phe Tyr Val Ser Phe Tyr Leu Phe Gln Ser Cys Ile Asn Phe Val Leu
          85          90          95          96

```

<210> 1464

<211> 132

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(132)

<223> Xaa = any amino acid or nothing

<400> 1464

<210> 1460
 <211> 116
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(116)
 <223> Xaa = any amino acid or nothing

<400> 1460
 His Glu Asp Leu Ser Ser Leu Leu Thr Arg Gly Ser Gly Asn Gln Glu
 1 5 10 15
 Arg Glu Arg Gln Leu Lys Lys Leu Ile Ser Leu Arg Asp Trp Met Leu
 20 25 30
 Ala Glu Leu Ala Phe Pro Val Gly Val Leu Ala Thr Cys Ala Xaa Ser
 35 40 45
 Leu Leu Ser Cys Xaa Tyr Cys Val Ile Leu Phe Pro Cys Ser Cys Phe
 50 55 60
 Phe Phe His Ser Pro Asp Ala Leu Phe Ser Leu Leu Leu Ser Cys
 65 70 75 80
 Tyr Phe Pro Ser Tyr Cys Phe Phe Tyr Tyr Leu Phe Phe Ser Ser Ser
 85 90 95
 Pro Leu Cys Leu Leu Ala Ser Ser Pro Phe Pro Leu Phe Ile Leu
 100 105 110
 Leu Ala Ser Leu
 115 116

<210> 1461
 <211> 114
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(114)
 <223> Xaa = any amino acid or nothing

<400> 1461
 Phe Thr Ser Thr Met Thr Lys Pro Phe Glu Lys Glu Ser Glu Gln Pro
 1 5 10 15
 Ala Xaa Ala Thr Leu Ala Phe Gly Ala Gln Thr Ser Thr Thr Ala Asp
 20 25 30
 Gln Cys Ala Leu Lys Pro Asp Leu Ser Tyr Leu Asn Asn Ser Ser Ser
 35 40 45
 Ser Ser Ser Thr Pro Ala Thr Ser Ala Gly Gly Gly Ile Phe Gly Ser
 50 55 60
 Ser Thr Ser Ser Ser Asn Pro Pro Val Ala Thr Phe Val Phe Gly Gln
 65 70 75 80
 Ser Ser Asp Pro Val Ser Ser Tyr Gly Phe Val Asn Thr Ala Glu Ser
 85 90 95
 Ser Thr Ser Asp Ser Leu Leu Phe Ser Gln Asp Ser Lys Leu Ala Thr
 100 105 110
 Thr Ser
 114

<210> 1462
 <211> 109
 <212> PRT

<210> 1458
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 1458
 Arg Val Ala Ile Ser Leu Leu Cys Ala Ala Ile Phe Ile Ser Phe Met
 1 5 10 15
 Val Gln Ser Ala Gly Lys Arg Trp Pro Thr Gly Val Met Leu Met Val
 20 25 30
 Val Val Leu Phe Ala Phe Leu Tyr Ser Trp Pro Ile Gln Ala Leu Leu
 35 40 45
 Pro Thr Tyr Leu Lys Thr Asp Leu Ala Tyr Asn Pro His Thr Val Ala
 50 55 60
 Asn Val Leu Ser Phe Ser Gly Phe Gly Ala Ala Val Gly Cys Cys Val
 65 70 75 80
 Gly Gly Phe Leu Gly Asp Trp Leu Gly Thr Arg Lys Ala Tyr Val Cys
 85 90 95
 Ser Leu Leu Ala Ser Gln Leu Leu Ile Ile Pro Val Phe Ala Ile Gly
 100 105 110
 Gly Ala Asn Val Trp Val Leu Gly Leu Leu Phe Phe Gln Gln Met
 115 120 125
 Leu Gly Gln Gly Ile Ala Gly Ile Leu Pro Lys Leu Ile Gly Gly Tyr
 130 135 140
 Phe Asp Thr Asp Gln Arg Ala Ala Gly Leu Gly Phe Thr Tyr Asn Val
 145 150 155 160
 Gly Ala Leu Gly Gly Ala Leu Ala Pro Ile Ile Gly Ala Leu Ile Ala
 165 170 175
 Gln Arg Leu Asp Leu Gly Thr Ala Leu Ala Ser Leu Ser Phe Ser Leu
 180 185 190
 Thr Phe Val Val Ile Leu Arg Asn Arg Arg Pro Gly Lys Ser Leu Val
 195 200 205
 Arg
 209

<210> 1459
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1459
 Val Leu Val Ala Leu Pro Asp Thr Val Thr Ser Glu Thr Val Val Thr
 1 5 10 15
 Glu Val Leu Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp
 20 25 30
 Ser His Asn Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr
 35 40 45
 Ser Gly Cys Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr
 50 55 60
 Ser Arg Lys Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly
 65 70 75 80
 Asp Val Ser Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val
 85 90 95
 Tyr Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile
 100 105 110
 Asn Val Arg Leu Asn Leu Gln Arg Ala Ser Thr Thr
 115 120 124

Ile Leu Ala Val Ile Asp Ser Ile Phe Val Trp Phe Ile Phe Ile Ser
 35 40 45
 Leu Ala Gln Thr Met Lys Thr Leu Arg Leu Arg Lys Asn Thr Val Lys
 50 55 60
 Phe Ser Leu Tyr Arg His Phe Lys Asn Thr Leu Ile Phe Ala Val Leu
 65 70 75 80
 Ala Ser Ile Val Phe Met Gly Trp Thr Thr Lys Thr Phe Arg Ile Ala
 85 90 95
 Lys Cys Gln Ser Asp Trp Met Glu Arg Trp Val Asp Asp Ala Phe Trp
 100 105 110
 Ser Phe Leu Phe Ser Leu Ile Leu Ile Val Ile Met Phe Leu Trp Arg
 115 120 125
 Pro Ser Ala
 130 131

<210> 1456
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 1456
 Glu Asp Gly His Gly Gly Trp Ser Ser Arg Cys Leu Val Asp His Ala
 1 5 10 15
 Glu Glu Gly His Arg Glu Pro Trp Lys Arg Leu Cys Ile Trp Gln Arg
 20 25 30
 Gly Gly His Glu Ile Arg Phe Ala Phe Tyr Phe Pro Gly His Pro Leu
 35 40 45
 Leu Ser Pro Gln Ile Cys Leu Ala Pro Glu Thr Pro Pro Arg Gly Cys
 50 55 60
 Pro Pro Val Ser Ser Leu His Phe Ile Ser Leu Gln Arg Leu Pro Arg
 65 70 75 80
 Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly Leu Phe
 85 90 95
 Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys Lys Met
 100 105 110
 Thr Ser Gly Thr Phe Trp Thr Cys Arg Thr Asp Ser Arg Val Phe Gln
 115 120 125
 Asn Ala Asn Pro Ser Asn Ala Ala His Ser Glu Asp Gln Pro Thr Pro
 130 135 140 144

<210> 1457
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 1457
 Phe Phe Phe Val Thr Arg Ser His Ser Val Ala Gln Ala Glu Cys Ser
 1 5 10 15
 Gly Val Phe Thr Ala His Arg Ser Leu Asp Leu Val Gly Ser Ser Asn
 20 25 30
 Tyr Pro Ala Leu Ser Leu Gln Ser Ser Trp Asp His Arg His Thr Trp
 35 40 45
 Leu Ile Phe Ala Phe Leu
 50 54

<213> Homo sapiens

<400> 1453

```

Cys His Ser Thr Glu Ser Ser Ser Asp Phe Ile Leu Pro Gly Asp Tyr
 1          5          10          15
Leu Leu Gly Gly Leu Cys Pro Leu His Ser Gly Cys Leu Gln Val Cys
          20          25          30
Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg Leu Ala
          35          40          45
Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile Thr Leu
          50          55          60
Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val Tyr Ala
          65          70          75          80
Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu Leu Gln
          85          90          95
Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile Gly Pro
          100          105          110
Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser Pro Phe
          115          120          125
Leu Val Pro Met Leu Leu Glu Gln
          130          135 136

```

<210> 1454

<211> 144

<212> PRT

<213> Homo sapiens

<400> 1454

```

Asn Ser Arg Val Glu Asp Arg Ser Asn Met Ser Leu Trp Thr Gln Asn
 1          5          10          15
Ile Thr Val Cys Pro Val Arg Asn Val Thr Arg Asp Gly Gly Phe Gly
          20          25          30
Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu Asp Gly Asp Asn Ser
          35          40          45
Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp Ser Pro Arg Pro Arg
          50          55          60
Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile His Ile Ala Asn Cys
          65          70          75          80
Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser Trp Ala Leu Cys Ser
          85          90          95
Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln Arg Ser Cys Ser Asn
          100          105          110
Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val Gly Lys Ser Arg Glu
          115          120          125
Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro Val Pro Ile Phe
          130          135          140          143

```

<210> 1455

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1455

```

Gly Leu Gly Leu Leu Tyr Leu Ile Phe Ala Ala Val Glu Gly Val Met
 1          5          10          15
Arg Val Ile Gly Gly Ser Asn His Leu Ala Val Val Leu Asp Asp Ile
          20          25          30

```

Arg His Gly Tyr Arg Val Asp Ser Asn Gln Val Trp Val Met Arg Asp
 225 230 235 240
 Val
 241

<210> 1451
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1451
 Asp Trp Pro Asp Leu Phe Thr Tyr Pro Leu Ile Gly Ser Pro Lys Cys
 1 5 10 15
 Phe Gln Ser Ala Arg Pro Glu Arg Met Tyr Arg Arg Thr Val Arg Ser
 20 25 30
 Ser His Gly Asn His Ala Leu Gln Glu Val Leu Pro Arg Ser Gly His
 35 40 45
 Gly Thr Glu Phe Thr Lys Gln Lys His Leu Glu Ala Ala Asp His Gly
 50 55 60
 His Pro Pro Ala Arg Met Ser Ile Phe Ser Arg
 65 70 75

<210> 1452
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 1452
 Ala His Leu Leu Met Leu Asn Leu Ala Leu Thr Asp Leu Leu Tyr Leu
 1 5 10 15
 Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly Glu Asn Trp
 20 25 30
 Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser Phe His Phe
 35 40 45
 Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser Ile Phe Arg
 50 55 60
 Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His Lys Thr
 65 70 75 80
 Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser Leu Val
 85 90 95
 Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg Thr Asn
 100 105 110
 Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn Thr Ile
 115 120 125
 Lys Trp Tyr Asn Leu Ile Leu Thr Ala Leu Leu Cys Leu Pro Leu Val
 130 135 140
 Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu Thr His Gly
 145 150 155 160
 His Ala Asn Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg Leu Thr Ile
 165 170 175
 Leu Leu Leu
 179

<210> 1453
 <211> 137
 <212> PRT

Leu Val Pro Glu Glu Leu Pro Pro Ser Arg Gly Gly Leu Gly Glu Ala
 355 360 365
 Leu Gly Ala Val Glu Leu Ser Leu Ser Glu Phe Leu Leu Phe Thr
 370 375 380
 Thr Ala Gly Ile Tyr Val Asp Gly Ala Gly Arg Lys Ser Arg Gly His
 385 390 395 400
 Glu Leu Leu Trp Pro Ala Ala Pro Met Gly Trp Gly Tyr Ala Ala Pro
 405 410 415
 Tyr Leu Thr Val Phe Ser Glu Asn Ser Ile Asp Val Phe Asp Val Arg
 420 425 430
 Arg Ala Glu Trp Val Gln Thr Val Pro Leu Lys Lys Val Arg Pro Leu
 435 440 445
 Asn Pro Glu Gly Ser Leu Phe Leu Tyr Gly Thr Glu Lys Val Arg Leu
 450 455 460
 Thr Tyr Leu Arg Asn Gln Leu Ala Glu Lys Asp Glu Phe Asp Ile Pro
 465 470 475 480
 Asp Leu Thr Asp Asn Ser Arg Arg Gln Leu Phe Arg Thr Lys Ser Lys
 485 490 495
 Arg Arg Phe Phe Phe Arg Val Ser Glu Glu Gln Gln Lys Gln Gln Arg
 500 505 510
 Arg Glu Met Leu Lys Asp Pro Phe Val Arg Ser Lys Leu Ile Ser Pro
 515 520 525
 Pro Thr Asn Phe Asn His Leu Val His Val Gly Pro Ala Asn Gly Arg
 530 535 540
 Pro Gly Ala Arg Asp Lys Ser Pro
 545 550 552

<210> 1450
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 1450
 Ser Leu Cys Val Pro Gly Pro Val Asp Thr Gly Thr Phe Ala Val Met
 1 5 10 15
 Ser Val Met Val Gly Ser Val Thr Glu Ser Leu Ala Pro Gln Ala Leu
 20 25 30
 Asn Asp Ser Met Ile Asn Glu Thr Ala Arg Asp Ala Ala Arg Val Gln
 35 40 45
 Val Ala Ser Thr Leu Ser Val Leu Val Gly Leu Phe Gln Val Gly Leu
 50 55 60
 Gly Leu Ile His Phe Gly Phe Val Val Thr Tyr Leu Ser Glu Pro Leu
 65 70 75 80
 Val Arg Gly Tyr Thr Thr Ala Ala Ala Val Gln Val Phe Val Ser Gln
 85 90 95
 Leu Lys Tyr Val Phe Gly Leu His Leu Ser Ser His Ser Gly Pro Leu
 100 105 110
 Ser Leu Ile Tyr Thr Val Leu Glu Val Cys Trp Lys Leu Pro Gln Ser
 115 120 125
 Lys Val Gly Thr Val Val Thr Ala Ala Val Ala Gly Val Val Leu Val
 130 135 140
 Val Val Lys Leu Leu Asn Asp Lys Leu Gln Gln Gln Leu Pro Met Pro
 145 150 155 160
 Ile Pro Gly Glu Leu Leu Thr Leu Ile Gly Ala Thr Gly Ile Ser Tyr
 165 170 175
 Gly Met Gly Leu Lys His Arg Phe Glu Ala Gly Pro Pro Val Ala Pro
 180 185 190
 Asn Thr Gln Leu Phe Ser Lys Leu Val Gly Ser Ala Phe Thr Ile Ala
 195 200 205
 Val Val Gly Phe Ala Ile Ala Ile Ser Leu Gly Lys Ile Phe Ala Leu
 210 215 220

Ala	Leu	Gln	Lys	Leu	Phe	Glu	Met	Asp	Ala	His	Gly	Arg	Val	Trp	Ser
50						55					60				
Gln	Asp	Leu	Ile	Leu	Gln	Val	Arg	Asp	Gly	Trp	Leu	Gln	Leu	Leu	Asp
65					70					75					80
Ile	Glu	Thr	Lys	Glu	Glu	Leu	Asp	Ser	Tyr	Arg	Leu	Asp	Ser	Ile	Gln
				85					90					95	
Ala	Met	Asn	Val	Ala	Leu	Asn	Thr	Cys	Ser	Tyr	Asn	Ser	Ile	Leu	Ser
			100					105					110		112

<210> 1449
 <211> 554
 <212> PRT
 <213> Homo sapiens

<400> 1449

Cys	Gly	Tyr	Phe	Cys	His	Thr	Thr	Cys	Ala	Pro	Gln	Ala	Pro	Pro	Cys
1				5					10					15	
Pro	Val	Pro	Pro	Asp	Leu	Leu	Arg	Thr	Ala	Leu	Gly	Val	His	Pro	Glu
			20					25					30		
Thr	Gly	Thr	Gly	Thr	Ala	Tyr	Glu	Gly	Phe	Leu	Ser	Val	Pro	Arg	Pro
		35					40					45			
Ser	Gly	Val	Arg	Arg	Gly	Trp	Gln	Arg	Val	Phe	Ala	Ala	Leu	Ser	Asp
	50				55					60					
Ser	Arg	Leu	Leu	Leu	Phe	Asp	Ala	Pro	Asp	Leu	Arg	Leu	Ser	Pro	Pro
	65				70					75					80
Ser	Gly	Ala	Leu	Leu	Gln	Val	Leu	Asp	Leu	Arg	Asp	Pro	Gln	Phe	Ser
			85					90						95	
Ala	Thr	Pro	Val	Leu	Ala	Ser	Asp	Val	Ile	His	Ala	Gln	Ser	Arg	Asp
			100					105					110		
Leu	Pro	Arg	Ile	Phe	Arg	Val	Thr	Ser	Gln	Leu	Ala	Val	Pro	Pro	
		115					120					125			
Thr	Thr	Cys	Thr	Val	Leu	Leu	Leu	Ala	Glu	Ser	Glu	Gly	Glu	Arg	Glu
	130					135					140				
Arg	Trp	Leu	Gln	Val	Leu	Gly	Glu	Leu	Gln	Arg	Leu	Leu	Leu	Asp	Ala
	145				150				155						160
Arg	Pro	Arg	Pro	Arg	Pro	Val	Tyr	Thr	Leu	Lys	Glu	Ala	Tyr	Asp	Asn
			165					170						175	
Gly	Leu	Pro	Leu	Leu	Pro	His	Thr	Leu	Cys	Ala	Ala	Ile	Leu	Asp	Gln
		180						185					190		
Asp	Arg	Leu	Ala	Leu	Gly	Thr	Glu	Glu	Gly	Leu	Phe	Val	Ile	His	Leu
		195					200					205			
Arg	Ser	Asn	Asp	Ile	Phe	Gln	Val	Gly	Glu	Cys	Arg	Arg	Val	Gln	Gln
	210					215					220				
Leu	Thr	Leu	Ser	Pro	Ser	Ala	Gly	Leu	Leu	Val	Val	Leu	Cys	Gly	Arg
	225				230					235					240
Gly	Pro	Ser	Val	Arg	Leu	Phe	Ala	Leu	Ala	Glu	Leu	Glu	Asn	Ile	Glu
			245						250					255	
Val	Glu	Val	Pro	Lys	Ile	Pro	Glu	Ser	Arg	Gly	Cys	Gln	Val	Leu	Ala
		260						265					270		
Ala	Gly	Ser	Ile	Leu	Gln	Ala	Arg	Thr	Pro	Val	Leu	Cys	Val	Ala	Val
		275					280					285			
Lys	Arg	Gln	Val	Leu	Cys	Tyr	Gln	Leu	Gly	Pro	Gly	Pro	Gly	Pro	Trp
	290					295					300				
Gln	Arg	Arg	Ile	Arg	Glu	Leu	Gln	Ala	Pro	Ala	Thr	Val	Gln	Ser	Leu
	305				310					315					320
Gly	Leu	Leu	Gly	Asp	Arg	Leu	Cys	Val	Gly	Ala	Ala	Gly	Gly	Phe	Ala
			325						330					335	
Leu	Tyr	Pro	Leu	Leu	Asn	Glu	Ala	Ala	Pro	Leu	Ala	Leu	Gly	Ala	Gly
			340					345					350		

Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe Val Glu Glu
 305 310 315 320
 Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp Ala Gln Leu
 325 330 335
 Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln Lys Leu Arg
 340 345 350
 Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly Asp Pro Lys
 355 360 365
 Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His Leu Lys Glu
 370 375 380
 Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His Glu Asp Lys
 385 390 395 400
 Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu Tyr Ala Arg
 405 410 415
 Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr Asp Tyr Arg
 420 425 430
 Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala Pro Lys Lys
 435 440 445
 Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg Asn Leu Ser
 450 455 460
 Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln Ala Lys Leu
 465 470 475 480
 Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr Glu Glu Trp
 485 490 495
 His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr Leu Ile Ile
 500 505 510
 Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser Leu Leu Phe
 515 520 525
 Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser Lys Gly Leu
 530 535 540
 Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg Arg Glu Cys
 545 550 555 560
 Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu Ser Gly Glu
 565 570 575
 Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu Phe Ile Val
 580 585 590
 Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu Lys Asp Ile
 595 600 605
 Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr Leu Gly Gln
 610 615 620
 Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe Leu Pro Lys
 625 630 635 640
 Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His Glu Pro Pro Lys
 645 650 655
 Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu Arg Phe Ala Arg Ile
 660 665 670
 Met Leu Ser Leu Ser Arg Thr Pro Ala Asp Gly Arg
 675 680 684

<210> 1448

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1448

Ser Gly Pro Ser Ser Arg Ala Ile Tyr Leu His Arg Lys Glu Tyr Ser
 1 5 10 15
 Gln Asn Leu Thr Ser Glu Pro Thr Leu Leu Gln His Arg Val Glu His
 20 25 30
 Leu Met Thr Cys Lys Gln Gly Ser Gln Arg Val Gln Gly Pro Glu Asp
 35 40 45

Leu Phe Val Pro Arg Arg His Gly Glu Arg Arg Asn Ser Asn Leu Ser
 370 375 380
 Gln Thr Ser Arg Ser Ser Arg Met Leu Ala Val Phe Pro Ala Asn Gly
 385 390 395 400
 Lys Met His Ser Thr Val Asp Cys Asn Gly Val Val Ser Leu Val Gly
 405 410 415
 Gly Pro Ser Val Pro Thr Ser Pro Val Gly Gln Leu Leu Pro Glu Val
 420 425 430
 Ile Ile Asp Lys Pro Ala Thr Asp Asp Asn Gly Thr Thr Thr Glu Thr
 435 440 445
 Glu Met Arg Lys Arg Arg Ser Ser Ser Phe His Val Ser Met Asp Phe
 450 455 460
 Leu Glu Asp Pro Ser Gln Arg Gln Arg Ala Met Ser Ile Ala Ser Ile
 465 470 475 480
 Leu Thr Asn Thr Val Glu
 485 486

<210> 1447
 <211> 685
 <212> PRT
 <213> Homo sapiens

<400> 1447
 Ile Gln Thr Gln Leu Pro Thr Lys Ser Ser Gln Gln Leu Arg Lys Gly
 1 5 10 15
 Gly Asn Cys Val Arg Cys Lys Met Gln Met Asn Phe Ile Ala Glu Glu
 20 25 30
 Val Leu Leu Lys Tyr Arg Ile Thr Phe Tyr Asn Asn Asn Lys Gly Pro
 35 40 45
 Asn Met Leu Tyr Ile Glu Ile Lys Ala Phe Val His Phe Met Ile Asn
 50 55 60
 Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val Asp
 65 70 75 80
 Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys Thr
 85 90 95
 Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser Ile
 100 105 110
 Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala Leu Ser
 115 120 125
 Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile Ser Ser
 130 135 140
 Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro Pro Asp
 145 150 155 160
 Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu Leu Ser
 165 170 175
 Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu Asn Asp
 180 185 190
 Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr Ile Glu
 195 200 205
 Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg Leu His
 210 215 220
 Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr Trp Ala
 225 230 235 240
 Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn Asp Ile
 245 250 255
 Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser Phe Gly
 260 265 270
 Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn Asp Lys
 275 280 285
 Ala Gln Phe Leu Ile Gln Glu Asp Leu Ile Lys Thr Gly Gln Pro Leu
 290 295 300

Ser Val Val Ala Tyr Thr Ile Glu Lys Glu Glu Asn Glu Gly Leu Ala
 130 135 140
 Thr Ile Pro Ala Cys Trp Trp Ala Thr Val Ser Met Thr Thr Val
 145 150 155 160
 Gly Tyr Gly Asp Val Val Pro Gly Thr Thr Ala Gly Lys Leu Thr Ala
 165 170 175
 Ser Ala Cys Ile Leu Ala
 180 182

<210> 1446
 <211> 489
 <212> PRT
 <213> Homo sapiens

<400> 1446
 Gln Leu Leu Pro Pro Ser Asn Arg Glu Asn Ala Gly Leu Leu Val Gly
 1 5 10 15
 Arg Cys Leu Cys Ser Ala Ala Leu Arg Pro Val Gly Asp Leu Ile Thr
 20 25 30
 Ser Ser Gly Gln Val Ala Val Arg Asn Ala Pro Gln Ala Gly Ser Ala
 35 40 45
 Lys Ala Gly Lys Gly Lys Phe Gln Asp Asn Phe Glu Phe Ile Gln Tyr
 50 55 60
 Phe Lys Lys Phe Phe Asp Ala Asn Cys Asn Glu Lys Asp Tyr Asn Pro
 65 70 75 80
 Val Ala Ala Gly Gln Gly Gln Glu Thr Glu Val Ala Pro Ser Ile Val
 85 90 95
 Ala Pro Val Leu Asn Lys Pro Asn Gln Cys Pro Glu Gly Tyr Ile Cys
 100 105 110
 Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp Thr
 115 120 125
 Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp Tyr
 130 135 140
 Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Glu Thr Thr Tyr
 145 150 155 160
 Met Ile Phe Leu Val Leu Val Ile Leu Leu Gly Ser Leu Tyr Leu Val
 165 170 175
 Thr Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn Gln
 180 185 190
 Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln Met
 195 200 205
 Leu Glu Gln Leu Lys Lys Gln Gln Glu Ala Ala Gln Gln Ala Ala Thr
 210 215 220
 Ala Thr Ala Ser Glu His Ser Arg Glu Pro Ser Ala Ala Gly Arg Leu
 225 230 235 240
 Ser Asp Ser Ser Ser Glu Ala Ser Lys Leu Ser Ser Lys Ser Ala Lys
 245 250 255
 Glu Arg Arg Asn Arg Arg Lys Lys Arg Lys Gln Lys Glu Gln Ser Gly
 260 265 270
 Gly Glu Glu Lys Asp Glu Asp Glu Phe Gln Lys Ser Glu Ser Glu Asp
 275 280 285
 Ser Ile Arg Arg Lys Gly Phe Arg Phe Ser Ile Glu Gly Asn Arg Leu
 290 295 300
 Thr Tyr Glu Lys Arg Tyr Ser Ser Pro His Gln Ser Leu Leu Ser Ile
 305 310 315 320
 Arg Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Thr Ser Leu Phe
 325 330 335
 Ser Phe Arg Gly Arg Ala Lys Asp Val Gly Ser Glu Asn Asp Phe Ala
 340 345 350
 Asp Asp Glu His Ser Thr Phe Glu Asp Asn Glu Ser Arg Arg Asp Ser
 355 360 365

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Thr Leu Ala His Glu Ala Ala Pro Leu Pro Ala Gly Arg Pro Arg Pro
      180      185      190
Thr Thr Asn Leu Phe Thr Lys Leu Thr Ser Lys Leu Thr Arg Arg Val
      195      200      205
Ala Asp Glu Pro Glu Arg Ile Gly Gly Pro Glu Val Thr Arg Arg Pro
      210      215      220
Arg Gln Glu Asp His Leu Ser Pro Gly Gly Arg Gly Cys Ser Glu Leu
      225      230      235      240

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<210> 1444
<211> 129
<212> PRT
<213> Homo sapiens

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<400> 1444
Lys Phe Ser Gln Trp Gly Leu Thr Lys Pro Lys Leu Ser Asn Ala Ser
  1      5      10      15
Pro Trp Ile Ser Leu Val Lys Lys Leu Met Lys Lys Trp Ser Val Thr
      20      25      30
Gln Asn Leu Thr Phe Arg Glu Gln Leu Glu Ala Gly Ile Arg Tyr Phe
      35      40      45
Asp Leu Arg Val Ser Ser Lys Pro Gly Asp Ala Asp Gln Glu Ile Tyr
      50      55      60
Phe Ile His Gly Leu Phe Gly Ile Lys Val Trp Asp Gly Leu Met Glu
      65      70      75      80
Ile Asp Ser Phe Leu Thr Gln His Pro Gln Glu Ile Ile Phe Leu Asp
      85      90      95
Phe Asn His Phe Tyr Ala Met Asp Glu Thr His His Lys Cys Leu Val
      100      105      110
Leu Arg Ile Gln Glu Ala Phe Gly Asn Lys Leu Cys Pro Ala Cys Arg
      115      120      125      128

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<210> 1445
<211> 184
<212> PRT
<213> Homo sapiens

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<400> 1445
Gly Pro Arg Asp Asn Pro Gly Glu Asp Pro Arg Phe Glu Ile Val Glu
  1      5      10      15
His Phe Gly Ile Ala Trp Phe Thr Phe Glu Leu Val Ala Arg Phe Ala
      20      25      30
Val Ala Pro Asp Phe Leu Lys Phe Phe Lys Asn Ala Leu Asn Leu Ile
      35      40      45
Asp Leu Met Ser Ile Val Pro Phe Tyr Ile Thr Leu Val Val Asn Leu
      50      55      60
Val Val Glu Ser Thr Pro Thr Leu Ala Asn Leu Gly Arg Val Ala Gln
      65      70      75      80
Val Leu Arg Leu Met Arg Ile Phe Arg Ile Leu Lys Leu Ala Arg His
      85      90      95
Ser Thr Gly Leu Arg Ser Leu Gly Ala Thr Leu Lys Tyr Ser Tyr Lys
      100      105      110
Glu Val Gly Leu Leu Leu Leu Tyr Leu Ser Val Gly Ile Ser Ile Phe
      115      120      125

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<210> 1442
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 1442
 Val Phe Asp Glu Glu Asn Ile Leu Asn Glu Leu Asn Asp Pro Leu Arg
 1 5 10 15
 Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Thr Met Pro
 20 25 30
 Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Ser Lys
 35 40 45
 Leu Arg Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu Gly
 50 55 60
 Ala Val Gly Lys Lys Met Tyr Phe Ile Gln His Gly Val Ala Gly Val
 65 70 75 80
 Ile Thr Lys Ser Ser Lys Glu Met Lys Leu Thr Asp Gly Ser Tyr Phe
 85 90 95
 Gly Glu Ile Cys Leu Leu Thr Lys Gly Arg Arg Thr Ala Ser Val Arg
 100 105 110
 Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe Asn
 115 120 125
 Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr Val
 130 135 140
 Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu Leu
 145 150 155 160
 Gln Lys Phe Gln Lys Asp Leu Asn Thr Gly Val Phe Asn Asn Gln Glu
 165 170 175
 Asn Glu Ile Leu Lys Gln Ile Val Lys His
 180 185 186

<210> 1443
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 1443
 Thr Val Pro Pro Pro Gly Gly Pro Ser Pro Ala Pro Leu His Pro
 1 5 10 15
 Lys Arg Ser Pro Thr Ser Thr Gly Glu Ala Glu Leu Lys Glu Glu Arg
 20 25 30
 Leu Pro Gly Arg Lys Ala Ser Cys Ser Thr Ala Gly Ser Gly Ser Arg
 35 40 45
 Gly Leu Pro Pro Ser Ser Pro Met Val Ser Ser Ala His Asn Pro Asn
 50 55 60
 Lys Ala Glu Ile Pro Glu Arg Arg Lys Asp Ser Thr Ser Thr Pro Asn
 65 70 75 80
 Asn Leu Pro Pro Ser Met Met Thr Arg Arg Asn Thr Tyr Val Cys Thr
 85 90 95
 Glu Arg Pro Gly Ala Glu Arg Pro Ser Leu Leu Pro Asn Gly Lys Glu
 100 105 110
 Asn Ser Ser Gly Thr Pro Arg Val Pro Pro Ala Ser Pro Ser Ser His
 115 120 125
 Ser Leu Ala Pro Pro Ser Gly Glu Arg Ser Arg Leu Ala Arg Gly Ser
 130 135 140
 Thr Ile Arg Ser Thr Phe His Gly Gly Gln Val Arg Asp Arg Arg Ala
 145 150 155 160
 Gly Gly Gly Gly Gly Gly Val Gln Asn Gly Pro Pro Ala Ser Pro
 165 170 175

Gln Leu Asn Tyr Thr Leu Leu Asp Gly Arg Tyr Leu Ser Glu Glu Pro
 165 170 175
 Glu Pro Tyr Leu Ala Val Tyr Leu His Ser Glu Pro Arg Pro Asn Glu
 180 185 190
 His Asn Cys Ser Ala Ser Arg Arg Ile Arg Pro Glu Ser Leu Gln Gly
 195 200 205
 Ala Asp His Arg Pro Tyr Thr Phe Phe Ile Ser Pro Gly Thr Arg Asp
 210 215 220
 Pro Val Gly Ser Tyr Arg Leu Asn Leu Ser Ser His Phe Arg Trp Ser
 225 230 235 240
 Ala Leu Glu Val Ser Val Gly Leu Tyr Thr Ser Leu Cys Gln Tyr Phe
 245 250 255
 Ser Glu Glu Asp Val Val Trp Arg Thr Glu Gly Leu Leu Pro Leu Glu
 260 265 270
 Glu Thr Ser Pro Arg Gln Ala Val Cys Leu Thr Arg His Leu Thr Ala
 275 280 285
 Phe Gly Thr Ser Leu Phe Val Pro Pro Ser His Ile Arg Phe Val Phe
 290 295 300
 Pro Glu Pro Thr Ala Asp Val Asn Tyr Ile Val Met Leu Thr Cys Ala
 305 310 315 320
 Val Cys Leu Val Thr Tyr Met Val Met Ala Ala Ile Leu His Lys Leu
 325 330 335
 Asp Gln Leu Asp Ala Ser Arg Gly Arg Ala Ile Pro Phe Cys Gly Gln
 340 345 350
 Arg Gly Arg Phe Lys Tyr Glu Ile Leu Val Lys Thr Gly Trp Gly Arg
 355 360 365
 Gly Ser Gly Thr Thr Ala His Val Gly Ile Met Leu Tyr Gly Val Asp
 370 375 380
 Ser Arg Ser Gly His Arg His Leu Asp Gly Asp Arg Ala Phe His Arg
 385 390 395 400
 Asn Ser Leu Asp Ile Phe Gln Ile Ala Thr Pro His Ser Leu Gly Ser
 405 410 415
 Met Trp Lys Ile Arg Val Trp His Asp Asn Lys Gly Leu Ser Pro Ala
 420 425 430
 Trp Phe Leu Gln His Ile Ile Val Arg Asp Leu Gln Thr Ala Arg Ser
 435 440 445
 Thr Phe Phe Leu Val Asn Asp Trp Leu Ser Val Glu Thr Glu Ala Asn
 450 455 460
 Gly Gly Leu Val Glu Lys Glu Val Leu Ala Ala Ser Lys Ala Ser Phe
 465 470 475 480
 Arg Val Pro Thr Pro Ser Ala Ala Leu Leu Arg Phe Arg Arg Leu Leu
 485 490 495
 Val Ala Glu Leu Gln Arg Gly Phe Phe Asp Lys His Ile Trp Leu Ser
 500 505 510
 Ile Trp Asp Arg Pro Pro Arg Ser Cys Phe Thr Arg Ile Gln Arg Ala
 515 520 525
 Thr Cys Cys Val Leu Leu Ile Cys Leu Phe Leu Gly Ala Asn Ala Val
 530 535 540
 Trp Tyr Gly Ala Val Gly Asp Ser Ala Tyr Ser Thr Gly Arg Val Ser
 545 550 555 560
 Arg Leu Asn Pro Leu Ser Val Asp Thr Val Ala Val Gly Leu Val Ser
 565 570 575
 Ser Val Val Val Tyr Pro Val Tyr Leu Ala Ile Leu Phe Leu Phe Arg
 580 585 590
 Met Ser Arg Ser Lys Val Gly Trp Gly Trp Gly Pro Gly Ser Thr Gly
 595 600 605
 Asn Gly Ala Trp Ala Ser Ala Pro Cys Pro Glu Pro Pro Leu Ser Ser
 610 615 620
 Ala Ala Ala Arg Gly Lys Gly Val His Gln Arg Leu Leu Gly Lys Gly
 625 630 635 640
 Gln His Thr
 643

Tyr Gly Phe Leu Pro Val Pro Leu Arg Ala His Ser Thr Leu Gln Asp
 195 200 205
 Glu Ala Glu Ser Phe Met His Val Gln Leu Glu Val Met Val Pro Ser
 210 215 220
 Ser Pro Ser Ser Ala Gln Ser Met Ala Val Val Ser Ala Asp His Ile
 225 230 235 240
 Gly Leu Val Ile Ser Tyr Leu
 245 247

<210> 1440
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1440
 Asn Lys Thr Ser Phe Ile Phe Tyr Leu Lys Asn Ile Val Val Ala Asp
 1 5 10 15
 Leu Ile Met Thr Leu Thr Phe Pro Phe Arg Ile Val His Asp Ala Gly
 20 25 30
 Phe Gly Pro Trp Asp Phe Lys Phe Ile Leu Cys Arg Tyr Thr Ser Val
 35 40 45
 Leu Phe Tyr Ala Asn Met Asp Thr Ser Ile Val Val Leu Gly Leu Ile
 50 55 60
 Thr Tyr Asp Arg Tyr Trp Lys Val Val Arg His Leu Trp Asp Ser Trp
 65 70 75 80
 Met Thr Gly Ile Ser Phe Thr Arg Val Tyr Leu Leu Gly Leu Gly Ala
 85 90 95
 Arg Leu Val Trp Phe Gly Lys Leu Ile Leu Ala Lys Gly Gly His Gly
 100 105 110
 Gly Ile Ser Trp Leu
 115 117

<210> 1441
 <211> 646
 <212> PRT
 <213> Homo sapiens

<400> 1441
 Leu Gly Ser Ser Asp Val Arg Ala Pro Gln Arg Ser Glu Leu Gly Ala
 1 5 10 15
 Glu Ser Pro Ser Arg Met Val Ala Ser Gln Ala Tyr Asn Leu Thr Ser
 20 25 30
 Ala Leu Thr Pro Ile Leu Thr Arg Ser Arg Val Leu Asn Glu Glu Pro
 35 40 45
 Leu Thr Leu Ala Gly Phe Ser Arg Ala Pro Ala Asn Leu Ser Asp Val
 50 55 60
 Val Gln Leu Ile Phe Leu Val Asp Ser Asn Pro Phe Pro Phe Gly Tyr
 65 70 75 80
 Ile Ser Asn Tyr Thr Val Ser Thr Lys Val Ala Ser Met Ala Phe Gln
 85 90 95
 Thr Gln Ala Gly Ala Gln Ile Pro Ile Glu Arg Leu Ala Ser Glu Arg
 100 105 110
 Ala Ile Thr Val Lys Val Pro Asn Asn Ser Asp Trp Ala Ala Arg Gly
 115 120 125
 His Arg Ser Ser Ala Asn Ser Val Val Gln Pro Gln Ala Phe Val Gly
 130 135 140
 Ala Val Val Thr Leu Asp Ser Ser Asn Pro Ala Ala Val Leu His Leu
 145 150 155 160

<211> 178
 <212> PRT
 <213> Homo sapiens

<400> 1438
 Pro Glu Phe Gly Thr Thr Ile Ser Cys Gly Tyr Leu Met Ala Thr Asp
 1 5 10 15
 Val Ser Arg Arg Pro Ser Val His Lys Ala Val Glu Ile Glu Gln Glu
 20 25 30
 Arg Val Lys Ser Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe
 35 40 45
 Arg Phe Tyr Trp Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu
 50 55 60
 Ile Val Leu Pro Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro
 65 70 75 80
 Pro Trp Ile Val Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp
 85 90 95
 Leu Val Leu Asn Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu
 100 105 110
 Ile Leu Leu Ala Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp
 115 120 125
 Phe Leu Val Asp Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu
 130 135 140
 Val Val Glu Leu Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala
 145 150 155 160
 Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg
 165 170 175
 Leu
 177

<210> 1439
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 1439
 Met Gly Phe Asp Glu Val Phe Met Ile Asn Leu Arg Arg Arg Gln Asp
 1 5 10 15
 Arg Arg Glu Arg Met Leu Arg Ala Leu Gln Ala Gln Glu Ile Glu Cys
 20 25 30
 Arg Leu Val Glu Ala Val Asp Gly Lys Val Gly Met Leu Thr Arg Ser
 35 40 45
 Asn Ala Ala Pro Gly Arg His Leu Ala Met Leu Glu Thr Leu Val Val
 50 55 60
 Val Ala Pro Arg Phe Val Asp Ala Asp Asn Leu Ile Leu Asn Pro Asp
 65 70 75 80
 Thr Leu Ser Leu Leu Ile Ala Glu Asn Lys Thr Val Val Ala Pro Met
 85 90 95
 Leu Asp Ser Arg Ala Ala Tyr Ser Asn Phe Trp Cys Gly Met Thr Ser
 100 105 110
 Gln Gly Tyr Tyr Lys Arg Thr Pro Ala Tyr Ile Pro Ile Arg Lys Arg
 115 120 125
 Asp Arg Arg Gly Cys Phe Ala Val Pro Met Val His Ser Thr Phe Leu
 130 135 140
 Ile Asp Leu Arg Lys Ala Ala Ser Arg Asn Leu Ala Phe Tyr Pro Pro
 145 150 155 160
 His Pro Asp Tyr Thr Trp Ser Phe Asp Asp Ile Ile Val Phe Ala Phe
 165 170 175
 Ser Cys Lys Gln Ala Glu Val Gln Met Tyr Val Cys Asn Lys Glu Glu
 180 185 190

```

Leu Pro Ser His Thr Cys Gly Asn Pro Gly Arg Leu Pro Asn Gly Ile
 1          5          10          15
Gln Gln Gly Ser Thr Phe Asn Leu Gly Asp Lys Val Arg Tyr Ser Cys
 20          25          30
Asn Leu Gly Phe Phe Leu Glu Gly His Ala Val Leu Thr Cys His Ala
 35          40          45
Gly Ser Glu Asn Ser Ala Thr Trp Asp Phe Pro Leu Pro Ser Cys Arg
 50          55          60
Ala Asp Asp Ala Cys Gly Gly Thr Leu Arg Gly Ala Glu Trp His His
 65          70          75          80
Leu Gln Pro Pro Leu Pro Leu Gly Ala Thr Lys Asn Asn Ala Asp Cys
 85          90          95
Thr Trp Thr Ile Leu Ala Glu Leu Gly Asp Thr Ile Ala Leu Val Phe
100          105          110
Ile Asp Phe Gln Leu Glu Asp Gly Tyr Asp Phe Leu Glu Val Thr Gly
115          120          125
Thr Glu Gly Ser Ser Leu Trp
130          135

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<210> 1437

<211> 247

<212> PRT

<213> Homo sapiens

<400> 1437

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Gly Thr Ala Arg Phe Gly Pro Met Val Gly Phe Gly Ala Asn Arg Arg
 1          5          10          15
Ala Gly Arg Leu Pro Ser Leu Val Leu Gly Val Leu Leu Val Ile
 20          25          30
Val Val Leu Ala Phe Asn Tyr Trp Ser Ile Ser Ser Arg His Val Leu
 35          40          45
Leu Gln Glu Glu Val Ala Glu Leu Gln Gly Gln Val Gln Arg Thr Glu
 50          55          60
Val Ala Arg Gly Arg Leu Glu Lys Arg Asn Ser Asp Leu Phe Ala Val
 65          70          75          80
Val Gly His Ala Gln Glu Thr Asp Arg Pro Glu Gly Gly Arg Leu Arg
 85          90          95
Pro Pro Gln Gln Pro Ala Ala Gly Gln Arg Gly Pro Arg Glu Glu Met
100          105          110
Glu Asp Asp Lys Val Lys Leu Gln Asn Asn Ile Ser Tyr Gln Met Ala
115          120          125
Asp Ile His His Leu Lys Glu Gln Leu Ala Glu Leu Arg Gln Glu Phe
130          135          140
Leu Arg Gln Glu Asp Gln Leu Gln Asp Tyr Arg Lys Asn Asn Thr Tyr
145          150          155          160
Leu Val Lys Arg Leu Glu Tyr Glu Ser Phe Gln Cys Gly Gln Gln Met
165          170          175
Lys Glu Leu Arg Ala Gln His Glu Glu Asn Ile Lys Lys Leu Ala Asp
180          185          190
Gln Phe Leu Glu Glu Gln Lys Gln Glu Thr Gln Lys Ile Gln Ser Asn
195          200          205
Asp Gly Lys Glu Leu Asp Ile Asn Asn Gln Val Val Pro Lys Asn Ile
210          215          220
Pro Lys Val Ala Glu Asn Val Ala Asp Lys Asn Glu Glu Pro Ser Ser
225          230          235          240
Asn His Ile Pro His Gly
245 246

```

<210> 1438

<223> Xaa = any amino acid or nothing

<400> 1434

```

Leu Gly Asp Val Gly Phe Trp Val Glu Arg Thr Pro Val His Glu Ala
 1           5           10           15
Ala Gln Arg Gly Glu Ser Leu Gln Leu Gln Gln Leu Ile Glu Ser Gly
           20           25           30
Ala Cys Val Asn Gln Val Thr Val Asp Ser Ile Thr Pro Leu His Ala
           35           40           45
Ala Ser Leu Gln Gly Gln Ala Arg Cys Val Gln Leu Leu Leu Ala Ala
           50           55           60
Gly Ala Gln Val Asp Ala Arg Asn Ile Asp Gly Ser Thr Pro Leu Cys
           65           70           75           80
Glu Cys Leu Arg Leu Gly Gln His Arg Val Cys Glu Ala Leu Ala Val
           85           90           95
Leu Arg Gly Gln Gly Gln Pro Ser Pro Val His Ser Val Pro Pro Ala
           100          105          110
Arg Gly Leu His Xaa Arg Glu Phe Arg Met Cys Xaa Gly Phe Leu Phe
           115          120          125
Asp Val Gly Xaa Asn Leu Glu Ala His Glu Phe His Phe Gly Glu Pro
           130          135          140          144

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<210> 1435

<211> 114

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(114)

<223> Xaa = any amino acid or nothing

<400> 1435

```

Lys Arg Ser Glu Glu Ala Ser Ala Pro Pro Phe Pro Leu Gly Gly Thr
 1           5           10           15
Gly Ala Ala Pro Thr Arg Ala Ser Leu Pro Glu Gln Ile Leu Leu Pro
           20           25           30
Arg Ser Cys Leu Glu Ala Arg Lys Ser Gln Pro Asp Glu Lys Leu Leu
           35           40           45
Ser Ala Leu His Asn Ser Arg Thr Trp Asn Xaa Glu Pro Arg Arg Ser
           50           55           60
Gln His Arg Leu Val Ser Pro Glu Val His Pro Gly Arg Arg Gly Ser
           65           70           75           80
Ser Pro Gly Val Ala Glu Cys Lys Leu Thr Ser Ala Tyr Phe Arg Thr
           85           90           95
Gly Arg Ser Pro Cys Pro Ser Leu Pro Gly Thr Thr Arg Thr Asn Ser
           100          105          110
Leu Leu
           114

```

<210> 1436

<211> 137

<212> PRT

<213> Homo sapiens

<400> 1436

```

Asp Phe Val Asp Ala Ala Arg Asn Leu Pro Leu Glu Ser Thr Lys Ser
 1          5          10          15
Pro Ala Glu Pro Ser Lys Ser Val Pro Ser Leu Glu Asp Pro Arg Ala
 20          25          30
Ser Ser Gln Gly Leu Pro Ser Gln Gly Pro Val Gln Asn Gln Gly Arg
 35          40          45
Arg Gly Glu Gln Arg Pro Lys Lys Phe Thr Val Ile Gln His Thr Ser
 50          55          60
Ser Phe Glu Lys Ser Asp Ser Leu Glu Gln Pro Ser Gly Leu Glu Gly
 65          70          75          80
Glu Asp Lys Pro Leu Ala Gln Phe Pro Ser Pro Pro Ala Pro His
 85          90          95
Gly Arg Ser Ala His Ser Leu Gln Pro Lys Leu Val Arg Gln Pro Asn
100          105          110
Ile Gln Val Pro Glu Ile Leu Val Thr Glu Glu Pro Asp Arg Pro Asp
115          120          125
Thr Glu Pro Glu Pro Pro Lys Glu Pro Glu Lys Thr Glu Glu Phe
130          135          140
Gln Trp Pro Gln Gly Ser Gln Thr Leu Ala Gln Phe Pro Val Glu Lys
145          150          155          160
Leu Pro Pro Lys Lys Lys Arg Leu Gly Leu Ala Lys Met Ala Gln Ser
165          170          175
Ser Gly Glu Ser Ser Phe Glu Ser Ser Val Pro Leu Phe Arg Ser Pro
180          185          190
Ser Gln Glu Ser Asn Val Ser Leu Ser Gly Ser Ser Arg Ser Ala Leu
195          200          205
Phe Glu Arg Asp Asp His Gly Lys Ala Glu Ala Pro Ser Pro Ser Phe
210          215          220
Asp Met Gly Pro Lys Pro Leu Gly Thr His Met Leu Thr Val
225          230          235          238

```

<210> 1433
 <211> 96
 <212> PRT
 <213> Homo sapiens

```

<400> 1433
Glu Ser Pro Gly Leu Ser Lys Val Leu Arg Thr Gly Ala Phe Ala Tyr
 1          5          10          15
Pro Phe Leu Phe Asp Asn Leu Pro Leu Phe Tyr Arg Leu Gly Leu Cys
 20          25          30
Trp Gly Arg Gly His Gly Cys Gly Gln Glu Ala Leu Ser Thr Ser His
 35          40          45
Gly Tyr His Leu Phe Cys Ala Leu Leu Thr Gly Phe Leu Phe Ala Ser
 50          55          60
His Leu Pro Glu Arg Leu Ala Pro Gly Arg Phe Asp Tyr Ile Gly His
 65          70          75          80
Ser His Gln Leu Phe His Ile Cys Ala Val Leu Gly Thr His Phe Gln
 85          90          95          96

```

<210> 1434
 <211> 144
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(144)

```

His Thr Gly Glu Lys Pro Tyr Met Cys Thr Ile Cys Glu Val Arg Phe
      85                      90                      95
Thr Arg Gln Asp Lys Leu Lys Ile His Met Arg Lys His Thr Gly Glu
      100                    105                    110
Arg Pro Tyr Leu Cys Ile His Cys Asn Ala Lys Phe Val His Asn Tyr
      115                    120                    125
Asp Leu Lys Asn His Met Arg
      130                    135

```

```

<210> 1430
<211> 58
<212> PRT
<213> Homo sapiens

```

```

<400> 1430
Glu Met Asn Glu Leu Ser Gln Gln Leu Ser Gln Gln Gly Gly Arg Gly
 1          5          10          15
Ala Ser Gln Cys Pro Ser Pro Pro Ala Pro Thr Leu Pro Asn Pro Thr
      20          25          30
Pro Leu Cys Gln Leu Gln Leu Gln Arg Val Asn Thr Gly Leu Pro Thr
      35          40          45
Pro Pro Cys His Pro Gly Ala Gly Ala Ala
      50          55          58

```

```

<210> 1431
<211> 110
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(110)
<223> Xaa = any amino acid or nothing

```

```

<400> 1431
Lys Thr Val Leu Asp Val Gly Ala Gly Thr Gly Ile Leu Ser Ile Phe
 1          5          10          15
Cys Ala Gln Ala Gly Ala Arg Arg Val Tyr Ala Val Glu Ala Ser Ala
      20          25          30
Ile Trp Gln Gln Ala Arg Glu Val Val Arg Phe Asn Gly Leu Glu Asp
      35          40          45
Arg Val His Val Leu Pro Gly Pro Val Glu Thr Val Glu Leu Pro Glu
      50          55          60
Gln Val Asp Ala Ile Val Ser Glu Trp Met Gly Tyr Gly Leu Leu His
      65          70          75          80
Glu Ser Met Leu Ser Ser Val Leu His Ala Arg Thr Lys Val Val Lys
      85          90          95
Asp Gly Gly Phe Phe Leu Pro Xaa Ser Ser Glu Leu Phe Met
      100                    105                    110

```

```

<210> 1432
<211> 240
<212> PRT
<213> Homo sapiens

```

```

<400> 1432

```

```

Phe Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu
      85          90          95
Gly Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys
      100        105        110
Lys Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met
      115        120        125
Glu Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys
      130        135        140
Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala
      145        150        155        160
Gly Met Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala
      165        170        175
Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val
      180        185        190
Pro Ser Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met
      195        200        205
Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly
      210        215        220
Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe
      225        230        235        240
Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr
      245        250        255
Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser
      260        265        270
Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu
      275        280        285
Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly
      290        295        300
Ala Glu Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn
      305        310        315        320
Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly
      325        330        335
Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln
      340        345        350
Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp
      355        360        365
Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val
      370        375        380
Ser Val Arg Glu Pro Gly Leu Leu Gly Gly Ser Phe Ser Thr Ala Gln
      385        390        395        400
Ser Pro Lys Cys Gln Gly Asp Ser Phe Pro Gly Val Ala Ala Glu Ser
      405        410        415
Leu Leu Leu Arg Gly Trp Val Leu Trp Leu Pro Gly Gly Gly
      420        425        430

```

<210> 1429

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1429

```

Pro Asn Asp Phe Phe Lys Asp Met Phe Pro Asp Leu Pro Gly Gly Pro
  1          5          10          15
Leu Gly Pro Ile Lys Ala Glu Asn Asp Tyr Gly Ala Tyr Leu Asn Phe
      20        25        30
Leu Ser Ala Thr His Leu Gly Gly Leu Phe Pro Pro Trp Pro Leu Val
      35        40        45
Glu Glu Arg Lys Leu Lys Pro Lys Ala Ser Gln Gln Cys Pro Ile Cys
      50        55        60
His Lys Val Ile Met Gly Ala Gly Lys Leu Pro Arg His Met Arg Thr
      65        70        75        80

```

<210> 1426
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 1426
 Pro Ile Ile Ser Ala Pro Ala Gln Asp Asp Pro Ile Leu Leu Ser Phe
 1 5 10 15
 Ile His Cys Leu His Ala Asn Leu Leu Cys Val Trp Arg Arg Asp Val
 20 25 30
 Lys Pro Asp Cys Lys Glu Ile Trp Ile Phe Trp Trp Gly Asp Glu Pro
 35 40 45
 Asn Leu Val Val Gln Tyr Ile Met Asn Cys Met Leu Trp Lys Lys Asp
 50 55 60
 Ser Gly Lys Met Ala Phe Pro Met Asn Val Gly Arg Cys Phe Phe Lys
 65 70 75 80
 Glu Ile His Asn Leu Leu Glu Arg Cys Leu Met Asp Lys Asn Phe Val
 85 90 95
 Leu Ile Gly Lys Trp Phe Val Arg Pro Tyr Tyr Lys Asp Glu Lys Pro
 100 105 110
 Val Asn Lys Ser Glu His Leu Ser Cys Ala Phe Thr
 115 120 124

<210> 1427
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1427
 Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr Pro Val Leu Ile
 1 5 10 15
 Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu Glu Leu Gln Gly Val
 20 25 30
 Leu Arg Gly Asn Leu Leu Arg Val Phe Arg Gln Val Glu Lys Val Gln
 35 40 45
 Glu Glu Asn Lys Trp Gln Ser Pro Leu Glu Asp
 50 55 59

<210> 1428
 <211> 431
 <212> PRT
 <213> Homo sapiens

<400> 1428
 Met Ala Glu Ser Ala Ser Pro Pro Ser Ser Ser Ala Ala Ala Pro Ala
 1 5 10 15
 Ala Glu Pro Gly Val Thr Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro
 20 25 30
 Ser Ser Pro Pro Gly Leu Glu Glu Pro Leu Asp Gly Ala Asp Pro His
 35 40 45
 Val Pro His Pro Asp Leu Ala Pro Ile Ala Phe Phe Cys Leu Arg Gln
 50 55 60
 Thr Thr Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp
 65 70 75 80

```

Trp Asp Leu Val Glu Arg Met Lys Asn Ser Pro Asp Ile Asn Leu Glu
  210          215          220
Lys Asp Trp Lys Leu Val Thr Leu Phe Ile Gly Gly Asn Asp Leu Cys
  225          230          235          240
His Tyr Cys Glu Asn Pro Glu Ala His Leu Ala Thr Glu Tyr Val Gln
          245          250          255
His Ile Gln Gln Ala Leu Asp Ile Leu Ser Glu
          260          265          267

```

```

<210> 1424
<211> 143
<212> PRT
<213> Homo sapiens

```

```

<400> 1424
Phe Arg Glu Pro Cys Leu Leu Val Pro Gly Asp His Gln Pro Leu Arg
  1          5          10          15
Glu Ala Ser Trp Leu Ala Leu Pro Pro Ile Gly Leu Trp Gly Thr Asp
          20          25          30
Ser Pro Leu Cys Cys Val Glu Val Ala Ile Pro Cys Asn Lys Gly Ala
          35          40          45
His Ser Val Gly Leu Lys Gly Trp Leu Leu Ala Gln Gly Val Leu Gly
          50          55          60
Met Arg Asp Thr Ile Pro Gln Glu His Pro Trp Glu Ser Thr Pro Asp
          65          70          75          80
Leu Cys Phe Cys Arg Asp Pro Glu Glu Ile Glu Val Glu Glu Gln Pro
          85          90          95
Ala Ala Asp Ala Ala Val Ala Lys Gly Glu Phe Gln Gly Glu Gln Ile
          100          105          110
Ala Pro Val Pro Ala Ile Ile Ala Ala His Pro Glu Ala Ala Asp Pro
          115          120          125
Ala Pro Val His Thr Thr Ala His Pro Lys Gly Ala
          130          135          140

```

```

<210> 1425
<211> 138
<212> PRT
<213> Homo sapiens

```

```

<400> 1425
Pro Phe Pro His Gln His Pro Gln Glu Pro Lys Gly Ser Cys Trp Pro
  1          5          10          15
Gln Ser Ala Leu Arg Gly Gln Cys Pro Gly Pro Val Leu Gly Val Thr
          20          25          30
Thr Thr Ser Asp Leu Cys Ser Leu Gln Val Pro Val Ser Ser His Arg
          35          40          45
Asn Pro Leu Leu Asp Leu Ala Ala Tyr Asp Gln Glu Gly Arg Arg Phe
          50          55          60
Asp Asn Phe Ser Ser Leu Ser Ile Gln Trp Glu Ser Thr Arg Pro Val
          65          70          75          80
Leu Ala Ser Ile Glu Pro Glu Leu Pro Met Gln Leu Val Ser Gln Asp
          85          90          95
Asp Glu Ser Gly Gln Lys Lys Leu His Gly Leu Gln Ala Ile Leu Val
          100          105          110
His Glu Ala Ser Gly Thr Thr Ala Ile Thr Ala Thr Ala Thr Gly Tyr
          115          120          125
Gln Glu Ser His Leu Ser Ser Ala Arg
          130          135          137

```

```

Pro Pro Asp Glu Leu Thr Ser Gly Pro Ser Met Leu Ala Gln Val Ser
      85                      90                      95
Pro His Gly Lys Leu Ser Ala Arg Arg Ser Trp Asp Leu Leu Ser Gly
      100                      105                      110
Phe Pro Arg Tyr Leu Val Leu Glu His Val Ser Gly Gly Glu Leu Phe
      115                      120                      125
Asp Tyr Leu Val Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys
      130                      135                      140
Phe Phe Arg Gln Ile Val Ser Ala Leu Asp Phe Cys His Ser Tyr Ser
      145                      150                      155                      160
Ile Cys His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys
      165                      170                      175
Asn Asn Ile Arg Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly
      180                      185                      190
Asp Ser Leu Leu Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro
      195                      200                      205
Glu Val Ile Lys Gly Glu Lys Tyr Asp Gly Arg Arg Ala Asp Met Trp
      210                      215                      220
Ser Cys Gly Val Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe
      225                      230                      235                      240
Asp Asp Asp Asn Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val
      245                      250                      255
Phe His Met Pro His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg
      260                      265                      270
Gly Met Ile Glu Val Glu Pro Glu Lys Arg Leu Ser Leu Glu Gln Ile
      275                      280                      285
Gln Lys His Pro Trp Tyr Leu Gly Gly Asn Phe Ile Ser
      290                      295                      300 301

```

<210> 1423

<211> 268

<212> PRT

<213> Homo sapiens

<400> 1423

```

Leu Arg Asn Ala Leu Asp Val Leu His Arg Glu Val Pro Arg Val Leu
1      5      10      15
Val Asn Leu Val Asp Phe Leu Asn Pro Thr Ile Met Arg Gln Val Phe
      20      25      30
Leu Gly Asn Pro Asp Lys Cys Pro Val Gln Gln Ala Met Leu Glu Pro
      35      40      45
Leu Gly Ser Lys Thr Glu Thr Leu Asp Leu Arg Ala Glu Met Pro Ile
      50      55      60
Thr Cys Pro Thr Gln Asn Glu Pro Phe Leu Arg Thr Pro Arg Asn Ser
      65      70      75      80
Asn Tyr Thr Tyr Pro Ile Lys Pro Ala Ile Glu Asn Trp Gly Ser Asp
      85      90      95
Phe Leu Cys Thr Glu Trp Lys Ala Ser Asn Ser Val Pro Thr Ser Val
      100      105      110
His Gln Leu Arg Pro Ala Asp Ile Lys Val Val Ala Ala Leu Gly Asp
      115      120      125
Ser Leu Thr Thr Ala Val Gly Ala Arg Pro Asn Asn Ser Ser Asp Leu
      130      135      140
Pro Thr Ser Trp Arg Gly Leu Ser Trp Ser Ile Gly Gly Asp Gly Asn
      145      150      155      160
Leu Glu Thr His Thr Thr Leu Pro Asn Ile Leu Lys Lys Phe Asn Pro
      165      170      175
Tyr Leu Leu Gly Phe Ser Thr Ser Thr Trp Glu Gly Thr Ala Gly Leu
      180      185      190
Asn Val Ala Ala Glu Gly Ala Arg Ala Arg Asp Met Pro Ala Gln Ala
      195      200      205

```

Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser Gln Gly Gly Phe
 100 105 110
 Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu Lys Asp Asp Trp Thr
 115 120 125
 Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly Glu His Thr Ala Tyr Pro
 130 135 140
 His Gly Trp Val Glu Thr Ala Val Lys Ser Ala Leu Arg Ala Ala Ile
 145 150 155 160
 Lys Ile Asn Ser Arg Lys Gly Pro Ala Ser Asp Thr Ala Ser Pro Glu
 165 170 175
 Gly His Ala Ser Asp Met Glu Gly Gln Gly His Val His Gly Val Ala
 180 185 190
 Ser Ser Pro Ser His Asp Leu Ala Lys Glu Glu Gly Ser His Pro Pro
 195 200 205
 Val Gln Gly Gln Leu Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser
 210 215 220
 His
 225

<210> 1421
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1421
 Gln Lys Gln Thr Leu Gln Asn Gly Tyr Leu Asp Ser Ser Met Asp Ile
 1 5 10 15
 Leu Tyr Leu Gly Ser Leu Pro Pro Glu Leu Gln Val Ser Ser Asp Glu
 20 25 30
 Pro Pro Gly Pro Pro Glu Gln Ala Gly Leu Ser Gln Phe His Leu Glu
 35 40 45
 Pro Glu Thr Gln Asn Pro Glu Thr Thr Glu Glu Ile Gln Ser Ser Leu
 50 55 60
 Gln Gln Glu Ala Ala Ala Gln Leu Pro Gln Leu Pro Glu Val Val Glu
 65 70 75 80
 Leu Ser Ser Thr Lys Ala Glu Ala Pro Ala Leu Pro Ser Gln Ser Leu
 85 90 95
 Glu Gly Val His Ser Ser Thr Glu Gln Lys Ala Pro Ala Gln Gln Leu
 100 105 110
 Pro Ala Phe Glu Glu Ile Leu Ala Pro Leu Leu Ile His His Glu
 115 120 125 127

<210> 1422
 <211> 302
 <212> PRT
 <213> Homo sapiens

<400> 1422
 His Ala Gln Tyr Val Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly Lys
 1 5 10 15
 Gly Gln Thr Gly Leu Val Lys Leu Gly Val His Cys Ile Thr Gly Gln
 20 25 30
 Lys Val Ala Ile Lys Ile Val Asn Arg Glu Lys Leu Ser Glu Ser Val
 35 40 45
 Leu Met Lys Val Glu Arg Glu Ile Ala Ile Leu Arg Leu Ile Glu His
 50 55 60
 Pro His Val Leu Lys Leu His Gly Val Tyr Glu Asn Lys Lys Tyr Phe
 65 70 75 80

Leu Val Ala Val Val Val Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr
 355 360 365
 Ala Leu Phe Arg Asn Val His Gln Asn Ile His Pro Glu Asn Gln Glu
 370 375 380
 Leu Val Arg Val Leu Arg Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro
 385 390 395 400
 Ala Ala Thr Arg Gln Gln Phe Tyr Thr Asp Met Tyr Cys Pro Ile Cys
 405 410 415
 Leu His Gln Ala Ser Phe Pro Val Glu Thr Asn Cys Gly His Leu Phe
 420 425 430
 Cys Gly Ser Leu Thr Pro Asn Ser Ile Trp
 435 440 442

<210> 1419
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1419
 Phe Asp Thr Ala Arg Leu His Glu Phe Gly Thr Ser Ile Thr Gln Ile
 1 5 10 15
 Phe Ala Val Asp Asn Arg Glu Asp Leu Gln Lys Trp Met Glu Ala Phe
 20 25 30
 Trp Gln His Phe Phe Asp Leu Ser Gln Trp Lys His Cys Cys Glu Glu
 35 40 45
 Leu Met Lys Ile Glu Ile Met Ser Pro Arg Lys Pro Pro Leu Phe Leu
 50 55 60
 Thr Lys Glu Ala Thr Ser Val Tyr His Asp Met Ser Ile Asp Ser Pro
 65 70 75 80
 Met Lys Leu Glu Ser Leu Thr Asp Ile Ile Gln Lys Lys Ile Glu Glu
 85 90 95
 Thr Asn Gly Gln Phe Leu Ile Gly Gln Arg Glu Glu Ser Leu Pro Ser
 100 105 110
 Ser Cys Gly Pro His Ser Leu Met Val Thr Ile Lys Trp Ser Ser Arg
 115 120 125
 Lys Arg Tyr Ser Tyr Pro Ala Ser Glu Pro Leu His Asp Glu Lys Gly
 130 135 140
 Lys Lys Arg Gln Ala Pro Leu Pro Pro Ser Asp Lys
 145 150 155 156

<210> 1420
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 1420
 Ala Leu Arg Arg Leu His Tyr Val Arg Ala Thr Lys Val Phe Leu Ser
 1 5 10 15
 Phe Arg Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser
 20 25 30
 Asn Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 35 40 45
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala Ala
 50 55 60
 Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu Asp Asp
 65 70 75 80
 Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp Asp Gly Thr
 85 90 95

```

Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys Ser Asp Ile Leu Arg
    35          40          45
Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser Val Lys Asn Gly Ser
    50          55          60
Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val Ile Ala Phe Leu Gly
    65          70          75          80
Val Leu Ser Cys Phe His Thr Ala Phe Met Leu Phe Cys Ile Ser Val
    85          90          95
Thr Arg Tyr Leu
    100

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<210> 1418
<211> 444
<212> PRT
<213> Homo sapiens

```

```

<400> 1418
Met Gly Lys Ile Ser Ala Thr Gly Ile Asn Met Gly Thr Lys Cys Ser
  1          5          10          15
Trp Ala Leu Val Trp His Leu Glu Ser Tyr Asp Pro Lys His Tyr Glu
    20          25          30
Arg Glu Gly Met Gln Asp Trp Lys Thr Ala Ser Gly Gln Ser Glu Glu
    35          40          45
Ala Thr Gln Gln Ser Ser Gln Lys Pro Gln Pro His Tyr Thr Thr Tyr
    50          55          60
Gln Ser Ser Ser Phe Leu Lys Tyr Ser Ser Glu Ser His Leu Leu Ala
    65          70          75          80
Trp Arg Glu Asn Ser Ser Glu Gly Ser Phe Gln Phe Pro Gly Arg Ser
    85          90          95
Arg Ala Arg Pro Pro Arg Thr Arg Gln Gln Arg Arg Gly Ala Ala Ala
    100          105          110
Gly Pro Gly Arg Gly Ala Val Arg Leu Gly His Pro Gln Ser Ala Ala
    115          120          125
Gln Pro Gln Leu Arg Ala Ala Arg Ile Pro Glu Ser Pro Ala Ala
    130          135          140
Phe Pro Ala Gln Pro Arg Pro Gly Ser Ala Arg Asn Ser Asp Ala Ser
    145          150          155          160
Gly Pro Ala Ser Leu Ser Arg Thr Leu Gly Arg Ala Ser Ser Pro Arg
    165          170          175
Pro Pro Gln Ala Pro Asp Val Thr Ala Pro Ser Pro Ala Ala Leu Ala
    180          185          190
Pro Arg Ala Ala Arg Gly Gly Ser Arg Ala Ala Ala Leu Ala Gly Ala
    195          200          205
Glu Ala Glu Glu Pro Leu Arg Thr Leu Ala Pro Arg Pro Thr Arg Ala
    210          215          220
Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Gly Ala
    225          230          235          240
Pro Pro Pro Pro Val Arg Cys Val Ser Arg Arg Ala Arg Ala Pro Pro
    245          250          255
Trp Arg Pro Ala Ala Thr Gly Pro Pro Arg Pro Val Ala Pro Ser
    260          265          270
Arg Lys Leu Gly Ser Ala Arg Ala Pro Ala Pro Ala Leu Gln Ile Arg
    275          280          285
Lys Gly Thr Ser Ser Gly Leu Pro Gly Arg Gly Gly Gly Ser Gly Pro
    290          295          300
Gly Asn Asn Leu Ser Ser Val Ala Gly Asn Trp Arg Gly Ser Ser Phe
    305          310          315          320
Ala Val Glu Arg Pro Gly Met Ala Lys Tyr Gln Gly Glu Val Gln Ser
    325          330          335
Leu Lys Leu Asp Asp Asp Ser Val Ile Glu Gly Val Ser Asp Gln Val
    340          345          350

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<210> 1415
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1415
 Pro Arg Ala Phe Glu Phe Val His Thr Glu Met Ile Val Gly Arg Val
 1 5 10 15
 Gln Asn Ile His Leu Phe Thr Leu Gln Val Leu Glu Asp Arg Ala Leu
 20 25 30
 Phe Thr Met Ser Val Gly Ser Ser Leu Trp Ser Thr Tyr Leu Ile His
 35 40 45
 Val Met Ala Leu Pro Asp Arg Glu Leu Leu Lys Pro Asn Ala Ser Val
 50 55 60
 Ala Leu His Lys Leu Ser Asn Ala Leu Val
 65 70 74

<210> 1416
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 1416
 His Glu Thr Cys Ser Val Thr His Ile Val Ser Phe Ser Leu Pro Phe
 1 5 10 15
 Leu Asn Pro Ser His Pro Ala Ser Thr Pro Gly His Thr Glu Asn Glu
 20 25 30
 Gln Pro Ser Leu Val Trp Phe Asp Arg Gly Lys Phe Tyr Leu Thr Phe
 35 40 45
 Glu Gly Ser Ser Arg Gly Pro Ser Pro Leu Thr Met Gly Ala Gln Asp
 50 55 60
 Thr Leu Pro Val Ala Ala Ala Phe Thr Glu Thr Val Asn Ala Tyr Phe
 65 70 75 80
 Lys Gly Ala Asp Pro Ser Lys Cys Ile Val Lys Ile Thr Gly Glu Met
 85 90 95
 Val Leu Ser Phe Pro Ala Gly Ile Thr Arg His Phe Ala Asn Asn Pro
 100 105 110
 Ser Pro Ala Ala Leu Thr Phe Arg Val Ile Asn Phe Ser Arg Leu Glu
 115 120 125
 His Val Leu Pro Asn Pro Gln Leu Leu Cys Cys Asp Asn Thr Gln Asn
 130 135 140
 Asp Ala Asn Thr Lys Glu Phe Trp Val Asn Met Pro Asn Leu Met Thr
 145 150 155 160
 His Leu Lys
 163

<210> 1417
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1417
 Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly Val Ser Val Val Gly
 1 5 10 15
 Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp Lys Thr Leu His Arg
 20 25 30

Ala Asn Leu Tyr Ala His Lys Lys Ile His Thr Gly Glu Lys Pro Tyr
 115 120 125
 Lys Cys Lys Glu Cys Gly Lys Ala Phe Lys Ser Tyr Tyr Ser Ile Leu
 130 135 140
 Lys His Lys Arg Thr His Thr Arg Gly Met Ser Tyr Glu Gly Asp Glu
 145 150 155 160
 Cys Gln Arg Ser Leu Asn Arg Ser Ser Ile Leu Ser Asn His Lys Ile
 165 170 175
 Ile His Asn Glu Glu Lys Pro Leu Lys Cys Glu Lys Cys Glu Lys Ala
 180 185 190
 Phe Asn His Thr Ser Ile Cys Cys Arg His Lys Lys Asn
 195 200 205

<210> 1414
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 1414
 Lys Lys Gln Asp Leu Ser Ser Ser Leu Thr Asp Asp Ser Lys Asn Ala
 1 5 10 15
 Gln Ala Pro Leu Ala Leu Thr Glu Ser His Leu Ala Thr Leu Ala Ser
 20 25 30
 Ser Ser Gln Ser Pro Glu Ala Ile Lys Gln Leu Leu Asp Ser Gly Leu
 35 40 45
 Pro Ser Leu Leu Val Arg Ser Leu Ala Ser Phe Cys Phe Ser His Ile
 50 55 60
 Ser Ser Ser Glu Ser Ile Ala Gln Ser Ile Asp Ile Ser Gln Asp Lys
 65 70 75 80
 Leu Arg Arg His His Val Pro Gln Gln Cys Asn Lys Met Pro Ile Thr
 85 90 95
 Ala Asp Leu Val Ala Pro Ile Leu Arg Phe Leu Thr Glu Val Gly Asn
 100 105 110
 Ser His Ile Met Lys Asp Trp Leu Gly Gly Ser Glu Val Asn Pro Leu
 115 120 125
 Trp Thr Ala Leu Leu Phe Leu Leu Cys His Ser Gly Ser Thr Ser Gly
 130 135 140
 Ser His Asn Leu Gly Ala Gln Gln Asp Gln Cys Lys Ile Ser Phe Ser
 145 150 155 160
 Phe Phe Ser Trp Leu Thr Thr Gly Leu Thr Thr Gln Gln Arg Thr Ala
 165 170 175
 Ile Glu Asn Ala Thr Val Ala Phe Phe Leu Gln Cys Ile Ser Cys His
 180 185 190
 Pro Asn Asn Gln Lys Leu Met Ala Gln Val Leu Cys Glu Leu Phe Gln
 195 200 205
 Thr Ser Pro Gln Arg Gly Asn Leu Pro Thr Ser Gly Asn Ile Ser Gly
 210 215 220
 Phe Ile Arg Arg Leu Phe Leu Gln Leu Met Leu Glu Asp Glu Lys Val
 225 230 235 240
 Thr Met Phe Leu Gln Ser Pro Cys Pro Leu Tyr Lys Gly Arg Ile Asn
 245 250 255
 Ala Thr Ser His Val Ile Gln His Pro Met Tyr Gly Ala Gly His Lys
 260 265 270
 Phe Arg Thr Leu His Leu Pro Val Ser Thr Thr Leu Ser Asp Val Leu
 275 280 285
 Asp Arg Val Ser Asp Thr Pro Ser Ile Thr Ala Lys Leu Ile Ser Lys
 290 295 300
 Gln Lys Asp Asp Lys Lys Lys Lys
 305 310 312

<213> Homo sapiens

<400> 1412

```

Val Val Glu Phe Leu Trp Ser Arg Arg Pro Ser Gly Ser Ser Asp Pro
 1      5      10      15
Arg Pro Arg Arg Pro Ala Ser Lys Cys Gln Met Met Glu Glu Arg Ala
 20      25      30
Asn Leu Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln Ser
 35      40      45
Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu Gln
 50      55      60
Gln Phe Phe Val Val Met Glu His Cys Leu Lys His Gly Leu Lys Val
 65      70      75      80
Lys Lys Ser Phe Ile Gly Gln Asn Lys Ser Phe Phe Gly Pro Leu Glu
 85      90      95
Leu Val Glu Lys Leu Cys Pro Glu Ala Ser Asp Ile Ala Thr Ser Val
 100     105     110
Arg Asn Leu Pro Glu Leu Lys Thr Ala Val Gly Arg Gly Arg Ala Trp
 115     120     125
Leu Tyr Leu Ala Leu Met Gln Lys Lys Leu Ala Asp Tyr Leu Lys Val
 130     135     140
Leu Ile Asp Asn Lys His Leu Leu Ser Glu Phe Tyr Glu Pro Glu Ala
 145     150     155     160
Leu Met Met Glu Glu Glu Gly Met Val Ile Val Gly Leu Leu Val Gly
 165     170     175
Leu Asn Val Leu Asp Ala Asn Leu Cys Leu Lys Gly Glu Asp Leu Asp
 180     185     190
Ser Gln Val Gly Val Ile Asp Phe Ser Leu Tyr Leu Lys Asp Val Gln
 195     200     205
Asp Leu Asp Gly Gly Lys Glu His Glu Arg Ile Thr Asp Val Leu Asp
 210     215     220
Gln Lys Asn Tyr Val Glu Glu Leu Asn Arg His Leu Ser Cys Thr Val
 225     230     235     240
Gly Asp Leu Gln Thr Lys Ile Asp Gly Leu Glu Lys Thr Asn Ser Lys
 245     250     255
Leu Gln Glu Arg Val Ser Ala Ala Thr Asp Arg Ile Cys Ser Leu Gln
 260     265     270
Glu Glu Gln Gln Gln Leu Arg Glu Gln Asn Glu Leu Ile Arg
 275     280     285     286

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<210> 1413

<211> 209

<212> PRT

<213> Homo sapiens

<400> 1413

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Ser Ser Phe Ala Lys His Lys Arg Ile His Thr Gly Glu Lys Pro Phe
 1      5      10      15
Ile Cys Leu Glu Cys Gly Lys Ala Phe Thr Ser Ser Thr Thr Leu Thr
 20      25      30
Lys His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Thr Cys Glu Glu
 35      40      45
Cys Gly Lys Ala Phe Arg Gln Ser Ala Ile Leu Tyr Val His Arg Arg
 50      55      60
Ile His Thr Gly Glu Lys Pro Tyr Thr Cys Gly Glu Cys Gly Lys Thr
 65      70      75      80
Phe Arg Gln Ser Ala Asn Leu Tyr Ala His Lys Lys Ile His Thr Gly
 85      90      95
Glu Lys Pro Tyr Thr Cys Gly Asp Cys Gly Lys Thr Phe Arg Gln Ser
 100     105     110

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Pro Tyr Lys Cys Asn Glu Cys Gly Arg Ala Phe Ser Gln Cys Ser Ser
  50          55          60
Leu Ile Gln His His Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
  65          70          75          80
Thr Gln Cys Gly Lys Ala Phe Thr Ser Ile Ser Arg Leu Ser Arg His
          85          90          95
His Arg Ile His Thr Gly Glu Lys Pro Phe His Cys Asn Glu Cys Gly
          100          105          110
Lys Val Phe Ser Tyr His Ser Ala Leu Ile Ile His Gln Arg Ile His
          115          120          125
Thr Gly Glu Lys Pro Tyr Ala Cys Lys Asp Val Gly Lys
          130          135          140 141

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<210> 1410
<211> 73
<212> PRT
<213> Homo sapiens

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<400> 1410
Gly Gly Pro Pro Gly Pro Phe Leu Ala His Thr His Ala Gly Leu Gln
  1          5          10          15
Ala Pro Gly Pro Leu Leu Ala Pro Ala Gly Asp Glu Gly Asp Leu Leu
          20          25          30
Leu Leu Ala Val Gln Gln Ser Cys Leu Ala Asp His Leu Leu Thr Ala
          35          40          45
Ser Trp Gly Gly Lys Asp Pro Ile Pro Thr Lys Ala Leu Gly Glu Gly
          50          55          60
Gln Glu Gly Leu Pro Leu Thr Val
          65          70          72

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<210> 1411
<211> 128
<212> PRT
<213> Homo sapiens

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<400> 1411
Arg His Ser Arg Ala His Leu Cys Gln Pro Phe His Leu Val Met Arg
  1          5          10          15
Asp Leu Leu Gln Leu Gly Gln Asp Ile Pro Gln Gly Cys His Tyr Leu
          20          25          30
Glu Glu Asn His Leu Ile His Arg Asp Ile Ala Ala Arg Asn Cys Leu
          35          40          45
Leu Ser Cys Ala Ala Pro Thr Arg Ala Ala Thr Ile Gly Asp Phe Gly
          50          55          60
Met Ala Arg Tyr Ile Tyr Arg Thr Arg Tyr Tyr Gln Leu Gly Asp Arg
          65          70          75          80
Ala Leu Leu Pro Arg Lys Trp Met Pro Pro Glu Ala Leu Leu Glu Gly
          85          90          95
Ile Phe Thr Tyr Asn Thr Asp Ser Trp Thr Phe Gly Val Leu Leu Trp
          100          105          110
Glu Ile Phe Ser Leu Gly Tyr Met Pro Tyr Pro Gly Arg Thr Asn
          115          120          125          127

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<210> 1412
<211> 287
<212> PRT

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<210> 1407
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 1407
 Gly Ala Tyr Ala Phe Glu Thr Asn Gly Phe Pro Ile Met Leu Val Leu
 1 5 10 15
 Thr Thr Asp Lys Ile Glu Gly Asp Val Gly Ile Ala Gly Leu Tyr Asp
 20 25 30
 Met His Ile Ser Leu Pro Met Ala Phe Leu Leu Arg Thr Leu Val Arg
 35 40 45
 Cys Thr Ser Tyr Ile Ile Pro Val Thr His Val Leu Ser Thr Pro Val
 50 55 60
 Thr Cys Leu Arg Arg Arg Glu Lys Asp Gly Val Ile Val Asp Val Leu
 65 70 75 80
 Ser Asp Thr Ala Ser Asn His Asn Gly Phe Pro Val Glu Glu His Ala
 85 90 95
 Asp Asp Thr His Pro Ala Arg Leu Gln Gly Pro Thr Leu Arg Ser Gln
 100 105 110
 Pro Met Gly Pro Leu Lys His Lys Ala Phe Glu Glu Arg Ala Asn Leu
 115 120 125
 Gly Leu Val Gln Arg Arg Leu Arg Leu Glu Asp
 130 135 139

<210> 1408
 <211> 54
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(54)
 <223> Xaa = any amino acid or nothing

<400> 1408
 Leu Lys His Arg Asp Thr Pro Val Val Gly Ala Asn Asn Arg Ala Leu
 1 5 10 15
 Ser Cys Thr Pro Leu Thr Ser Leu Thr Leu Cys Ala Leu Cys Pro Leu
 20 25 30
 Pro Cys Leu Gly Cys Pro Thr Xaa Ala Thr Cys Arg Leu Tyr Gln Thr
 35 40 45
 Thr Val Ala Val Val Phe
 50 54

<210> 1409
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 1409
 Lys Ala Phe Ser Phe Thr Thr Ser Leu Ile Gly His Gln Arg Met His
 1 5 10 15
 Thr Gly Glu Arg Pro Tyr Lys Cys Lys Glu Cys Gly Lys Thr Phe Lys
 20 25 30
 Gly Ser Ser Ser Leu Asn Asn His Gln Arg Ile His Thr Gly Glu Lys
 35 40 45

```

Met Ile Thr Thr Leu Lys Lys Leu Gly Ile Asp Gly Lys Tyr Leu Asn
      20      25      30
Thr Ile Lys Ala Ile Asp Asp Arg His Thr Val Ser Thr Ile Leu Asn
      35      40      45
Val Glu Lys Leu Lys Ala Phe Leu Xaa Arg Ser Gly Thr Arg Gln Arg
      50      55      60
Phe Pro Ile Ser Gly Ser Gly Ala Arg Ile
      65      70      74

```

<210> 1405
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<400> 1405
His Ala Ser Val Asp Gly Asp Glu Gly Ser Asp Asp Val Tyr Tyr Tyr
  1      5      10      15
Tyr Thr Pro Ala Ile Leu Arg Glu Leu Gln Ala Leu Asn Thr Ala Glu
      20      25      30
Ala Ala Glu His Arg Pro Glu Glu Asp Arg Met Leu Ser Glu Asp Pro
      35      40      45
Trp Arg Pro Ala His Met Ile Lys Gly Tyr Met Pro Leu His Asn Ile
      50      55      60
Pro His Thr Glu Val Ile Asp Val Thr Gly Leu Asn Gln Ser His Leu
      65      70      75      80
Tyr Gln His Leu Asn Lys Gly Thr Pro Met Lys Thr Gln Lys Arg Ala
      85      90      95
Ala Leu Tyr Thr Trp His Val Leu Glu Gln Leu Glu Ile Leu Arg Gln
      100      105      110
Ile Asn Gln Gln Ser His Gly Pro Gly
      115      120 121

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<210> 1406
 <211> 141
 <212> PRT
 <213> Homo sapiens

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<400> 1406
Ser Val Leu Thr Leu Gln Thr Arg Ser Pro Ser Lys Pro Leu Ser Arg
  1      5      10      15
Lys Leu Met Asp Trp Glu Val Val Ser Arg Asn Ser Ile Ser Glu Asp
      20      25      30
Arg Leu Glu Thr Gln Ser Arg Ala Ser Arg Ser Pro Pro Val Thr Pro
      35      40      45
Asn Gln Ser Gln Glu Thr Pro Val Asp Gly Lys Pro Leu Ala Leu Pro
      50      55      60
Pro Asn Gln Ser Gln Lys Asn Ile Arg Tyr His Ile His Tyr Leu His
      65      70      75      80
Leu Gln Tyr Tyr Leu Asp Arg His Ile Ser Ala Thr Leu Pro Ile Pro
      85      90      95
Ser Ser Ser Gly Ile Pro Thr Pro Ile Ala Val Ile Thr Asp Ala Leu
      100      105      110
Thr Asp Leu Val Glu Leu Ile Leu Gly Gln Pro Cys Ser Glu Glu Ser
      115      120      125
Gly Arg Ala Pro Gly Thr Leu Phe Leu Leu Ala Leu
      130      135      140

```


Lys Thr Arg His Glu Lys Glu Ile Thr Cys Pro Leu Ile Gly Gln Glu
 115 120 125
 Glu Lys Xaa Phe Ser Xaa Phe Val Gly Asp Met Asn Thr Cys Val Glu
 130 135 140
 Asn Lys Lys Glu Ser Lys Lys Leu Leu Glu
 145 150 154

<210> 1403
 <211> 210
 <212> PRT
 <213> Homo sapiens
 <221> misc_feature
 <222> (1)...(209)
 <223> Xaa = any amino acid or nothing

<400> 1403
 Pro Glu Val Ile Gln Gln Ser Ala Tyr Asp Ser Lys Ala Asp Ile Trp
 1 5 10 15
 Ser Leu Gly Ile Thr Ala Ile Glu Leu Ala Lys Gly Glu Pro Pro Asn
 20 25 30
 Ser Asp Met His Pro Met Arg Val Leu Phe Leu Ile Pro Lys Asn Asn
 35 40 45
 Pro Pro Thr His Cys Trp Arg Arg Leu Leu Glu Ser Phe Lys Glu Val
 50 55 60
 Xaa Leu Met Leu Ala Xaa Thr Lys Asp Pro Ser Ile Arg Pro Thr Ala
 65 70 75 80
 Lys Glu Leu Leu Lys His Lys Phe Ile Val Lys Asn Ser Lys Lys Thr
 85 90 95
 Ser Tyr Leu Thr Glu Leu Ile Asp Arg Phe Lys Arg Trp Lys Ala Glu
 100 105 110
 Gly His Ser Asp Asp Glu Ser Asp Ser Glu Gly Ser Asp Ser Glu Ser
 115 120 125
 Thr Ser Arg Glu Asn Asn Thr His Pro Glu Trp Ser Phe Thr Thr Val
 130 135 140
 Arg Lys Lys Pro Asp Pro Lys Lys Val Gln Asn Gly Ala Glu Gln Asp
 145 150 155 160
 Leu Val Gln Thr Leu Ser Cys Leu Ser Met Ile Ile Thr Pro Ala Phe
 165 170 175
 Ala Glu Leu Lys Gln Gln Asp Glu Asn Asn Ala Ser Arg Asn Gln Ala
 180 185 190
 Ile Glu Glu Leu Glu Lys Ser Ile Ala Val Ala Glu Ala Ala Gly Pro
 195 200 205
 Gly
 209

<210> 1404
 <211> 75
 <212> PRT
 <213> Homo sapiens
 <221> misc_feature
 <222> (1)...(74)
 <223> Xaa = any amino acid or nothing

<400> 1404
 Ile Ser Ile Asp Ala Xaa Lys Ala Phe Asp Lys Ile Gln His Cys Phe
 1 5 10 15

Ala Thr Arg Ala Gln Thr Val Ala Thr Thr Ala Asn Thr Ser Ser Pro
 355 360 365
 Met Ser Thr Arg Pro Ser Pro Ser Lys His Met Pro Ser Asp Thr Ala
 370 375 380
 Ala Ser Pro Val Pro Pro Met Arg Pro Gln Ala Gln Gly Pro Ile Ser
 385 390 395 400
 Gln Val Ser Val Asp Gln Pro Val Val Asn Thr Thr Asn Lys Ser Thr
 405 410 415
 Pro Met Pro Ser Asn Thr Thr Pro Glu Pro Ala Pro Thr Pro Thr Val
 420 425 430
 Val Thr Thr Thr Lys Ala Gln Ala Arg Glu Pro Thr Ala Ser Pro Val
 435 440 445
 Pro Val Pro His Thr Ser Pro Ile Pro Glu Met Glu Ala Met Ser Pro
 450 455 460
 Thr Thr Gln Pro Ser Pro Met Pro Tyr Thr Gln Arg Ala Ala Gly Pro
 465 470 475 480
 Gly Thr Ser Gln Ala Pro Glu Gln Val Glu Thr Glu Ala Thr Pro Gly
 485 490 495
 Thr Asp Ser Thr Gly Pro Thr Pro Arg Ser Ser Gly Gly Thr Lys Met
 500 505 510
 Pro Ala Thr Asp Ser Cys Gln Pro Ser Thr Gln Gly Gln Tyr Met Val
 515 520 525
 Asp His His Xaa Ala Pro His Pro Gly Arg Gly Arg Gln Asn Ser Pro
 530 535 540
 Ser Gly Gly Ala Val Thr Arg Gly Asp Pro Phe His His Ser Leu Gly
 545 550 555 560
 Phe Val Cys Pro Ala Gly Leu Xaa Glu Leu Gln Glu Glu Gly Leu His
 565 570 575
 Pro Gly Gly Leu Leu Asn Gln Arg Asp Val Cys Gly Leu Arg Asn Val
 580 585 590
 Arg Gly Ala Gly Ala Trp Arg Glu Ala Trp Pro Leu Pro Arg Pro Phe
 595 600 605
 Leu Leu Pro Leu Arg Pro Asn Gln Val Leu Pro Asn Ser Phe Gly Ala
 610 615 620
 Ile Glu Glu Ile Cys Gln Met Leu Lys His Ile
 625 630 635

<210> 1402

<211> 156

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(154)

<223> Xaa = any amino acid or nothing

<400> 1402

Glu Ser Gly Glu Phe Leu Val Ser Phe Thr Leu Lys Lys Pro Thr Asn
 1 5 10 15
 Val Phe His His Ile Asn Gly Met Lys Phe Phe Asn Lys Leu Ile Phe
 20 25 30
 Xaa Ser His Thr Asp Ile Ala Phe Tyr Lys Ile Gln His Pro Phe Met
 35 40 45
 Leu Lys Ala Leu Thr Lys Trp Ala Xaa Glu Gly Thr Xaa Pro Asp Arg
 50 55 60
 Arg Tyr Leu His Xaa Ser Leu Arg Leu Asn Gly Glu Gln Leu Lys Thr
 65 70 75 80
 Phe Pro Leu Arg Ser Gly Met Arg Xaa Gly Cys Ala Ile Leu Pro Leu
 85 90 95
 Val Leu Asn Ala Met Leu Ser Ile Val Pro Ala Val Val Pro Ala Gly
 100 105 110

Leu Tyr Phe Ala Cys Leu Pro Glu Glu Lys Val Pro Tyr Val Asn Ser
 85 90 95
 Pro Gly Glu Lys His Arg Ile Lys Gln Leu Leu Tyr Gln Leu Pro Pro
 100 105 110
 His Asp Asn Glu Val Arg Tyr Cys Gln Ser Leu Ser Glu Glu
 115 120 125 126

<210> 1401

<211> 637

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(635)

<223> Xaa = any amino acid or nothing

<400> 1401

Ile Arg Ile Arg His Glu Ala Ala Arg Ser Cys Leu Gly Cys Ala Ala
 1 5 10 15
 Gly His Val Pro Ala Pro Gly Leu Arg Leu Leu Pro Thr Val Arg Gly
 20 25 30
 Pro Pro Gly Arg Arg Gly Pro Ala Ala Pro Gly Cys Val Cys Tyr Xaa
 35 40 45
 Ser Gly Glu Ser Thr Phe Val Ser His Val Pro Gln Arg Met Ala Trp
 50 55 60
 Pro Gly Ser Ala Pro Pro Arg Gly Phe His Pro Leu Gln Ser Gln Thr
 65 70 75 80
 Ser Pro Ser Asp Thr Val Ser Ser Pro Gln Leu Ser Lys Glu Glu Asp
 85 90 95
 Gly Pro Gly Trp Glu His Pro Leu Ser Ser Ser Leu Xaa Ser Leu Gly
 100 105 110
 Gln Ala Gly Gly Asn His Xaa Gln Pro Glu Glu Leu Ala Gly Trp Glu
 115 120 125
 Pro Arg Gly Pro Pro Ser Leu Ala Pro Ser Ser Pro Thr Thr Met Trp
 130 135 140
 Thr Ala Leu Val Leu Ile Trp Ile Phe Ser Leu Ser Leu Ser Glu Ser
 145 150 155 160
 His Ala Ala Ser Asn Asp Pro Arg Asn Phe Val Pro Asn Lys Met Trp
 165 170 175
 Lys Gly Leu Val Lys Arg Asn Ala Ser Val Glu Thr Val Asp Asn Lys
 180 185 190
 Thr Ser Glu Asp Val Thr Met Ala Ala Ala Ser Pro Val Thr Leu Thr
 195 200 205
 Lys Gly Thr Ser Ala Ala His Leu Asn Ser Met Glu Val Thr Thr Glu
 210 215 220
 Asp Thr Ser Arg Thr Asp Val Ser Glu Pro Ala Thr Ser Gly Val Ala
 225 230 235 240
 Ala Asp Gly Val Thr Ser Ile Ala Pro Thr Ala Val Ala Ser Ser Thr
 245 250 255
 Thr Ala Ala Ser Ile Thr Thr Ala Ala Ser Ser Met Thr Val Ala Ser
 260 265 270
 Ser Ala Pro Thr Thr Ala Ala Ser Ser Thr Thr Val Ala Ser Ile Ala
 275 280 285
 Pro Thr Thr Ala Ala Ser Ser Met Thr Ala Ala Ser Ser Thr Pro Met
 290 295 300
 Thr Leu Ala Leu Pro Ala Pro Thr Ser Thr Ser Thr Gly Arg Thr Pro
 305 310 315 320
 Ser Thr Thr Ala Thr Gly His Pro Ser Leu Ser Thr Ala Leu Ala Gln
 325 330 335
 Val Pro Lys Ser Ser Ala Leu Pro Arg Thr Ala Thr Leu Ala Thr Leu
 340 345 350

<400> 1398

His Phe Thr Pro Asp Arg Ile Ala Ile Val Lys Asn Thr Arg Asp Ser
 1 5 10 15
 His Cys Trp Arg Gly Cys Xaa Glu Glu Gly Ala Pro Ala Arg Cys
 20 25 30 31

<210> 1399

<211> 156

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(155)

<223> Xaa = any amino acid or nothing

<400> 1399

Pro Arg Lys Arg Glu Ser Trp Trp Gly Glu Arg Leu Pro Pro Arg Gly
 1 5 10 15
 Phe Pro Pro Ala Ala Glu Asp Ala Pro Ala Pro Gly Trp Lys Gly Arg
 20 25 30
 Lys His Ala Ser Arg Thr Ala Arg Ala His Val Phe His Pro Ile Arg
 35 40 45
 Gln Ser Ile Arg Ser Pro Val Arg Gly Arg Pro Gly Asp Pro Arg Ala
 50 55 60
 Ala His Thr Arg Ser Ala Gly Thr Arg Leu Gln Cys Lys Ala Ser Arg
 65 70 75 80
 Gly Gly Xaa Gly Lys Gly Pro Ala Pro Thr Arg Xaa Glu Gly Gly Pro
 85 90 95
 Gly Ser Ala Pro Ala Pro Leu Pro Ala Ser Ser Gly Cys Ser Leu Phe
 100 105 110
 Pro Asp Ser Ser Pro Trp Thr Pro Pro Pro Ala Pro Gly Ala Ala
 115 120 125
 Ala Ala Gln Pro Xaa Xaa Thr Pro Arg Cys Pro Ala Ala Leu Arg Ala
 130 135 140
 Gly Ala His Ile Gly Arg Val Gly Arg Pro Tyr
 145 150 155

<210> 1400

<211> 127

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(126)

<223> Xaa = any amino acid or nothing

<400> 1400

Glu Lys Cys Ile Gln Ala Leu Asp Val Phe Val Phe Cys Tyr Ile Asp
 1 5 10 15
 His Ser Ser His Cys Leu Met Ser Cys Asp Xaa Glu Asp Gln Ala Leu
 20 25 30
 Asn Phe Met Pro Leu Glu Met Glu Pro Lys Met Ser Lys Leu Ala Phe
 35 40 45
 Gly Cys Gln Arg Ser Ser Thr Ser Asp Asp Asp Ser Gly Cys Ala Leu
 50 55 60
 Glu Glu Tyr Ala Trp Val Pro Pro Gly Leu Arg Pro Glu Gln Ile Gln
 65 70 75 80

<210> 1396
 <211> 124
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(122)
 <223> Xaa = any amino acid or nothing

<400> 1396
 Thr Thr Lys Lys Thr Leu Ile Ser Asn Asn Val Ser Ser Arg Ser Leu
 1 5 10 15
 Pro Ile Leu Pro Glu Leu Lys Ala Phe Ser Leu Ala Phe Asn Asp Pro
 20 25 30
 Leu Glu Ile Gln Lys Tyr Met Arg Thr Asp Gln Xaa Cys Val Thr His
 35 40 45
 Asp Ile Ser Leu Tyr Ile Val Thr Lys Leu Ala Leu Ile Phe Leu Ile
 50 55 60
 Pro Arg Val Phe Leu Phe His Gln Leu Asn Ile Thr Xaa Xaa Cys Leu
 65 70 75 80
 His Phe Phe Thr Met Thr Thr Phe Ile Ala Ile Pro Phe Ser Phe Leu
 85 90 95
 Phe Leu Gly Arg Asp Lys Ser Leu Ala Met Leu Pro Arg Leu Val Ser
 100 105 110
 Asn Ser Trp Pro Gln Val Ile Leu Pro Pro
 115 120 122

<210> 1397
 <211> 54
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(53)
 <223> Xaa = any amino acid or nothing

<400> 1397
 Gln Leu Gln Asn Leu Ala Ser Arg Gly Cys Leu Xaa Ser Gln Leu Leu
 1 5 10 15
 Arg Arg Leu Arg Arg Glu Asn Arg Leu Asn Pro Gly Gly Gly Cys
 20 25 30
 Ser Glu Ile Ala Pro Cys Thr Pro Ala Trp Val Thr Gln Arg Asp Phe
 35 40 45
 Phe Arg Lys Lys Lys
 50 53

<210> 1398
 <211> 31
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(31)
 <223> Xaa = any amino acid or nothing

```

Ser Leu Pro Ala Thr Pro Pro Leu Leu Thr Pro Pro His Thr Leu Leu
  50                      55                      60
Pro Gln Arg Pro Met Leu Pro Pro Ser His Ala Gly Leu Ala Arg Pro
  65                      70                      75                      80
Pro Pro Pro Glu Pro Ile Ser Val Pro
                      85                      89

```

```

<210> 1394
<211> 152
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(150)
<223> Xaa = any amino acid or nothing

```

```

<400> 1394
Leu Pro Gln Tyr Cys Phe Phe Pro Arg Leu Ser Pro Lys Ser Lys Leu
  1                      5                      10                      15
Val Lys His Ser Ala Leu Xaa Xaa Pro Ser Ala Leu Lys Pro Pro Thr
                      20                      25                      30
Lys Ser Pro Arg Cys Ile Pro Arg Thr Ser Leu Tyr Phe Thr Ile Cys
                      35                      40                      45
Cys Pro Pro Ala Leu Gln Leu Ser Pro Ile Glu Asp Pro Pro Ala Ile
                      50                      55                      60
Tyr Arg Ser Pro Pro Thr His Met Leu Arg Ser Ala Ser Gln Pro Leu
                      65                      70                      75                      80
Asn Gln Ala Pro Thr Leu Val Lys Gly His Pro Pro Ser Arg Phe Leu
                      85                      90                      95
Gln Gly Gln Val Ser Cys Pro Pro Gln Pro Thr Leu Pro Arg Glu Lys
                      100                      105                      110
Pro Leu Pro Leu His Leu Arg Pro Pro Pro Arg Pro Ala Gln Pro Pro
                      115                      120                      125
Leu Pro Arg Pro Leu Thr Phe Ser Thr Arg Arg Asn Val Asp Pro Glu
                      130                      135                      140
Ile Pro Glu Arg Phe Arg
145                      150

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<210> 1395
<211> 74
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(73)
<223> Xaa = any amino acid or nothing

```

```

<400> 1395
Gly Val Tyr Pro Pro Thr Val Phe Asp Asn Tyr Ser Val Gln Thr Ser
  1                      5                      10                      15
Val Asp Gly Gln Ile Val Ser Leu Asn Thr Trp Asp Thr Ala Gly Gln
                      20                      25                      30
Glu Glu Tyr Asp Arg Leu Arg Thr Leu Ser Xaa Pro Gln Thr Ser Ile
                      35                      40                      45
Phe Val Ile Cys Phe Ser Ile Gly Asn Leu Glu Phe Pro Ile Tyr Gly
                      50                      55                      60
Thr Trp Leu Ser Met Ser Met Gly Lys
65                      70                      73

```

<223> Xaa = any amino acid or nothing

<400> 1391

```

Ser Met Leu Lys Glu Arg Lys Val Phe Gln Phe Pro Ser Cys Leu Phe
 1           5           10           15
Phe Gln Tyr Ile Thr Trp Leu Gly Pro Pro Tyr His Val Leu Phe Asp
           20           25           30
Ser Ser Val Thr Asn Phe Ser Ile Gly Ala Lys Xaa Asp Ile Leu Gln
           35           40           45
Ser Val Met Asn Cys Leu Tyr Ala Lys Arg Ile Pro Cys Val Thr
 50           55           60           63

```

<210> 1392

<211> 139

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(138)

<223> Xaa = any amino acid or nothing

<400> 1392

```

Gly Ser Thr His Ala Ser Gly Tyr Asp Lys Thr Pro Asp Phe Ile Leu
 1           5           10           15
Gln Val Pro Val Ala Val Glu Gly His Ile Ile His Trp Ile Glu Ser
           20           25           30
Lys Ala Ser Phe Gly Asp Glu Cys Ser His His Ala Tyr Leu His Asp
           35           40           45
Gln Phe Trp Ser Tyr Trp Asn Ser Leu Lys His Arg Thr Trp Gln Gly
 50           55           60
Ile Gly Thr Val Ala Ser Asn Leu Ser Gln Leu Xaa Thr Leu Asn Ala
 65           70           75           80
Pro Phe Pro Glu Leu Leu Phe Arg Ser Leu Ala Arg Thr Gly Phe
           85           90           95
Val Leu Thr Xaa Arg Phe Gly Pro Gly Leu Val Ile Tyr Trp Tyr Gly
           100          105          110
Phe Ile Gln Glu Leu Asp Cys Asn Arg Glu Arg Gly Ile Leu Leu Lys
           115          120          125
Ala Cys Phe Pro Thr Asn Ile Val Thr Leu
130           135           138

```

<210> 1393

<211> 89

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(89)

<223> Xaa = any amino acid or nothing

<400> 1393

```

Pro Ala Leu Ser Pro Ala Pro Val Pro Gln Lys Lys Gly Ser Pro Leu
 1           5           10           15
Pro Leu Asp Pro Cys Leu Gly Pro Ser Ser Trp Leu Leu Ser Val Gly
           20           25           30
Leu Gly Trp Pro Arg Leu Xaa Pro Arg Arg Gly Pro Gly Asp Pro Gly
           35           40           45

```

```

His Arg Pro Leu Gln Glu Thr Val Leu Arg Arg Ala Pro Ala Pro Ala
145          150          155          160
Ser Gly Val Pro Ser Pro Ser Gly Val Gly Trp Asp Arg Xaa Ala Gly
          165          170          175
Pro Ala Glu Pro Ser Pro Ser Thr Pro Ala Thr Val Ile Ile Ser Val
          180          185          190
Pro Trp Tyr Leu Gly Leu Met Phe Arg Thr Arg Lys Glu Asp Ser Val
          195          200          205
Leu Met Glu Ala Thr Ser Gly Gly Pro Thr Ser Phe Arg Leu Gln Val
          210          215          220
Thr Gly Ala Pro Cys His Gln Gly Thr Cys Xaa Val Gly Ala Arg Gly
225          230          235          240
Arg Asp Pro Met Leu Ser Gly Leu Arg Val Thr Asp Gly Glu Trp His
          245          250          255
His Leu Leu Ile Glu Leu Lys Asn Val Lys Glu Asp Ser Glu Met Lys
          260          265          270
His Leu Val Thr Met Thr Leu Asp Tyr Gly Met Asp Gln Val Ser Trp
          275          280          285
His Leu His Leu Leu Trp Gly Xaa Thr Leu Pro Pro Ala Gln Gly Lys
          290          295          300
Thr Gly Ala Ser Glu Asp Lys Val Ser Val Arg Arg Gly Phe Arg Gly
305          310          315          320
Cys Met Gln Val Arg Gly Gly Cys Gly Gly Arg Gly Glu Ala Cys Pro
          325          330          335
Ser Gln Ala Ala Pro Arg Leu
          340          343

```

```

<210> 1390
<211> 111
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(110)
<223> Xaa = any amino acid or nothing

```

```

<400> 1390
Ile His Lys Ile Ile Ile His Lys Glu Asp Leu Asn Lys Trp Lys Tyr
1          5          10          15
Ile Leu Cys Ser Gly Met Glu Arg Leu Ser Thr Val Met Ile Pro Val
          20          25          30
Val Pro Gln Ile Ile Tyr Lys Phe Asn Ala Xaa Gln Val Ile Leu Lys
          35          40          45
Phe Thr Trp Xaa Glu Xaa Gly Ala Lys Ile Thr Ile Leu Arg Lys Asn
          50          55          60
Lys Leu Arg Gly Leu Val Leu Val Pro Leu Ser Thr Cys Xaa Val Lys
          65          70          75          80
Tyr Leu Leu Asp Lys Val Leu Pro His Ile Lys Thr Tyr Tyr Glu Ala
          85          90          95
Arg Val Asn Lys Ser Val Val Leu Val Gln Val Thr Ile Met
          100          105          110

```

```

<210> 1391
<211> 63
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(63)

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<210> 1388
 <211> 144
 <212> PRT
 <213> Homo sapiens
 <221> misc_feature
 <222> (1)...(142)
 <223> Xaa = any amino acid or nothing

<400> 1388
 Phe Arg Ala Met Val Ser Ser Thr Leu Lys Leu Gly Ile Ser Ile Leu
 1 5 10 15
 Asn Gly Gly Asn Ala Glu Val Gln Gln Gly Asn Arg Gly Lys Gly Thr
 20 25 30
 Ser Glu Glu Gly Lys Glu Gly Xaa Glu Val Pro Val Xaa Leu Pro Val
 35 40 45
 Ser Pro Pro Leu Pro Arg Pro Leu Gln Lys Met Leu Asp Tyr Leu Lys
 50 55 60
 Asp Lys Lys Glu Val Gly Phe Phe Gln Ser Ile Gln Ala Leu Met Gln
 65 70 75 80
 Thr Cys Gly Glu Lys Val Met Ala Asp Asp Glu Phe Thr Gln Asp Leu
 85 90 95
 Phe Arg Phe Leu Gln Leu Leu Cys Glu Gly His Asn Asn Asp Phe Gln
 100 105 110
 Asn Tyr Leu Arg Thr Gln Thr Gly Asn Thr Thr Thr Ile Asn Ile Ile
 115 120 125
 Ile Cys Thr Val Asp Tyr Leu Leu Arg Leu Gln Glu Ser Ile
 130 135 140 142

<210> 1389
 <211> 344
 <212> PRT
 <213> Homo sapiens
 <221> misc_feature
 <222> (1)...(343)
 <223> Xaa = any amino acid or nothing

<400> 1389
 Thr Leu Asp Leu Thr Gly Pro Leu Leu Leu Gly Gly Val Pro Asn Val
 1 5 10 15
 Pro Lys Asp Phe Arg Gly Arg Asn Arg Gln Phe Gly Gly Cys Met Arg
 20 25 30
 Asn Leu Ser Val Asp Gly Lys Asn Val Asp Met Ala Gly Phe Ile Ala
 35 40 45
 Asn Asn Gly Thr Arg Glu Gly Cys Ala Ala Arg Arg Asn Phe Cys Asp
 50 55 60
 Gly Arg Arg Arg Gln Asn Gly Gly Thr Cys Val Asn Arg Trp Asn Met
 65 70 75 80
 Tyr Leu Cys Glu Cys Pro Leu Arg Phe Gly Gly Lys Asn Cys Glu Gln
 85 90 95
 Gly Glu Trp Pro Ala Ser Ser Ile Pro Pro Val Thr Ala Ala Trp Glu
 100 105 110
 Ala Leu Leu Asp Val Pro Gly Thr Thr Val Arg Gly Leu His Ile
 115 120 125
 Gln Val Arg Gln Pro Leu Val Val Tyr Ala Ala Phe Thr Val Asp Ser
 130 135 140

```

Arg Pro Arg Leu Arg Ser Leu Pro Val Leu Gly Leu Pro Ala Pro Arg
      435              440              445
Cys Pro Val Ser Ala His Pro Trp His Arg Arg Ser Gly Ser Ser Cys
      450              455              460
His Ala Ala Arg Leu Val Pro Arg His Pro Ala Pro Gly Cys Pro Xaa
465              470              475              480
Xaa Thr Gly Xaa Pro Leu Ile Thr Gly Phe Pro Glu Pro Xaa Ala Xaa
      485              490              495
Gly Leu Pro Asn His Gln Ala Val Gly Leu Glu Ala Ser Gly Ala Leu
      500              505              510
Gln Ala Gly His Arg Asp Glu Leu Pro Thr Met Val Gln Leu Leu Asp
      515              520              525
His Ser Pro Asp Tyr Pro Leu Lys Gly Arg Pro His Ala Pro
      530              535              540              542

```

<210> 1387

<211> 278

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(276)

<223> Xaa = any amino acid or nothing

<400> 1387

```

Phe Arg Leu Pro Leu Ala Ala Gly Ala Arg Gly Ala Ala Glu Pro Arg
1              5              10              15
Val Ala Val Ser Met Ala Pro Asp Pro Ser Ala Lys Ile His Trp Glu
      20              25              30
Ala Ser Pro Glu Met Gln Ser Lys Cys His Gln Lys Gly Lys Asn Asn
      35              40              45
Gln Thr Glu Cys Phe Asn His Val Arg Phe Leu Gln Arg Leu Asn Ser
      50              55              60
Thr His Leu Tyr Ala Cys Gly Thr His Ala Phe Gln Pro Leu Cys Ala
      65              70              75              80
Ala Ile Asp Ala Glu Ala Phe Thr Leu Pro Thr Ser Phe Glu Glu Gly
      85              90              95
Lys Glu Lys Cys Pro Tyr Asp Pro Ala Arg Gly Phe Thr Gly Leu Ile
      100             105             110
Ile Asp Gly Gly Leu Tyr Thr Ala Thr Arg Tyr Glu Phe Arg Ser Ile
      115             120             125
Pro Asp Ile Arg Arg Ser Arg His Pro His Ser Leu Arg Thr Glu Glu
      130             135             140
Thr Pro Met His Trp Leu Asn Gly Xaa Glu Asp Glu Ala Gln Asp Asp
145             150             155             160
Gly Gly Xaa Gly Thr Ile Ser Ser Phe Leu Leu Pro Trp Pro Ala Asp
      165             170             175
His Pro Thr Pro Lys Ser Pro Gly Glu Pro Val His Ser Ile Pro Val
      180             185             190
Cys Cys Gln Val Arg Gly Gln Pro Gln Ser Gly Gly Lys Glu Ser Pro
      195             200             205
Ala Cys Leu Lys Ser Leu Ser Asn Cys Leu Thr His Asp Ala Glu Phe
      210             215             220
Val Phe Ser Val Leu Val Arg Glu Ser Lys Ala Ser Ala Val Gly Asp
225             230             235             240
Asp Asp Lys Val Tyr Tyr Phe Phe Thr Glu Arg Ala Thr Glu Lys Glu
      245             250             255
Ser Gly Ser Phe Thr Gln Ser Arg Ser Ser His Arg Val Ala Arg Gly
      260             265             270
Ile Pro Pro Leu
      275 276

```

<211> 549
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(542)
 <223> Xaa = any amino acid or nothing

<400> 1386
 Phe Phe Phe Ser Phe Val Cys His Leu Tyr Cys Val Ser Pro Thr Pro
 1 5 10 15
 Gly Pro His Gly Arg Leu Ala Thr Trp Leu Pro Gly Leu Leu Ala Phe
 20 25 30
 Leu Gly Leu Ala Ala Gly Gly Gln Thr Leu Cys Pro Ala Gly Glu Leu
 35 40 45
 Pro Gly His Ala Arg Ala Gln Ala Ser Gly Ala Pro Gly Ser Val Leu
 50 55 60
 Ile Ala Val Pro Gly Arg Arg Arg Val His Thr Cys Gly Pro Gly Pro
 65 70 75 80
 Ala Ala Pro Ser Thr Arg Gly Glu Cys Pro Pro Pro Ala Leu Gly His
 85 90 95
 Thr Arg Pro Ala Arg Pro Arg Pro Val Pro Phe Ala Pro Ala Val Pro
 100 105 110
 Gln Glu Pro Gly Gly Gln Gly His Gly Ala Ala Pro Pro Ala Thr Gly
 115 120 125
 His Ser Ala Pro Arg Gly Cys Pro Pro Ala Arg Ala Ala Pro Thr Gly
 130 135 140
 Ser Ala Thr Pro Ala Pro Pro Pro Ala Ala Cys Ala Ala Phe His Ser
 145 150 155 160
 Ala Trp Ser Val Pro Pro Ala Gly Arg Gln Gln Gly Xaa Arg Val Pro
 165 170 175
 Ala Pro Ala Phe Arg Arg Thr Thr Pro Gly Thr Pro Gly Gln His Leu
 180 185 190
 Leu Asp Arg Pro Gly Ala Pro Pro Ala Gln Gly Ser Gly Pro Ala Pro
 195 200 205
 Ala Pro Pro Pro Arg Leu Ala Gly Pro Ala Gly Pro Ala Ala Pro Pro
 210 215 220
 Pro Gly Pro Pro Ala Ala Ser Trp His Ser Ser Leu Ser Lys Ser Ser
 225 230 235 240
 Ser Ser Leu Gly Trp Ser Pro Pro Leu Pro Val Gly Pro Gly Ser Leu
 245 250 255
 Gln Xaa Thr Pro Pro Pro Gln Gly Pro His Leu Ser Gly Ser Cys Gly
 260 265 270
 Gly Thr Ser Ser Trp Arg Gly Gln Arg Ala Ala Val Ala Arg Arg Leu
 275 280 285
 Arg Ser Trp Asn Ala Cys Gly Leu Ser Arg Val Ala Gly Arg Ser Ser
 290 295 300
 Ala Ser Tyr Pro Gly Arg Glu Gly Arg Pro Ser Gln Ser Gln Xaa Pro
 305 310 315 320
 Ala Gly Pro Pro Gly Met Arg Gly Cys Cys Leu Arg Gly Trp Xaa Pro
 325 330 335
 Ser Ser Ser Gly Ser Asp Gly Pro Gly Pro His Pro Ala Ser Thr Trp
 340 345 350
 Leu Arg Ala Gly Lys Thr Gly Pro Ser Pro Pro Ala Cys Gly Cys Ala
 355 360 365
 Xaa Leu Pro Pro Pro Ser Val Ser Ala Ala Pro Gln Ser Pro Arg Thr
 370 375 380
 Arg Cys Pro Arg Gly Cys Ala Ala Ala Ala Gly Leu Cys Val Leu Ala
 385 390 395 400
 Ala Ala Gly Ala Ser His Gly Ala Gly Leu Pro Gly Val Arg Val His
 405 410 415
 Thr Gln Arg Val His Ile His Xaa Gly Ala Gly Gly Cys Gln Thr Pro
 420 425 430

<210> 1384
 <211> 142
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(140)
 <223> Xaa = any amino acid or nothing

<400> 1384
 Ala Pro Gly Ala Ser Val Gly Arg Ala Gln Ala Ala Glu Gly Xaa Arg
 1 5 10 15
 Gly Gly Pro Thr Gly Arg Pro Pro Ser Ala Leu Gly Val Ser Glu Ala
 20 25 30
 Gly Arg Ala Gly Arg Ala Gly Glu Gly Arg Pro Val Pro Pro Ala Tyr
 35 40 45
 Pro Leu Cys Lys Ser Ala Gln Thr Ser Gly Pro Pro Lys Ala Arg Leu
 50 55 60
 Ser Pro Pro Leu Ala Ser Cys Gly Gly Arg Gly Pro Pro Gly Gly Ala
 65 70 75 80
 Ala Cys Ala Thr Cys Ala Pro Pro Ala Gly Pro Ala Arg Ser Ser Arg
 85 90 95
 Cys Arg Arg Arg Ser Pro Pro Glu Xaa Gly Pro Arg Xaa Pro Ser Arg
 100 105 110
 Pro Ala Arg Pro Ser Pro Gly Ser Ala Ala Ser Arg Arg Gln Lys Leu
 115 120 125
 Thr Pro Cys Arg Cys Gln Phe Arg Gly Leu Cys Ala
 130 135 140

<210> 1385
 <211> 109
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(107)
 <223> Xaa = any amino acid or nothing

<400> 1385
 Pro Thr Pro Tyr Pro Gly Glu Xaa Gln Ala Ala Phe Leu Leu Arg Gly
 1 5 10 15
 Pro Gly Leu Arg Pro Pro Ala Asp Pro Ser Leu Arg His Arg Asn Leu
 20 25 30
 Thr Glu Leu Val Val Ala Val Thr Asp Glu Asn Ile Val Gly Leu Phe
 35 40 45
 Ala Ala Leu Leu Ala Glu Arg Arg Val Leu Leu Thr Ala Ser Lys Leu
 50 55 60
 Ser Thr Leu Thr Ser Cys Asp His Ala Phe Cys Ala Leu Leu Tyr Pro
 65 70 75 80
 Met Arg Trp Glu His Val Leu Ile Pro Thr Leu Pro Pro His Leu Leu
 85 90 95
 Asp Tyr Cys Xaa Cys Pro Pro Leu Pro Arg Thr
 100 105 107

<210> 1386

Gly Gly Ser Ala Gly Ser Xaa Gly Leu Pro Ser Ala Gly Gly Ser Arg
 100 105 110
 Gly Arg Lys Gly Trp Arg Ala Ala Gly Arg Gln Pro Ser Thr Arg Xaa
 115 120 125
 Gly Arg Pro Gly Arg His Gly Gly Arg Gly Glu Xaa Ala Gly His Pro
 130 135 140
 Glu Pro Arg Gln Ser Ala Leu Gln Ser Ala Gly Leu Ala Ser Ser Pro
 145 150 155 160
 Glu Pro Met Gly Ala Ala Leu Ala Glu Asp Gly Ser Gly Asp Ser Arg
 165 170 175
 Gly Ala Gly Pro Arg Pro Gln Glu Xaa Pro Pro Ser Val Leu Ser Arg
 180 185 190
 Ser Gly Ser Xaa Gly Xaa Gly Xaa Ala Ala Ser Gly Thr Ala Ser Ser
 195 200 205
 Pro Arg Ser His Ser Ser Arg Leu Gly Pro Pro Ser Ala Gly Phe His
 210 215 220
 Gly Leu Arg Cys Gly Gln Pro Pro Phe Ala Ala Pro Pro Gly Pro
 225 230 235 240
 Trp Pro Gly Thr Gly Arg Pro Ala Gly Gly Ala Gly Ser Pro Pro Ala
 245 250 255
 Ala Ala Gly Thr Ala Pro Pro Ala Thr Arg Gly Ala Gln Ser Arg Arg
 260 265 270
 Gln Asn Arg Thr Ala Gly Arg Asn Ala Ser Pro Gln Thr Ala Ala Gly
 275 280 285
 Ala Gly Ser Pro Val Gln Trp Ala Leu Ser Arg Ala Thr Gly Xaa Thr
 290 295 300
 Gly Glu Thr Gly Ser Trp Cys Ala Gly Gly Thr His Gln Ala Thr His
 305 310 315 320
 Leu Thr Ala Ala Trp Val Cys Pro Pro Thr Trp Ser Val Arg Pro Gly
 325 330 335
 Gly Ser Gly Pro Ala Ala Gly Leu Gly Arg Xaa Gly Arg His Pro Ala
 340 345 350
 Gln Ser Pro Pro Leu Pro Val Pro Arg Gly Xaa Pro Ala Trp Pro Gln
 355 360 365
 Glu Ala Pro Ser Pro Ser Pro Ala Ser Ser Glu Val Ala Leu Ser Ser
 370 375 380
 Gly Ser Cys Trp Pro Asp Gln Ala Pro Gly Pro Ala Arg Gly Ser Pro
 385 390 395 400
 Pro Ala Pro Leu Ala Pro Ala Trp Pro Ala Ala Gly Arg Gly Arg Gln
 405 410 415
 Arg Xaa Gly Arg Gln Ser Ala His Pro Pro Pro Arg Arg Xaa Ser Thr
 420 425 430
 Ala Val Ser Leu Ser Gly Thr Ser Xaa Trp Arg Arg Ser Pro Xaa Ala
 435 440 445
 Gly Thr Arg Thr Gln Gln Cys Xaa Ser Pro Trp Leu Val Pro Ala Cys
 450 455 460
 Ser Ser Arg Pro Leu Xaa Arg Gly Thr Arg Arg Pro Ser Thr Gln Gln
 465 470 475 480
 Ser Pro Gln Thr Thr Gly Thr Pro Gly Arg Ser Ala Gly Pro Gly His
 485 490 495
 Pro Arg Ser Xaa Gly Gly Arg Ser Pro Ala Gly Thr Gly His Leu Gly
 500 505 510
 Ala Gln Thr Val Ala Ser Pro His Xaa Gly His Trp Pro Thr Ala Leu
 515 520 525
 Ser Cys Leu Trp Ala Ser Ala Ser Pro Pro Gly Pro Glu Ala Pro Pro
 530 535 540
 Gln Thr Gly Ala Cys Ile Gly Thr Asn Cys Arg Tyr Arg Ala Ala Ser
 545 550 555 560
 Ala Arg Arg Ser Ser Val Ala Pro Ala Cys Ala Xaa Gly Trp Gln Xaa
 565 570 575
 Ala Gly Ser Pro Pro Ala Val Leu Arg Gly Pro Pro Xaa Arg Val Arg
 580 585 590
 Glu Arg Gly Ala Leu Thr His Arg Pro Arg Ala Pro Asp Glu
 595 600 605 606

```

Ala Lys Thr Ser Lys Ala Gln Ser Thr Lys Thr Asn Lys Xaa Lys Arg
      85          90          95
Gln Thr Arg Tyr Ile Lys Leu Lys Lys Lys Ser Thr Ala Ser Lys Glu
      100        105        110
Asn Asn Arg Val Lys Arg Gln Pro Leu Glu Xaa Glu Lys Ile Phe Ala
      115        120        125
Asn
129

```

```

<210> 1382
<211> 119
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(116)
<223> Xaa = any amino acid or nothing

```

```

<400> 1382
Val Lys Pro Tyr Glu Ile Ala Val Phe Leu Val Lys Pro Ile Glu Tyr
 1          5          10          15
Lys Xaa His Leu Ser Asp Pro Ala Ile Pro Leu Ser Gly Ile Xaa
      20          25          30
Leu Lys Glu Ile Lys Ala Tyr Thr Arg Arg Ile Cys Thr Pro Met Phe
      35          40          45
Ala Ala Pro Val Ser Val Ile Ala Arg Asn Xaa Lys Gln Ser Lys Cys
      50          55          60
Gln Lys Gln Xaa Tyr Val His Arg Met Glu Tyr Tyr Thr Thr Ile Lys
      65          70          75          80
Arg Ser Glu Ile Leu Ile Cys Thr Thr Thr Trp Val Asp Phe Arg Asn
      85          90          95
Thr Ile Leu Arg Glu Thr Asp Arg Ile His Lys Thr Thr Tyr Asp Val
      100        105        110
Ile Ser Leu Ile
      115 116

```

```

<210> 1383
<211> 612
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(606)
<223> Xaa = any amino acid or nothing

```

```

<400> 1383
Lys Ser Ala Cys Ser Phe Ile Cys Ser Glu Glu Gln Pro Ala Ser Pro
 1          5          10          15
Ser Pro Leu Lys Pro Gly Thr Tyr Ala Ser Glu Thr Arg Pro Arg Asp
      20          25          30
Pro His Ala Ala Gly Pro Arg Arg Asp Ser Ser Glu Ala Glu Thr Arg
      35          40          45
Arg Pro Arg Gly Ala Asp Gly Ser Gly Thr Val Val Lys Gly Thr Pro
      50          55          60
Gly Ser Pro Ala Pro Pro Cys Ser Trp Gly His Gly Gly Glu Thr Glu
      65          70          75          80
Gly Ala Gly Xaa Cys Pro Ala Ala Pro Gly Thr Asp Leu Arg Ala Pro
      85          90          95

```

<223> Xaa = any amino acid or nothing

<400> 1379

```

Ile Tyr Ser Lys Met Cys Met Glu Arg Gln Arg Leu Asn Asn Xaa Ile
 1           5           10           15
Leu Lys Lys Asn Lys Val Arg Gly Ile Ala Val Pro Asp Val Lys Val
      20           25           30
Tyr Tyr Lys Pro Thr Val Ile Lys Thr Ser Trp Ile Leu Xaa Lys Asp
      35           40           45
Ser His Ile Val Glu Trp Asn Arg Leu Glu Asn Leu Glu Ile Asp Pro
      50           55           60
Asn Ile Lys Arg Leu Ile Leu Asp Lys Gly Ala Glu Ala Thr Glu Trp
      65           70           75           80
Arg Lys Asp Ser Phe Phe Arg Gln Trp Gln
              85           90

```

<210> 1380

<211> 77

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(75)

<223> Xaa = any amino acid or nothing

<400> 1380

```

Phe Phe Phe Glu Thr Glu Ser His Ser Val Thr Gln Ala Gly Val Gln
 1           5           10           15
Trp Cys Asn Pro Gly Phe Lys Arg Phe Ser Cys Phe Gly Leu Ser Ser
      20           25           30
Ser Trp Asp Tyr Arg Tyr Ala Pro Pro Arg Pro Ala Asn Phe Xaa Phe
      35           40           45
Leu Val Glu Thr Gly Phe Tyr Tyr Val Ala Gln Ala Gly Leu Lys Leu
      50           55           60
Leu Ser Pro Gly Asp Leu Pro Ala Leu Ala Ser
      65           70           75

```

<210> 1381

<211> 132

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(129)

<223> Xaa = any amino acid or nothing

<400> 1381

```

Gln Leu Met Phe Asp Lys Gly Val Lys Asn Ile His Trp Gly Trp Thr
 1           5           10           15
Pro Pro Phe Thr Lys Xaa Tyr Trp Lys Asn Trp Ile Ser Ile Cys Arg
      20           25           30
Arg Met Asn Leu Asn Pro Tyr Leu Ser Arg Tyr Ile Lys Ile Asn Ser
      35           40           45
Arg Lys Asp Leu Thr Val Arg Pro Glu Pro Ile Lys Leu Val Glu Glu
      50           55           60
Asn Thr Gly Lys Thr Ile Gln Asp Thr Gly Leu Gly Lys Xaa Phe Ile
      65           70           75           80

```

<211> 94
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(92)
 <223> Xaa = any amino acid or nothing

<400> 1377
 Lys Ser Lys Ala Thr Gly Tyr Met Val Asn Ile Xaa Lys Leu Ile Val
 1 5 10 15
 Phe Leu Tyr Ala Asn Asp Glu Gln Leu Glu Ile Glu Met Asn Lys Ile
 20 25 30
 Val Pro Phe Asn Gly Ser Lys Asn Lys Ile Ala Phe Thr Asn Leu Thr
 35 40 45
 Lys Tyr Gln Asn Ile Gln Asn Arg His Ala Glu Asn Tyr Lys Ile Leu
 50 55 60
 Val Asn Lys Ile Glu Asp Leu Asn Lys Trp Arg Asn Val Leu Leu Ser
 65 70 75 80
 Trp Ile Gly Arg Arg Asn Ile Ile Asn Thr Met Thr
 85 90 92

<210> 1378
 <211> 143
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(138)
 <223> Xaa = any amino acid or nothing

<400> 1378
 Thr Ile Cys Thr Asn Lys Phe Asn Asn Leu Asp Glu Ile Lys Phe Leu
 1 5 10 15
 Glu Arg His Lys Leu Ser Lys Leu Thr Gln Glu Glu Val Glu Asn Leu
 20 25 30
 Ile Thr Leu Lys Thr Ser Arg Glu Thr Glu Leu Val Ile Asn Lys Xaa
 35 40 45
 Val Ile Pro His Lys Glu Lys Pro Gly Pro Asp Ser Phe Thr Gly Glu
 50 55 60
 Phe Tyr Gln Thr Phe Lys Glu Glu Leu Ile Ile Ile Leu His Lys Leu
 65 70 75 80
 Phe Gln Thr Ile Lys Tyr Gly Arg Ile Leu Pro Asn Ser Val Tyr Glu
 85 90 95
 Thr Ser Ile Thr Leu Lys Pro Lys Pro Glu Lys Asp Leu Lys Glu Asn
 100 105 110
 Tyr Arg Pro Leu Pro Leu Ser Asn Ile Asp Ala Lys Leu Asn Lys Thr
 115 120 125
 Leu Ala Asn Arg Ile Xaa Xaa His Ile Arg
 130 135 138

<210> 1379
 <211> 92
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(90)

<400> 1374

```

Gly Arg Ala Leu Asp Thr Ala Ala Gly Ser Pro Val Gln Thr Ala His
 1           5           10           15
Gly Leu Pro Ser Asp Ala Leu Ala Pro Leu Asp Asp Ser Met Pro Trp
           20           25           30
Glu Gly Arg Thr Thr Ala Gln Trp Ser Leu His Arg Lys Arg His Leu
           35           40           45
Ala Arg Thr Leu Leu Val Ser Arg Val Arg Gly Pro Gln
           50           55           60 61

```

<210> 1375

<211> 82

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(82)

<223> Xaa = any amino acid or nothing

<400> 1375

```

Tyr Leu Ile Thr Thr Ile Leu Glu Thr Gly Tyr Leu Trp Lys Asn Arg
 1           5           10           15
His Ser Asp Gln Xaa Lys Arg Thr Glu Asn Pro Glu Arg Asp Gln His
           20           25           30
Lys Tyr Pro Lys Val Asp Phe Cys Lys Ser Asn Ser Met Lys Asn Arg
           35           40           45
Leu Cys Asn Lys Trp His Trp Thr Asn Trp Ile Phe Thr Asp Lys Lys
           50           55           60
Ile Asn Leu Asn Leu Lys Pro His Thr Lys Leu Thr Pro Asn Ile Lys
           65           70           75           80
Lys Asn
           82

```

<210> 1376

<211> 73

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(73)

<223> Xaa = any amino acid or nothing

<400> 1376

```

Glu Val Lys Asn Thr Asn Pro Phe Ile Phe Ser Gly Thr Asn Leu Thr
 1           5           10           15
Ile Trp Ile Arg Ser Ile Xaa Arg Lys Ser Asp Glu Ile Asn Gln Arg
           20           25           30
Thr Lys Xaa Met Glu Lys Tyr Ser Ile Ser Leu Asp Arg Arg Leu Asn
           35           40           45
Thr Val Lys Met Ser Phe Leu Pro Asn Leu Ile Tyr Lys Phe Asn Thr
           50           55           60
Ile Ser Ile Lys Ile Pro Ala Asn Phe
           65           70           73

```

<210> 1377

```

<400> 1372
Pro His Leu Glu Asn Pro His Pro Glu His Ser Phe Pro Gly Ala Pro
 1          5          10          15
Leu Thr Xaa Ser Thr Leu Ser Trp Ser Ile Leu Ser Pro Arg Glu Pro
 20          25          30
Ser Pro Gly Ala Pro Cys Tyr Pro Gly His Pro His Leu Glu Asn Pro
 35          40          45
His Leu Glu His Leu Leu Thr Trp Arg Thr Val Thr Trp Ser Thr Leu
 50          55          60
Leu Pro Gly Ala Pro Cys Tyr Pro Glu His Pro His Leu Glu His Pro
 65          70          75          80
Leu Thr Trp Ser Thr Pro His Leu Glu His Pro Ser Pro Gly Glu Pro
 85          90          95
Leu Ser Cys Arg Thr Pro Thr Arg Ser Ile Leu His Arg Asp His Pro
100          105          110
Leu Pro Xaa Cys Leu Ser Thr Glu Glu Ser Pro Ile Xaa Gly Trp Gly
115          120          125
Ser Leu Pro Ala Pro Pro Ser Thr Pro Leu Val Leu Asp Val Ala Pro
130          135          140
Pro Gly Pro Gln Pro Ala Ser Ser Cys Pro Gly Arg Asp Ser Cys Tyr
145          150          155          160
Ser Val Pro Gly Thr Val Val Ser Pro
          165          169

```

```

<210> 1373
<211> 133
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(132)
<223> Xaa = any amino acid or nothing

```

```

<400> 1373
Cys Ile Val Ser Ser Cys Gln Gly Thr Arg Lys Pro Cys His Leu Glu
 1          5          10          15
Asp Ala Asn Lys Ile Asn Lys Gln Ser Pro Thr Leu Glu Lys Ile Glu
 20          25          30
Ser Leu Gln Glu Ser Leu Xaa Val Lys Gln Xaa Leu Ile Val Ala Glu
 35          40          45
Lys Tyr Val Gln Ile Leu His Pro Arg Lys Lys Tyr Phe Gln Arg Pro
 50          55          60
Leu Asn Asn Glu Lys Arg Lys Met Lys Lys Arg Lys Glu Glu Lys Lys
 65          70          75          80
Lys Cys Arg Glu Arg Met Gln Arg Arg Ser Lys Trp Arg Arg Glu Glu
 85          90          95
Lys Lys Glu Xaa Arg Arg Glu Glu Glu Glu Arg Lys Lys Glu Lys Glu
100          105          110
Asp Arg Lys Glu Arg Arg Lys Glu Thr Ser Pro Arg Gly Ser Arg Arg
115          120          125
Leu Leu Arg Asp
130          132

```

```

<210> 1374
<211> 61
<212> PRT
<213> Homo sapiens

```

Leu Pro Ala Val Arg Gln Thr Lys Ser Trp Arg Trp Arg Asn Glu Glu
 420 425 430
 Glu Ile Thr Arg Pro Trp Ala Leu Val Arg Ser Arg Gly Gly
 435 440 445 446

<210> 1371
 <211> 263
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(263)
 <223> Xaa = any amino acid or nothing

<400> 1371
 Gly Ser Gln Val Leu Pro Pro Pro Pro Ser Gln Asp Ser Ala Thr Leu
 1 5 10 15
 Pro Gln Asp Ala Xaa Gly Pro Arg Ala Pro Gly Gln Pro Val Cys
 20 25 30
 Glu Xaa Gly Leu Gln Gly Ala Gly Val Arg Arg Leu Arg Gly Glu Val
 35 40 45
 Leu Cys Gln Pro Gln Pro Xaa Gly Ala Leu Xaa Glu Gln Cys Leu Pro
 50 55 60
 His Leu Ser Phe Ser Pro Arg Gln Gly Ala Ala Pro Asp Thr Glu Pro
 65 70 75 80
 Ser Ala Trp Gly Pro Ala Pro Thr Gly Ala Thr Gly Pro Gly Leu Pro
 85 90 95
 Leu Arg His Val Arg Leu Phe Ser Ala Gly Ala Pro Arg Gly Ala Ala
 100 105 110
 Thr Pro Cys Pro Pro Ala Leu Leu His Gly Pro Ala Trp Pro Pro Ala
 115 120 125
 Arg Pro Met Phe Arg Gly His Pro Pro Val Arg Pro Leu Gly Pro Trp
 130 135 140
 Gly Lys Val Ala Ala Gly Pro Arg Ala Leu Cys Leu Ala Gly Val Pro
 145 150 155 160
 Ala Val Gln Gly Glu Cys Ala Thr Lys Pro Ser Gly Xaa Gly Leu Xaa
 165 170 175
 Pro Ala His Leu Arg Gly Pro Pro Gly Pro Glu Val Leu Gln Trp His
 180 185 190
 Trp Gln Leu Ser Ala Gly Arg Asp Pro Val Pro Ala Glu Asp Pro Pro
 195 200 205
 Leu Xaa Glu Gly Pro Leu Gly Pro Gly Gly Pro Ala Ala Ala Gln Ala
 210 215 220
 Glu Pro Gly Ala Asp Pro Glu Pro Glu Asp Lys Asp Gln Ala Ala Glu
 225 230 235 240
 Ser Arg Pro Ala Gly Ala Met Ser Leu Ser Ala Gln Gly Ser Gly Pro
 245 250 255
 Val Gly Gly Gln Gly Leu Arg
 260 263

<210> 1372
 <211> 169
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(169)
 <223> Xaa = any amino acid or nothing

<210> 1370
 <211> 449
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(446)
 <223> Xaa = any amino acid or nothing

<400> 1370
 Phe Phe Phe Cys Gly Lys Glu Val Pro Leu Phe Glu Gln Asn Lys His
 1 5 10 15
 Pro Gly Pro Arg Ala Thr Thr Ser Pro Gly Ala His Ala Arg Ala Leu
 20 25 30
 Leu Ser Ala Gly Glu Phe Thr Ala Gly Val Gly Leu Ser Pro Xaa Ala
 35 40 45
 Ile His Ser Phe Val Trp Leu Cys Thr Phe Ile Gln His Gly Ala Gly
 50 55 60
 Gly Pro Cys His Gln Pro Gly Gly Ser Pro Gly Pro Trp Met His Thr
 65 70 75 80
 Thr Gln Ala Gly His Leu Trp Glu Gly Ala Tyr Pro Gly Gly Ser Ser
 85 90 95
 Thr Trp His Gln Val Pro Gly Gln Leu Gly Gly Ser Trp Gly Pro Arg
 100 105 110
 Glu Arg Ser Leu Leu Gly Ser Phe Ile Lys Cys Ser Pro Cys Pro His
 115 120 125
 Pro Pro Gly Phe Arg Leu Trp Met Ser Pro Asn Gln Lys Pro Pro Thr
 130 135 140
 Glu Asn Pro Gly Val Met Gly Arg Val Trp Arg Leu Met Pro Gly Glu
 145 150 155 160
 Ser Pro Leu Ile Trp Glu Ala Glu Gly Lys Glu Asp His Leu Ser Pro
 165 170 175
 Glu Gly Gln Gly His Ser Glu Pro Val Ala Pro Leu His Ser Ser Leu
 180 185 190
 Gly Asn Thr Val Lys Pro Xaa Pro Lys Asn Gln Lys Pro Lys Gln Asn
 195 200 205
 Arg Ser Arg His Gly Gln Gly Phe Met Ala Gly Gln Gly Gln Ser Arg
 210 215 220
 Pro Ala Ala Arg Xaa Pro Pro Cys Pro Ala Leu Thr Pro Ala Ser His
 225 230 235 240
 Ser Ala Gly Thr Trp Pro Pro Arg Ile Cys Arg Thr Val Pro Gly Gly
 245 250 255
 Pro Cys Pro Ser Pro Ser Gly Phe Arg Ser Cys Arg Arg Xaa Gly Phe
 260 265 270
 Ser Ala Xaa Thr Arg Ser Trp Pro Asp Ala Glu Pro Pro Ser Thr Pro
 275 280 285
 Asp Thr Ala Pro Arg Cys Cys Thr Gln Ser Asp Thr Ser Ser Gln Gly
 290 295 300
 Pro Gln Xaa Ser Xaa Trp Arg Arg Cys Arg Ala Leu Pro Gly Arg Leu
 305 310 315 320
 Cys Ser Ala Pro Ala Ala Gly Leu Arg Arg Ala Arg Pro Arg Leu Ser
 325 330 335
 Glu Ser Arg Arg Gly Asn Ser Pro Pro Ala Ser Pro Ala Ala Ala Ser
 340 345 350
 Ala Arg Cys Pro Ser Trp Gly Pro Ser Cys Pro Ala Arg Pro Pro Ser
 355 360 365
 Arg Pro Ala Ala Gly Thr Glu Pro Ala Ala Pro Ser Arg Cys Thr Ala
 370 375 380
 Trp Leu Arg Gly Glu Arg Glu Pro Gly Pro Arg Pro Pro Gly Arg Arg
 385 390 395 400
 Pro Arg Ser Gly Arg Gly Pro Val Ser Phe Ala Pro Glu Val Leu Ser
 405 410 415

```

Pro Thr Ile Asn Leu Ile Leu Leu Ile Ile Pro Gly Asn Leu Asn
      85                      90                      95
Ile Phe Lys Pro Asn Met Gly Trp Leu Gly Pro Lys Thr Ala Phe Val
      100                    105                    110
Xaa Lys Asp Glu Val Leu Ser Gly Ile Pro Phe Ala Lys Gly Arg Cys
      115                    120                    125
Arg Trp Lys Xaa Asp Tyr Xaa Cys Leu Gln Glu Val Thr Asp Pro Ile
      130                    135                    140
Met Glu Lys Gly Lys Lys Lys Lys Arg Thr Ala Ser Phe Phe Lys Gly
      145                    150                    155                    160
Gln Pro His Gln Ser Thr Asn Ala Leu Leu Arg Arg Cys Val Arg Xaa
      165                    170                    175
Arg Tyr His Leu Ser Thr Val Glu Thr Ala Gly Leu Pro Xaa Lys Asn
      180                    185                    190
Thr Gly His Ile Pro Gly Gln Pro Phe Leu Phe Lys Leu Val Phe Lys
      195                    200                    205
Cys Xaa Asn Val Ile Cys Ile Xaa Xaa Gln Tyr Lys Trp Xaa Gln Asn
      210                    215                    220
Ile Gly Val Lys Asn Lys Ser Phe Cys Pro His Xaa Ser Ser Ser Pro
      225                    230                    235                    240
Ser Leu Xaa Phe Ile Gly His His Ser Arg Asn Phe Cys Ser Phe Lys
      245                    250                    255
Thr Glu Pro His Ser Val Val Gln Ala Gly Gly Gln Trp Arg Asn Leu
      260                    265                    270
Ser Ser Leu Gln Ala Pro Pro Pro Gly Leu Met Pro Leu Ser Arg Ile
      275                    280                    285
Ser Leu Met Ser Ser Trp Asp Tyr Arg Arg Pro Pro Gln
      290                    295                    300 301

```

<210> 1369

<211> 151

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1) ... (148)

<223> Xaa = any amino acid or nothing

<400> 1369

```

Asn Ser Pro Ser Arg Trp Ala Lys Ile Gln Met Phe Glu His Thr Phe
  1          5          10          15
Cys Gly Xaa Gly Cys Gly Glu Arg Asn Val His Ile His Cys Ser Trp
      20          25          30
Ile Cys Arg Leu Arg Pro Leu Leu Trp Arg Ala Val Arg Glu Tyr Leu
      35          40          45
Ser Lys Leu Lys Asn Ala Glu Leu Ser Phe Asp Pro Gly Val Ser Leu
      50          55          60
Leu Arg Ile Tyr Ala Ile Asp Met Pro Thr Ser Ile Xaa Asp Glu Lys
      65          70          75          80
Glu Ala Leu Leu Phe Ala Phe Leu Ala Phe His Glu Xaa His Cys Lys
      85          90          95
Ser Arg Ile Trp Ala Val Ile Gln Cys Ile His Leu Trp Asp Trp Leu
      100         105         110
Arg Lys Leu Xaa Cys Phe His Arg Met Lys Phe Tyr Ala Ala Val Xaa
      115         120         125
Asn Lys Pro Arg His Leu Leu Ser His Ile Trp Lys Asp Val Gln Asn
      130         135         140
Ile Leu Leu Lys
      145         148

```

<213> Homo sapiens

<400> 1366

```

Phe Cys Ile Phe Arg Thr Thr Glu Glu Asp Arg Gly Gly Asp Asp Cys
 1           5           10           15
Val Val Ser Val Trp Thr Lys Gln Arg Asn Asn Ser Cys Val Lys Ser
          20           25           30
Lys Asp Val Phe Ser Lys Pro Val Asn Ile Phe Trp Ala Leu Glu Glu
          35           40           45
Ser Val Leu Gly Val Lys Ala Arg Gln Pro Lys Pro Phe Phe Ala Ala
          50           55           60
Gly Asn Thr Phe Glu Met Thr Cys Lys Val Ser Ser Lys Asn Ile Lys
          65           70           75           80
Ser Pro Arg Tyr Ser Val Leu Ile Met Ala Glu Lys Pro Val Gly Asp
          85           90           95
Leu Ser Ser Pro Asn Glu Thr Lys Tyr Ile Ile Ser Leu Asp Gln Asp
          100          105          110
Ser Val Val Lys Leu Glu Asn Trp Thr Asp Ala Ser Arg Val
          115          120          125 126

```

<210> 1367

<211> 47

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(47)

<223> Xaa = any amino acid or nothing

<400> 1367

```

Arg Lys Arg Thr Asn Asn Pro Ile Lys Leu Asp Lys Lys Phe Glu His
 1           5           10           15
Phe Lys Asn Glu Asp Ile Xaa Ile Thr Ser Lys His Thr Lys Met Trp
          20           25           30
Val Ser Ser Leu Ala Met Lys Glu Met Leu Thr Lys Thr Thr Met
          35           40           45           47

```

<210> 1368

<211> 304

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(301)

<223> Xaa = any amino acid or nothing

<400> 1368

```

Leu Val Val Gly Ile Thr Gly Thr Arg His His Ala Arg Val Ile Phe
 1           5           10           15
Ile Phe Leu Val Glu Thr Gly Phe Pro His Val Gly Gln Ala Gly Leu
          20           25           30
Glu Leu Leu Thr Ser Gly Asp Pro Pro Ala Leu Ala Ser Gln Ser Ala
          35           40           45
Gly Ile Thr Gly Met Ser His Cys Ala Arg Pro Lys Gly His Phe Gly
          50           55           60
Ile His Leu Lys Xaa Met Phe Tyr Thr Met Ser Gln Lys Met Pro Xaa
          65           70           75           80

```

<210> 1364
 <211> 124
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(124)
 <223> Xaa = any amino acid or nothing

<400> 1364
 Tyr Leu Leu Thr Xaa Ile Gly Asn Leu Met Met Leu Leu Val Ile Asn
 1 5 10 15
 Ala Asp Ser Cys Leu Arg Thr Xaa Met Xaa Phe Phe Leu Gly His Phe
 20 25 30
 Phe Phe Leu Asp Ile Cys Tyr Ser Ser Val Thr Ala Gln Asp Ala Ala
 35 40 45
 Glu Phe Pro Val Ser Xaa Lys Pro Ile Leu Val Trp Gly Tyr Ile Thr
 50 55 60
 Xaa Ser Phe Phe Phe Ile Phe Ser Trp Gly Thr Asn Gly Cys Leu Leu
 65 70 75 80
 Ser Ala Ile Thr Tyr Ala Cys Tyr Ala Ala Ile Cys His Pro Leu Leu
 85 90 95
 Ser Thr Met Val Met Asn Arg Pro Leu Cys Thr Ala Thr Val Asn Ala
 100 105 110
 Thr Asn Lys Met Gly Phe Leu Asn Ser Gln Val Asn
 115 120 124

<210> 1365
 <211> 120
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(119)
 <223> Xaa = any amino acid or nothing

<400> 1365
 Thr His Ala Lys Phe Leu Asn Lys Lys Phe Asn Ile Pro Lys Leu Val
 1 5 10 15
 Ile Leu Pro Lys Leu Val Tyr Ile Val Lys Ala Ile Pro Thr Lys Met
 20 25 30
 Ala Ile Glu Phe Leu Leu Glu Cys Asp Gln Asn Ile Thr Lys Leu Ile
 35 40 45
 Cys Glu Asn Thr Xaa Lys Asn Ile Ala Lys Asn Ile Xaa Lys Arg Arg
 50 55 60
 Val Thr Phe Thr Pro Ile Glu Thr Xaa His Pro Val Lys Gln Met Ile
 65 70 75 80
 Lys Trp Gln Xaa Leu Thr Ala Trp Leu Arg Asn Arg Gly Tyr Lys Lys
 85 90 95
 Ile Lys Gln Thr Pro Asn Ser Glu Thr Ala Pro Ser Val Cys Arg Asn
 100 105 110
 Leu Val Phe Asp Lys Cys Gly
 115 119

<210> 1366
 <211> 126
 <212> PRT

<211> 136
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(135)
 <223> Xaa = any amino acid or nothing

<400> 1362
 Leu Ile Pro Ser Glu Pro Ala Leu Asp Ser Leu Val Asp Pro Arg Val
 1 5 10 15
 Arg Ser Arg Lys Gln Pro Phe Val Ile Tyr Pro Val Tyr Asp Thr Ala
 20 25 30
 Ile Asp Thr Lys Ile His Phe Ser Leu Leu Asp Gly Asn Val Gly Glu
 35 40 45
 Pro Asp Met Ser Ala Gly Phe Cys Pro Asn His Lys Ala Ala Met Val
 50 55 60
 Leu Phe Leu Asp Arg Val Tyr Gly Ile Glu Val Gln Asp Phe Leu Leu
 65 70 75 80
 His Leu Leu Glu Gly Gly Phe Leu Pro Asp Leu Arg Ala Ala Ala Ser
 85 90 95
 Leu Asp Thr Ala Glu Ile Gly Ala Met Asp Phe Leu Leu Ser Xaa Leu
 100 105 110
 Phe Thr Leu Cys Leu Met Met Phe Phe Ile Tyr Pro Phe Ile Asn
 115 120 125
 Leu Leu Thr Met Asn Val Tyr
 130 135

<210> 1363
 <211> 145
 <212> PRT
 <213> Homo sapiens

 <221> misc_feature
 <222> (1)...(144)
 <223> Xaa = any amino acid or nothing

<400> 1363
 Trp Thr Phe His Arg His Leu Ser Pro Ala Pro Leu Ile Val Cys Asp
 1 5 10 15
 Gln Gly Thr Cys Val Val Ser Tyr Tyr Pro Gln Asn Ile Val Gln Met
 20 25 30
 Pro Asp Thr Gln Met Glu Gln Gly Leu Asn His Leu Phe Leu Asp Gly
 35 40 45
 Asn Ala Xaa Pro His Ser Val Glu Cys Tyr Cys Pro Ser Thr Phe Glu
 50 55 60
 Ile Ala Ile Lys Ile Thr Ser Phe Val Leu Tyr Phe His Arg Tyr Arg
 65 70 75 80
 Ala Pro Glu Val Leu Leu Arg Ser Ser Val Tyr Ser Ser Pro Ile Asp
 85 90 95
 Val Trp Ala Val Gly Ser Ile Met Ala Glu Leu Tyr Met Leu Arg Pro
 100 105 110
 Leu Phe Pro Gly Thr Ser Glu Val Asp Glu Ile Phe Lys Ile Cys Gln
 115 120 125
 Val Leu Gly Thr Pro Lys Lys Val Ser Thr Leu Val Pro Lys Leu Leu
 130 135 140 144


```

Thr Val Ala Ile Asp Phe Thr Ala Ser Asn Gly Asp Pro Arg Asn Ser
      260                265                270
Cys Ser Leu His Tyr Ile His Pro Tyr Gln Pro Asn Glu Tyr Leu Lys
      275                280                285
Ala Leu Val Ala Val Gly Glu Ile Cys Gln Asp Tyr Asp Ser Asp Lys
      290                295                300
Met Phe Pro Ala Phe Gly Phe Gly Ala Arg Ile Pro Pro Glu Tyr Thr
      305                310                315
Asp Ser His Asp Phe Ala Ile Asn Phe Asn Glu Asp Asn Pro Glu Cys
      325                330                335
Ala Gly Ile Gln Gly Val Val Glu Ala Tyr Gln Ser Cys Phe Pro Lys
      340                345                350
Ala Pro Thr Phe Thr Gly Pro Thr Asn Ile Cys Pro His Ser Ser Arg
      355                360                365
Lys Val Ala Lys Phe Arg Arg Ser Glu Gly Asn Xaa His Gln Gly Arg
      370                375                380
Ala Phe Ala Ile Ile Phe Ile Leu Val Asp Pro Gly Gln Val Gly Val
      385                390                395
Tyr Ser Gln Asp Met Gly Pro Asp Asn Pro Gly Gly His Phe Val
      405                410                415

```

<210> 1361

<211> 204

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(202)

<223> Xaa = any amino acid or nothing

<400> 1361

```

Ala Cys Ala Arg Lys Gln Leu Leu Gly Arg Thr Val Phe Ile Trp Phe
  1      5      10      15
Val Gly Gln Leu Gly Gly Glu Leu Lys Gly Tyr Ser Lys Thr Asn
      20      25      30
Thr Thr Ser Ser Arg Pro Ala Ser Ser Arg Gly Thr Leu Ser Ser Ser
      35      40      45
Ser Ser Ser Ser Ser Leu Thr Lys Asp Ala Leu Pro Ser Ser Leu
      50      55      60
Lys Ser Asp Ser Thr Thr Ile Thr Ser Gly Leu Val Phe Pro Phe Arg
      65      70      75      80
Ser Leu Cys Val Asn Pro Ala Lys Ser Ser Val Ser Glu Ser Val Ser
      85      90      95
Ser Ile Lys Ile Leu Leu Ser Ser Ser Val Lys Tyr Leu Glu Xaa Lys
      100      105      110
Arg Thr Ser Cys Cys Phe Pro Asp Ser Ser Glu Ser Lys Leu Ser Gln
      115      120      125
Leu Ser Ser Asp Glu Arg Val Ser Met Gly Thr Ser Ser Arg Lys Pro
      130      135      140
Thr Asn Ser Ser Ser Ser Leu Gly Ala Leu Lys Met Ser Ala Thr Ser
      145      150      155      160
Xaa Gly Ser Gly Ser Glu Ser Pro Thr Pro Phe Phe Leu Thr Gly Leu
      165      170      175
Gln Ser Pro Pro Ser Thr Arg Pro Arg Glu Pro Gly Leu Thr Thr Ala
      180      185      190
Arg Asn Ser Thr Thr Leu Thr Arg Asp Cys
      195      200      202

```

<210> 1362

Thr Leu Thr
115

<210> 1359
<211> 46
<212> PRT
<213> Homo sapiens

<400> 1359
Gln Ala Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly Asp Thr Gly
1 5 10 15
Gly Pro Ala Val Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys Ser
20 25 30
Ser Glu Phe Asn Glu Gly Pro Glu Arg Glu Arg Met Asp Val
35 40 45 46

<210> 1360
<211> 416
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(415)
<223> Xaa = any amino acid or nothing

<400> 1360
Lys Gly Cys Arg Thr Gln Glu Lys Val Asp Arg Thr Glu Val Ile Arg
1 5 10 15
Thr Cys Ile Asn Pro Val Tyr Ser Lys Leu Phe Thr Val Asp Phe Tyr
20 25 30
Phe Glu Glu Val Gln Arg Leu Arg Phe Glu Val His Asp Ile Ser Ser
35 40 45
Asn His Asn Gly Leu Lys Glu Ala Asp Phe Leu Gly Gly Met Glu Cys
50 55 60
Thr Leu Gly Gln Ile Val Ser Gln Arg Lys Leu Ser Lys Ser Leu Leu
65 70 75 80
Lys His Gly Asn Thr Ala Gly Lys Ser Ser Ile Thr Val Ile Ala Glu
85 90 95
Glu Leu Ser Gly Asn Asp Asp Tyr Val Glu Leu Ala Phe Asn Ala Arg
100 105 110
Lys Leu Asp Asp Lys Asp Phe Phe Ser Lys Ser Asp Pro Phe Leu Glu
115 120 125
Ile Phe Arg Met Asn Asp Asp Ala Thr Gln Gln Leu Val His Arg Thr
130 135 140
Glu Val Val Met Asn Asn Leu Ser Pro Ala Trp Lys Ser Phe Lys Val
145 150 155 160
Ser Val Asn Ser Leu Cys Ser Gly Asp Pro Asp Arg Arg Leu Lys Cys
165 170 175
Ile Val Trp Asp Trp Asp Ser Asn Gly Lys His Asp Phe Ile Gly Glu
180 185 190
Phe Thr Ser Thr Phe Lys Glu Met Arg Gly Ala Met Glu Gly Lys Gln
195 200 205
Val Gln Trp Glu Cys Ile Asn Pro Lys Tyr Lys Ala Lys Lys Lys Asn
210 215 220
Tyr Lys Asn Ser Gly Thr Val Ile Leu Asn Leu Cys Lys Ile His Lys
225 230 235 240
Met His Ser Phe Leu Asp Tyr Ile Met Gly Gly Cys Gln Ile Gln Phe
245 250 255

```

Ile Val Ala Gly Ala Val Ser Asn Gln Leu Leu Val Trp Tyr Pro Ala
      20      25      30
Thr Ala Leu Ala Asp Asn Lys Pro Val Ala Pro Asp Arg Arg Ile Ser
      35      40      45
Gly His Val Gly Ile Ile Phe Ser Met Ser Tyr Leu Glu Ser Lys Gly
      50      55      60
Leu Leu Ala Thr Ala Ser Glu Asp Arg Ser Val Arg Ile Trp Lys Gly
      65      70      75      80
Gly Asp Leu Arg Val Pro Gly Gly Arg Val Gln Asn Ile Gly His Cys
      85      90      95
Phe Gly His Ser Ala Arg Val Trp Gln Val Lys Leu Leu Glu Asn Tyr
      100      105      110
Leu Ile Ser Ala Gly Glu Asp Cys Val Cys Leu Val Trp Ser His Glu
      115      120      125
Gly Glu Ile Leu Gln Ala Phe Arg Gly His Gln Gly Arg Gly Ile Arg
      130      135      140
Ala Ile Ala Ala His Glu Arg Gln Ala Trp Val Ile Thr Gly Gly Asp
      145      150      155      160
Asp Ser Gly Ile Arg Leu Trp His Leu Val Gly Arg Gly Tyr Arg Gly
      165      170      175
Leu Gly Asp Leu Gly Ser Leu Leu Gln Val Pro Xaa Xaa Ala Arg Tyr
      180      185      190
Thr Gln Gly Cys Asp Ser Gly Trp Leu Leu Ala Thr Ala Gly Ser Asp
      195      200      205
Xaa Tyr Arg Gly Pro Val Ser Leu Xaa Arg Arg Gly Gln Val Leu Gly
      210      215      220
Ala Ala Ala Arg Gly Xaa Thr Phe Pro Val Leu Leu Pro Ala Gly Gly
      225      230      235      240
Ser Ser Trp Ser Arg Gly Leu Arg Ile Val Cys Tyr Gly Gln Trp Gly
      245      250      255
Arg Ser Cys Gln Gly Cys Pro His Gln His Ser Asn Cys Cys Gly
      260      265      270
Pro Asp Pro Val Ser Trp Glu Gly Ala Gln Leu Glu Leu Gly Pro Ala
      275      280      285
Trp Leu
      290

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<210> 1358

<211> 117

<212> PRT

<213> Homo sapiens

<221> misc_feature

<222> (1)...(115)

<223> Xaa = any amino acid or nothing

<400> 1358

```

Phe Ser Ser Leu Leu Ser Gly Arg Ile Ser Thr Leu Arg Asp Glu Thr
  1      5      10      15
Gly Ala Ile Leu Ile Asp Gly Asp Pro Ala Ala Cys Ala Pro Ile Ile
      20      25      30
Lys Phe Leu Leu Thr Glu Glu Leu His Leu Arg Gly Val Ser Ile Tyr
      35      40      45
Val Leu Arg His Glu Ala Gln Ile Tyr Gly Ile Thr Pro Leu Val Cys
      50      55      60
Ala Leu Leu Ile Cys Arg Arg Leu Xaa Ser Asp Ser Cys Met Arg Ala
      65      70      75      80
Ala Leu Asn Asp Arg Gly Leu Tyr Gln Val Leu Ile Leu Asp Gly Leu
      85      90      95
Val Gln Cys Leu Gly Phe Val Asp Ser Asp Ser Arg Lys Met Val Ser
      100      105      110

```

```

Gly Glu Glu Val Asn Ala Gly Arg Ile Gly Leu Thr Ile Val Ile Ala
      85          90          95
Gly Met Leu Gly Ala Val Ile Ser Gly Ile Trp Leu Asp Arg Ser Lys
      100        105        110
Thr Tyr Lys Glu Thr Thr Leu Val Val Tyr Ile Met Asp Thr Gly Gly
      115        120        125
Ala Trp Trp Cys Tyr Thr Phe Tyr Leu Gly Thr Gly Asp Thr Cys Gly
      130        135        140
Xaa Cys Phe Ile Thr Ala Gly Thr Met Gly Phe Phe Met Thr Gly Tyr
145          150          155          160
Leu Pro Leu Gly Phe Glu Phe Ala Val Glu Leu Ser Tyr Pro Glu Ser
      165        170        175
Glu Gly Ile Ser Ser Gly Leu Leu Asn Ile Ser Ala Gln Val Phe Gly
      180        185        190
Ile Ile Phe Thr Ile Ser Gln Gly Gln Ile Ile Asp Asn Tyr Gly Thr
      195        200        205
Lys Pro Gly Asn Ile Phe Leu Cys Val Phe Leu Thr Leu Gly Ala Ala
      210        215        220
Leu Thr Ala Phe Ile Lys Ala Asp Leu Arg Arg Gln Lys Ala Asn Lys
225          230          235          240
Glu Thr Leu Glu Asn
      245

```

```

<210> 1356
<211> 94
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(93)
<223> Xaa = any amino acid or nothing

```

```

<400> 1356
Glu Trp Phe Ser Tyr Met Leu Gly Ser Asn Met Ser Val Tyr His Ser
 1          5          10          15
Pro Xaa Ser Leu Glu Pro Leu Cys Lys Val Leu Ser Glu Ser Xaa Ala
      20          25          30
Tyr Leu Arg Val Pro Phe Ile Arg Ile Leu Leu Asn Ala Arg Xaa Ile
      35          40          45
Arg Lys Ala Tyr Lys Arg Met Ser Leu Glu Ile Lys Leu Leu Ile Arg
      50          55          60
Glu Xaa Cys Leu Phe Gln Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr
      65          70          75          80
Ser Ala Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu
      85          90          93

```

```

<210> 1357
<211> 291
<212> PRT
<213> Homo sapiens

<221> misc_feature
<222> (1)...(290)
<223> Xaa = any amino acid or nothing

```

```

<400> 1357
Thr Leu Ser Ser Ala Cys Leu Ile Gly Asp Ala Trp Lys Glu Leu Thr
 1          5          10          15

```

```

Glu Gln Gln Leu Gly Ala Thr Gly Ala Tyr Arg Ala Arg Ala Leu Glu
      20          25          30
Leu Glu Ala Glu Val Ala Glu Met Arg Gln Met Leu Gln Leu Glu His
      35          40          45
Pro Phe Val Asn Gly Ala Asp Lys Leu Arg Pro Asp Ser Met Tyr Val
      50          55          60
His Leu Asn Glu Leu Xaa Gln Ser Leu Val Glu Asn Met Leu Leu Thr
      65          70          75          80
Val Val Asp Thr His Arg Thr Pro Ile Xaa Arg Ser Cys Asn Tyr Thr
      85          90          95
Leu Ala Leu Ile Leu Phe Leu
      100          103

```

```

<210> 1354
<211> 98
<212> PRT
<213> Homo sapiens

```

```

<221> misc_feature
<222> (1)...(97)
<223> Xaa = any amino acid or nothing

```

```

<400> 1354
Thr Ala Ser Ala Leu Phe Ser Cys Pro Asp Gly Gly Ser Leu Ala Gly
  1          5          10          15
Phe Ala Gly Arg Arg Ala Ser Phe His Leu Glu Cys Leu Lys Arg Gln
      20          25          30
Lys Asp Arg Gly Gly Asp Ile Ser Gln Lys Thr Val Leu Pro Leu His
      35          40          45
Leu Val His His Gln Val Ala His Thr Phe Gly Gln Ala Thr Val Thr
      50          55          60
Cys Gln Gln Ala Arg Gln Ser Pro Gly Xaa Arg Thr Asn Pro Glu Ala
      65          70          75          80
Leu Gln Trp Val Leu Pro Val Ser Asp Gly Trp His Val Leu Pro Leu
      85          90          95
Pro
97

```

```

<210> 1355
<211> 247
<212> PRT
<213> Homo sapiens

```

```

<221> misc_feature
<222> (1)...(245)
<223> Xaa = any amino acid or nothing

```

```

<400> 1355
Glu Asn Cys Arg Val Ala Ser Asn Leu Pro Gly Val Phe Phe Ser Glu
  1          5          10          15
Asp Thr Ala Gln Ser Gly Ser Tyr Met Arg Ile Ser Ala His Pro Pro
      20          25          30
Asn Ala Gly Gly Glu Val Ser Asn Gly Pro Lys Arg Lys Leu Thr Leu
      35          40          45
Met Leu Asn Phe Ser Leu Pro Ser Ser Gly Leu Asn Ala Gly Ala Phe
      50          55          60
Tyr Ala Leu Ser Thr Leu Leu Asn Arg Met Val Ile Trp His Tyr Pro
      65          70          75          80

```

<221> misc_feature
 <222> (1)...(112)
 <223> Xaa = any amino acid or nothing

<400> 1351
 Thr Pro Ser Leu Ile His Gln Ala Pro Thr Pro Cys Pro Ala Gly Leu
 1 5 10 15
 Trp Gly Pro Pro Asn Gly His Tyr His Gly Ser Xaa Pro Gly Cys His
 20 25 30
 Trp Pro Gln Ala Pro His Arg Ala Xaa Xaa Xaa Gly Leu Leu Pro Pro
 35 40 45
 Arg Trp Leu Gly His Gly Leu Pro Gly Gly Pro Ala Ala Pro Trp Ala
 50 55 60
 Ala Ser Gln Trp Val Asp Gly Val Ala Gly Arg Leu Pro Gly Pro Ala
 65 70 75 80
 Trp Ser Trp His Ala Ser Gly Ala Ala Pro Ala Gln Pro Gly Pro Leu
 85 90 95
 Xaa Leu Leu Val Pro Gly Ser Ser Gly Leu Pro Asp Pro Arg Asp Pro
 100 105 110 112

<210> 1352
 <211> 91
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(89)
 <223> Xaa = any amino acid or nothing

<400> 1352
 Ile Arg Asn Ser Ser Ile Arg Pro Met Lys Glu Arg Glu Thr Lys Leu
 1 5 10 15
 Ser Ala Lys His Met Ile Thr Cys Ser Ala Ser Tyr Asp Ile Arg Gly
 20 25 30
 Leu Gln Ile Glu Thr Thr Tyr His His Thr Pro Ile Arg Met Ala Lys
 35 40 45
 Ile Gln Lys Thr Gly His His Gln Cys Xaa Xaa Glu Cys Gly Ala Thr
 50 55 60
 Gly Thr Leu Ile His Gly Trp Trp Gly Cys Lys Val Val Glu Pro Leu
 65 70 75 80
 Gly Lys Thr Val Trp Gln Ile Pro Lys
 85 89

<210> 1353
 <211> 104
 <212> PRT
 <213> Homo sapiens

<221> misc_feature
 <222> (1)...(103)
 <223> Xaa = any amino acid or nothing

<400> 1353
 His Ala Ser Ala His Ala Ser Val Val Leu Lys Asp Asn Ser Glu Leu
 1 5 10 15

gcacagaagc	attgaagcca	agctgaggca	gttttcgagc	gctttaattg	attgtctgat	360
aaacccactt	caagaacaga	tggaagaatg	gaagaaagtg	gcccaaccagc	tggataaaga	420
ccacgcacaaa	gaatataaga	aagcccgcga	agagataaaa	aagaagtcct	cggatacgct	480
gaaactgcag	aagaaagcaa	aaaaagggag	aggtgatatc	cagcctcagt	tggacagtgc	540
tctccaagat	gtcaatgata	agtatctctt	attggaagaa	acagaaaagc	aggctgtccg	600
gaaggctttg	attgaagaac	gtggcgcgatt	ctgtaccttc	atctctatgc	tgcggccagt	660
gattgaagaa	gaaatctcaa	tgctagggga	aataacccac	cttcagacca	tctcgggaaga	720
tctaaaaagc	ctgacccatg	acccctcaca	actgccctcc	tcaagtgaac	aggtgattct	780
ggacttgaaa	ggttctgatt	acagctggtc	gtatcagaag	ccaccctctt	ccccagcac	840
caccatgtcc	agaaagtcca	gtgtctgcag	cagcctgaac	agtgtcaaca	gcagtgtacc	900
ccggtccagc	ggotcccact	cgcattcccc	cagctcacat	taccgctacc	gcagctccaa	960
cctggcccgag	caggctcctg	tgaggtgtc	cagcgtgtcc	tcccatgact	caggattcat	1020
atcccaggat	gccttccagt	ccaagtcacc	atcccccatg	ccgccagagg	cccccaacca	1080
gcgccgcaaa	gagaagcgag	aaccggaccc	caacggggga	ggaccacta	ccgccagcgg	1140
cccacctgca	gcagctgagg	aggctcagag	accacggagc	atga		1184

<210> 1350
 <211> 1828
 <212> DNA
 <213> Homo sapiens

<400> 1350						
tttttttttt	ttcgttccat	gttttttatt	tgtgcactgg	gaaagaagtc	ttccctccca	60
tcacatgagc	cacgtggtga	gtcctctgga	ggcttgaaga	ttatccccct	ccctgggagt	120
cttggggccat	ggagggtggg	ggcgggtgaac	ggaaggggat	tttgtctctg	ccctcagcct	180
ggtgccctct	ccttccagga	atgtcccagc	ggaattgtca	atgaggagaa	cttcaagcag	240
atttactccc	agttctttcc	tcaaggaggt	gaggggacaa	gggccaaggg	gaagcagttg	300
tccttctcta	ggctgagggg	gggagggatt	ccggaggagt	tgggaatgcc	aaggtgatgg	360
ggggtatggg	gagctcctta	gagggaggaa	gtcctctcct	gtgtggaagc	caacttctcc	420
acactcacc	tgccagactcc	agcaccatg	ccacttttct	cttcaatgcc	tttgacacca	480
accatgatgg	ctcggctcagt	tttgaggtga	gctgggagag	gtggggccagg	gaagcctgtt	540
tccctggagt	cagggccagg	atctccaggc	caaaccacga	gaaggagtgg	ggtgaagagt	600
acccgaggac	acagctccct	cctgcctcct	tcccaggact	ttgtggctgg	tttgtccgtg	660
attcttcggg	gaactgtaga	tgacaggcct	aattgggcct	tcaacctgta	tgaccttaac	720
aaggacggct	gcacaccaa	ggaggaaatg	cttgacatca	tgaagtccat	ctatgacatg	780
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<211> 3044

<212> DNA

<213> Homo sapiens

<400> 1347

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